

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 1, 2004, 15:01:21; Search time 343 Seconds
(without alignments)
5982.887 Million cell updates/sec

Title: US-09-965-830-1_COPY_6_3257

Perfect score: 6089

Sequence: 1 atgcggccatgcgggacct.....aagaagccacaggggtctga 3252

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5
Xgapop 10.0, Xgapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 2034082

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p_model -DEV=xlp
-Q=/cgm2_1/USFO_spool_p/US995830/runat_01092004_160110_4801/app_query.fasta_1.3399
-DB=SPITREMBL_25 -QFMT=fastan -SUFFIX=rspt -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US995830 @CGN 1.1 536 runat_01092004_160110_4801 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: sp_archea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2489	40.9	1097	11 Q8BX82	Q8bx82 mus musculus

2	1909	31.4	351	4 Q8N500	Q8n500 homo sapien
3	1901	31.2	1284	5 Q9V899	Q9v899 drosophila
4	1901	31.2	1284	5 Q23974	Q23974 drosophila
5	1537.5	25.3	1117	11 Q80XE8	Q80xe8 mus musculus
6	1511.5	24.8	1058	4 Q81Z12	Q81zi2 homo sapien
7	1416	23.3	1011	5 Q7YW98	Q7yw98 manduca sex
8	1405.5	23.1	1186	13 Q8JH78	Q8jhr8 brachydanio
9	1387	22.8	1174	5 Q3VX26	Q3vxz6 drosophila
10	1342.5	22.0	988	11 Q8C035	Q8cc35 mus musculus
11	1261.5	20.7	956	5 Q9XYX7	Q9xyx7 caenorhabdi
12	1259.5	20.7	956	5 Q44164	Q44164 caenorhabdi
13	1185.5	19.5	772	4 Q8G0U7	Q8g0u7 homo sapien
14	1084	17.8	791	5 Q18325	Q18325 caenorhabdi
15	1075.5	17.7	732	4 Q8IV15	Q8iv15 homo sapien
16	1046	17.2	855	5 Q02497	Q02497 drosophila
17	720.5	11.8	422	4 Q86X11	Q86x11 homo sapien
18	537.5	8.8	515	11 Q8C782	Q8c782 mus musculus
19	534	8.8	522	11 Q8CC38	Q8cc38 mus musculus
20	507	8.3	395	11 Q8BYS2	Q8bya2 mus musculus
21	474.5	7.8	774	4 Q86WJ5	Q86wj5 homo sapien
22	474	7.8	890	4 Q86WJ6	Q86wj6 homo sapien
23	449	7.4	678	5 Q96777	Q96777 heliothis v
24	443	7.3	5146	6 Q8SPM4	Q8spm4 bos taurus
25	439	7.2	1463	5 Q9USE2	Q9use2 drosophila
26	434	7.1	767	5 Q76977	Q76977 strongyloce
27	431	7.1	945	5 Q9YLJ9	Q9ylj9 drosophila
28	431	7.1	1327	5 Q9V702	Q9v702 drosophila
29	430	7.1	1324	5 Q8IR35	Q8ir35 drosophila
30	429.5	7.1	1696	5 Q9VXV8	Q9vxv8 drosophila
31	428.5	7.0	632	11 Q9ER32	Q9er32 rattus norv
32	420	6.9	631	11 Q8CFV6	Q8cfv6 mus musculus
33	417.5	6.9	670	11 Q9ER33	Q9er33 rattus norv
34	415.5	6.8	611	11 Q9QWN7	Q9qwn7 rattus norv
35	414	6.8	907	10 Q8H569	Q8h569 oryza sativ
36	413.5	6.8	900	5 Q97119	Q97119 limulus pol
37	413	6.8	686	6 Q9N0H4	Q9n0h4 sus scrofa
38	411	6.7	849	10 Q9SM12	Q9sm12 zea mays (m
39	401	6.6	664	11 Q80XH6	Q80xh6 mus musculus
40	401	6.6	1414	5 Q26634	Q26634 strongyloce
41	397	6.5	1218	5 Q9W201	Q9w201 drosophila
42	396	6.5	1461	4 Q76045	Q76045 homo sapien
43	395.5	6.5	1953	5 Q9BIT7	Q9bit7 nephila ina
44	394.5	6.5	1464	4 Q8N473	Q8n473 homo sapien
45	391	6.4	1453	11 Q810J9	Q810j9 mus musculus

ALIGNMENTS

RESULT 1

Q8BX82 PRELIMINARY; PRT; 1097 AA.

ID Q8BX82

AC Q8BX82; (TREMBlrel. 23, Created)

DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE ELK channel 3 (Fragment).

GN C13090D05RIK.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Head;

RX MEDLINE=22354683; PubMed=12466851;

RA The FANTOM Consortium,

RA the RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs."

RL Nature 420:563-573(2002).

DR EMBL; AK048629; BAC33401.1; -.

DR PIR; PT0566; PT0566.

DR PIR; PT0633; PT0633.

DR MGD; MGI:2445160; C130090D05R1K.
 DR GO; GO:0016020; C-membrane; IEA.
 DR GO; GO:0000155; P:two-component sensor molecule activity; IEA.
 DR GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR GO; GO:0006813; P:potassium ion transport; IEA.
 DR GO; GO:0000160; P:two-component signal transduction system (p...); IEA.
 DR InterPro; IPR000595; CNMP binding.
 DR InterPro; IPR003967; Erg channel.
 DR InterPro; IPR005821; Ion trans.
 DR InterPro; IPR001622; K-channel_pore.
 DR InterPro; IPR005820; M-channel_nlg.
 DR InterPro; IPR001610; PAC.
 DR InterPro; IPR000700; PAS-associ C.
 DR InterPro; IPR000014; PAS domain.
 DR Pfam; PF00027; CNMP binding; 1.
 DR Pfam; PF00520; ion_trans; 1.
 DR Pfam; PF00785; PAC; 1.
 DR PRINTS; PR01470; ERGCHANNEL.
 DR SMART; SM00100; CNMP; 1.
 DR SMART; SM00086; PAC; 1.
 DR TIGRfam; TIGR00229; sensory box; 1.
 DR PROSITE; PS0042; CNMP_BINDING_3; 1.
 DR PROSITE; PS0113; PAC; 1.
 FT NON TER 1
 SQ SEQUENCE 1097 AA; 122704 MW; D7E37630C1E93B5F CRC64;

Alignment Scores:

Pred. No.: 1,14e-132 Length: 1097
 Score: 2489.00 Matches: 550
 Percent Similarity: 61.63% Conservative: 147
 Best Local Similarity: 48.63% Mismatches: 286
 Query Match: 40.88% Indels: 148
 DB: 11 Gaps: 26

US-09-965-830-1_COPY_6_3257 (1-3252) x Q8BX82 (1-1097)

QY 16 GGCTCTGCGGCTCAGAACACCTTCTCGACACCATCTCGGCTTCCGAGCGGACG 75
 DB 1 GlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThrArgPheAspGlyThr 20
 QY 76 CACAGTAATCTGCTGGGCAACGCCAGGTGGGGGCTCTTCCCGTGGTCTACTGC 135
 DB 21 HisSerAsnPheIleLeuAlaAsnAlaGlnValAlaLysGlyPheProIleValTyrCys 40
 QY 136 TCTGATGGCTCTGTGACCTCAGGGCTTCTCCGGGCTGAGTTCATGACGGGGTGT 395
 DB 41 SerAspGlyPheCysGlnLeuAlaGlyPheAlaArgThrGluValMetGlnLysSerCys 60
 QY 196 GCCTGCTCTCTCTTATGGGCGCACACCCAGTGAGCTCTCGGCCAACAGATCCCGCAAG 255
 DB 61 SerCysLysPheLeuPheGlyValGluThrAsnGluGlnLeuMetLeuGlnLeuLys 80
 QY 256 GCCCTGACAGACACAGAGATTCAGGCTGAGTGTATCTGTACCGAGAGAGCGGCTC 315
 DB 81 SerLeuGluLysValGluPheLysGlyGluIleMetPheTyrLysLysAsnGlyAla 100
 QY 316 CCGTCTCTGCTCTCTGATGTATACCCATAAGATGAGAAAGGGAGGTGGCTCTC 375
 DB 101 ProPheTrpCysLeuLeuAspIleValProIleLysAsnGluLysGlyAspValValLeu 120
 QY 376 TTCCTAGTCTCTCACAGGACATCAGCGAAACCAAGAACCGAGGGGCGCCGACAGATGG 435
 DB 121 PheLeuAlaSerPheLysAspIleThrAspThrLysValLysIleThrSerGluAspLys 140
 QY 436 AAGAGACAGGTGGTGGCGCGCGGATATGGCGGCGCAGATCC----AAGGCTTCAAT 492
 DB 141 LysGluAsp-----ArgThrLysGlyArgSerArgAlaGlySerHisPheAsp 156
 QY 493 GCCAACCGGGCGGAGCGGGCGTCTCTACCACTGTCCGGGCGACCTGCAGAACAG 552
 DB 157 SerAlaArgArgSerArgAlaValLeuTyrHisIleSerGlyHisLeuGlnArgArg 176

QY 553 CCCAAGGGCAAGCACAGCTCAATAGGGGGTGTGGGGAGAAACCAACTTGCCTGAG 612
 DB 177 GluLysAsnLysLeuLysIleAsnAsnValPheValAspLysProAlaPheProGlu 196
 QY 613 TACAAGTAGCCGCCATCCGGAAGTCGCCCTTCATCTCTGCTGTGACGTGGGGCACTGAGA 672
 DB 197 TyrLysAlaSerAspAlaLysLysSerLysPheIleLeuLeuHisPheSerThrPheLys 216
 QY 673 GCACCTGGGATGGCTTCACTCTGTCTGCGCACACTCTATGTGGCTCTCACTGTGCCCTAC 732
 DB 217 AlaGlyTrpAspTrpLeuIleLeuLeuAlaThrPheTyrValAlaValThrValProTyr 236
 QY 733 AGCTGTGTGTGAGCACACGAGCGGAGCCAGTGGCGCGCGCGCGCGCGCGCGCTGT 792
 DB 237 AsnValCysPheIleGlyAsnGluAspLeuSerThrArgSer---ThrThrValSer 255
 QY 793 GACCTGGCGGTGGGTCTCTTCACTTGTGATGTCTGAATTCGTGAATTCGTACACATTC 852
 DB 256 AspIleAlaValGluIleLeuPheIleIleAspIleIleLeuAsnPheArgThrThrTyr 275
 QY 853 GTGTCCAGTCCGGCCAGGTGTGTGGCCCAAGTCCATTTGCTCCACTACGTCAACC 912
 DB 276 ValSerLysSerGlyGlnValIlePheGluAlaArgSerIleCysIleHisTyrValThr 295
 QY 913 ACCTGTTCTGCTGATGTCATCGAGCGGCTGCTTGAACCTGTACATGCTACATGCTCAAG 972
 DB 296 ThrTrpPheIleIleAspLeuIleAlaLeuProPheAspLeuLeuTyrAlaPheAsn 315
 QY 973 GTCAACGTGTACTTCCGGGCCCATCTGTCAAGACGCTGCGCTGTGGCGCTGTGCGC 1032
 DB 316 ValThrValValSerLeuValHisLeuLeuLysThrValArgLeuLeuArgLeuLeuArg 335
 QY 1033 CTGCTTCCCGCGTGGACCGGTACTCGCAGTACAGCGCCGTGTGTGTGACACTGTCTCATG 1092
 DB 336 LeuLeuGlnLysLeuAspArgTyrSerGlnHisSerThrIleValLeuThrLeuLeuMet 355
 QY 1093 GCGGTGTCCTGCTGCTGCGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCGC 1152
 DB 356 SerMetPheAlaLeuLeuAlaHisTrpMetAlaCysIleTrpTyrIleIleGlyLysMet 375
 QY 1153 GAGATCGAGACGACGAAATCCGAGCTGCTGAGATTGGCTGCGTGGAGAGTGGCGCCG 1212
 DB 376 GluArgGluAsnSerLeuLeuLysTyrGluValGlyTrpLeuHisGluLeuGlyLys 395
 QY 1213 CGACTGAGACTCCCTACTACTGCTGGTGGCGCGGAGCCAGCTGGAGGAAACAGCTCCGGC 1272
 DB 396 ArgLeuGluSerProTyrTyr-----GlyAsnAsnThr--- 406
 QY 1273 CAGATGTACACTGTGACGACGACGAGCGGAGCCACCGGACGGGGTGGAGTGTGCTGGC 1332
 DB 407 -----LeuGly 408
 QY 1333 GGCCCGTGTGCGAGCGCTACATCCTCCTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 1392
 DB 409 GlyProSerIleArgSerAlaTyrIleAlaAlaLeuTyrPheThrLeuSerSerLeuThr 428
 QY 1393 AGCTGGCTTCCGCAACGCTGCTCGCCCAACACCGACACCGAGAGATCTTCTCATCTGC 1452
 DB 429 SerValGlyPheGlyAsnValSerAlaAsnThrAspAlaGluLysIlePheSerIleCys 448
 QY 1453 ACCATGCTCATCGCGGCTGATCGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1512
 DB 449 ThrMetLeuIleGlyAlaLeuMetHisAlaLeuValPheGlyAsnValThrAlaIle 468
 QY 1513 CAGCGCATGTACCGCGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1572
 DB 469 GlnArgMetTyrSerArgTrpSerLeuTyrHisThrArgThrLysAspLeuLysAspPhe 488
 QY 1573 ATCCGATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGTGTGGAGTACTTCCAGGCC 1632
 DB 489 IleArgValHisLeuProGlnGlnLysGlnArgMetLeuGluTyrPheGlnThr 508
 QY 1633 ACCTGGCGGTGAACATGTCATCGACACCGAGCTGTGTCGAGACCTCTCTGTCGAGCAG 1692


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RX MEDLINE=94211879; PubMed=8159766;
RA Warmke J.W., Ganetzky B.;
RT "A family of potassium channel genes related to eag in Drosophila and
RL mammals.";
RN Proc. Natl. Acad. Sci. U.S.A. 91:3438-3442(1994).
RP [2]
RC STRAIN=Berkley;
RA Celniker S.E., Aghavani A., Arcaina T.T., Baxter E., Blazej R.G.,
RA Chew M., Doyle C.M., Farfan D.E., Flanagan J., Houston K.A.,
RA Hummasti S.R., Karra K., Kearney L., Kim S.H., Lee B., Lomotan M.A.,
RA Mazda P., Mok M.S., Moshrefi A.R., Moshrefi M., Nixon K., Pacleb J.M.,
RA Park S., Pfeiffer B., PUNCH D., Snir E., Twomey B., Wan K.H.,
RA Whitelaw K.R., Yee A., Zhang R., Zieran L.L., Kimmel B.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 103-1284 FROM N.A.
RC STRAIN=Berkley;
RA Harris N.L., Aghayani A., Arcaina T.T., Baxter E., Blazej R.G.,
RA Chavez C., Chew M., Doyle C.M., Farfan D.E., Flanagan J.,
RA Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim S.H., Lee B.,
RA Lomotan M.A., Mak J., Mazda P., Mok M.S., Moshrefi A.R., Moshrefi M.,
RA Nixon K., Pacleb J.M., Park S., Pfeiffer B., PUNCH E., Snir E.,
RA Twomey B., Wan K.H., Whitelaw K.R., Yee A., Zhang R., Zieran L.L.,
RA Kimmel B.E.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RC STRAIN=Berkley;
RA Celniker S.E., George R.A., Galle R.P., Hoskins R.A., Svirskas R.R.,
RA Harris N.L., Aghayani A., Arcaina T.T., Baxter E., Blazej R.G.,
RA Chavez C., Chew M., Doyle C.M., Farfan D.E., Flanagan J.,
RA Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim S.H., Lee B.,
RA Lomotan M.A., Mak J., Mazda P., Mok M.S., Moshrefi A.R., Moshrefi M.,
RA Nixon K., Pacleb J.M., Park S., Pfeiffer B., PUNCH E., Snir E.,
RA Twomey B., Wan K.H., Whitelaw K.R., Yee A., Zhang R., Zieran L.L.,
RA Kimmel B.E.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; U04246; AAA62472.1; -.
DR EMBL; AC004640; -. NOT ANNOTATED_CDS.
DR EMBL; AC005298; -. NOT ANNOTATED_CDS.
DR PIR; T13168; T13168.
DR FLYBASE; FBgn0011589; elk.
DR GO; GO:0008076; C:voltage-gated potassium channel complex; NAS.
DR GO; GO:0005249; F:voltage-gated potassium channel activity; NAS.
DR GO; GO:0006813; P:potassium ion transport; NAS.
DR InterPro; IPR000595; cNMP binding.
DR InterPro; IPR003967; Erg channel.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR001622; K-channel_pore.
DR InterPro; IPR005820; M-channel_nlg.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000700; PAS-assoc C.
DR InterPro; IPR000014; PAS domain.
DR Pfam; PF00027; cNMP binding; 1.
DR Pfam; PF00520; ion.trans; 1.
DR Pfam; PF00785; PAC; 1.
DR PRINTS; PR01470; ERGCHANNEL.
DR SMART; SM00100; cNMP; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 1.
DR TIGREMS; TIGR00229; sensory_box; 1.
DR PROSITE; PS50042; cNMP_BINDING_3; 1.
DR PROSITE; PS50113; PAC; 1.
DR PROSITE; PS50112; PAS; 1.
DR KX Ionic channel; Polymorphism; Transmembrane.
FT VARIANT 1127 1127 I -> L (IN STRAIN BERKELEY).
SQ SEQUENCE 1284 AA; 141377 MW; F09C418E19394A04 CRC64;

Alignment Scores:
Pred. No.: 2,2e-99 Length: 1284
Score: 1901.00 Matches: 455
Percent Similarity: 53.85% Conservative: 146
Best Local Similarity: 40.77% Mismatches: 273
Query Match: 31.22% Indels: 242
DB: 5 Gaps: 31

US-09-965-830-1_COPY_6_3257 (1-3252) x Q23974 (1-1284)

QY 1 ATCGCGGCATCGCGGGCTCTCTGGCGCTCAGACACCTTCCTGGACACCATCGCTACG 60
Db 1 MetProAlaArgLysGlyLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20
QY 61 CGCTTCGACGCGCACGACAGTAACCTCTGCTGGGCAACGCCAGGTGGGGCTCTTC 120
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Db 21 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnAlaAsnGly---Asn 39
QY 121 CCCTGGTGTACTGCTCTGTGATGGCTTCTGTACCTCAGCGGCTTCTCCGGGCTAGGTC 180
Db 40 ProfileValTyrCysSerAspGlyPheValAspLeuThrGlyTyrSerArgAlaGlnIle 59
QY 181 ATGCAGCGGGCTGCTGCTCTCTCTTATGGCCAGACACGAGTGTCTCTCGC 240
Db 60 MetGlnLysGlyCysSerCysHisPheLeuTyrGlyProAspThrLysGlnLysHis 79
QY 241 CAACAGATCCCAAGGCGCTCGACGACGACAGAGGAGTTCAGAGGTGAGCTCATCTG 300
Db 80 GlnGlnIleGluLysSerLeuSerAsnLysMetGluLeuLysLeuGluValIlePheTyr 99
QY 301 CGAAGAGCGGGCTCCGCTTCTGCTGCTCTCTGATGTGATACCATTAAGAGAGAAA 360
Db 100 LysLysGluGlyAlaProPheTyrCysLeuPheAspIleValProLysAsnGluLys 119
QY 361 GGGAGGTGGCTCTCTTCCTAGTCTCTCACAGGACATCAGCGAAACCAAG----- 411
Db 120 ArgAspValValLeuPheLeuAlaSerHisLysAspIleThrHisThrLysMetLeu 139
QY 411 ----- 411
Db 140 MetAsnValAsnGluGluCysAspSerValPheAlaLeuThrAlaAlaLeuLeuGly 159
QY 412 -----AACCGAGG 420
Db 160 ArgPheArgAlaGlySerAsnAlaGlyMetLeuGlyLeuGlyGlyLeuProGlyLeu 179
QY 421 GGGCCC-----GACAGATGCAAGAGAGACAGTGTGGCGCGCGCGATATGGCGG 471
Db 180 GlyProAlaAlaSerAspGlyAspThrGluAlaGlyGluGlyAsnAsnLeuAspVal 199
QY 472 GCAGATCCCAAGGCTTCAATGCCAACCGGGCGGAGCGCGGCGTCTCTACCCACTG 531
Db 200 Ala-----GlyCysAsnMetGlyArgArgArgSerArgAlaValLeuTyrGlnLeu 216
QY 532 TCCGGGCACTGCGAGAGAGCGCCCAAGGGC---AAGCAACAGCTCAATAAGGGG----- 582
Db 217 SerGlyHisTyrLysProGluLysGlyGlyValLysThrLysLeuLysLeuGlyAsn 236
QY 583 ---GTGTTTGGGAGAAACCAACTTCCCTGAGTACAAAGTAGCGCCATCGGAAGTCG 639
Db 237 PheMetHisSerThrGluAlaProPheProGluTyrLysThrGlnSerIleLysLys 256
QY 640 CCCTTCATCTCTGTTGCATCTGTGGGCGCATGAGAGCCACCTGGGATGGCTTCATCT 699
Db 257 ArgLeuIleLeuProHisTyrGlyValPheLysGlyIleTyrAspTrpValIleVal 276
QY 700 GCACACTCTATGTGGCTGTCTGTGCCCTTACAGCGTGTGTGTGAGCAGACGAGGAG 759
Db 277 AlaThrPheTyrValAlaLeuMetValProTyrAsnAlaAlaPheAlaLysAlaAsp 296
QY 760 CCCAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 819
Db 297 GlnThr-----LysValSerAspValIleValGluAlaLeuPheIle 310
QY 820 CTTGACATTTGTGTAATTTCCGTACCATTTCCGTGTCCTCAAGTCGGCGAGGTGGT 879
Db 311 ValAspIleLeuLeuAsnPheArgThrPheValSerArgLysGlyGluValValSer 330
QY 880 GCCCAAGTCCATTTCCTCCACTACGTCAACACCTGGTTCCTGCTGGATGTCATGCA 939
Db 331 AsnSerLysGlnIleAlaIleAsnTyrLeuArgGlyTrpPheAlaLeuAspLeuAla 350
QY 940 GCGCTGGCTTGTGACCTGCTACATGCTCCCTCAAGTCAACGTGTACTTCGGG----- 990
Db 351 AlaLeuProPheAsp-----HisLeuTyrAlaSerAspLeuTyrAspGlyGluAsp 368
QY 991 ---GCCCATCTGCTGAAGACGGTGGCGCTGCTGGCGCTGCTGGCGCTGCTTCGCCG 1047
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369	HisIleHisLeuValLysLeuThrArgLeuLeuArgLeuAlaArgLeuGlnLysIle	388
1048	GACCGTACTCGCAGTACAGCGCGTGGTGTCTGACACTGCTCATGGCGGTGTTCGCCCTG	1107
389	AspArgTyrSerGlnHisThrAlaMetIleLeuThrLeuLeuMetPheSerPheThrLeu	408
1108	CTCGGCAGTGGGTGGCTGGCTGGTGTGTTCATATTGGCCAGCGGGAGATCGAGAGCAGC	1167
409	AlaAlaHisTrpLeuAlaCysIleTrpTyrValIleAlaValLysGlnTyrGlu-----	426
1168	GAATCCGAGTCCCTGGAG-----ATTGGGTGGCTGCAGCAGTGGCGCCGCCACTGGAG	1221
427	-----TrpPheProGluSerAsnIleGlyTrpLeuGlnLeuLeuAlaGluArg-----	442
1222	ACTCCCTACTACTGTGGTGGCGGAGCCAGCTGGAGGAGAACAGCTCCGCCACAGATGAC	1281
442	-----	442
1282	AACTGCAGCAGCAGCAGCGAGGCGCAACGGGACGGGGCTGCAGCTGTGGGCGGCCGTGC	1341
443	-----LysAsnAlaSerValAlaIleLeuThrAlaGlu-----	454
1342	CTGCGCAGCGCTATCATCACTCCCTCTACTTCGCATCTAGCAGCCTCACAGCGTGGGC	1401
455	-----ThrTyrSerThrAlaLeuTyrPheThrPheThrSerLeuThrSerValGly	471
1402	TTCGGCAACGTGTCGCCCAACACGACGACGAGAGATCTTCCATCTGCACCATGCTCTC	1461
472	PheGlyAsnValSerAlaAsnThrThrAlaGlnLysValPheThrIleIleMetMetLeu	491
1462	ATCGGCGCCTGATGCACGGCGTGGTGTGGGAACGTGACGGGCATCATCCAGCGCATG	1521
492	IleGlyAlaLeuMetHisAlaValAlaPheGlyAsnValThrAlaIleIleGlnArgMet	511
1522	TACGCCCGCGCTTCTGTATCCACAGCGGACGCGCGACCTGCGCGACTCATCCCGATC	1581
512	TyrSerArgArgSerLeuTyrGluSerLysTrpArgAspLeuLysAspPheValAlaLeu	531
1582	CACCGTATCCCAAGCCCTCAAGCAGCGGATGTGTGAGTACTTCCAGGCGCATCGGCGC	1641
532	HisAsnMetProLysGluLeuLysGlnArgIleGluAspTyrPheGlnThrSerTrpSer	551
1642	GTGAACAAATGGCATCGACACACCGAGCTGTGCAGAGCCTCCCTGACAGTGTGCGGCA	1701
552	LeuSerHisGlyIleAspIleTyrGluThrLeuArgGluPheProGluGluLeuArgGly	571
1702	GACATCGCATGCACTGCACAAAGAGTCTCTGAGCTGCCACTGTGTTGAGGCGGCCAGC	1761
572	AspValSerMetHisLeuHisArgGluIleLeuGlnLeuProIlePheGluAlaAspSer	591
1762	CGCGCTGCTCGTGGCGGCACTGTCTCTCGCCCTTGGCGCCGCTTCTGCACCGCGGCGAG	1821
592	GlnGlyCysLeuLysLeuLeuSerLeuHisIleLysThrAsnPheCysAlaProGlyGlu	611
1822	TACCTCATCCACCAAGCGATGCCCTGCAGGCCCTCTACTTGTCTGCTCTGCTCCATG	1881
612	TyrLeuIleHisLysGlyAspAlaLeuAsnTyrIleTyrLeuCysAsnGlySerMet	631
1882	GAGTGTCTCAAGGTGGCACCGTCTCGCCATCTTAGGGAAGGCGCACCTGATCGGCTGT	1941
632	GluValIleLysAspAspMetValValAlaIleLeuGlyLysGlyAspLeuValGlySer	651
1942	GAGCTG-----	1947
652	AspIleAsnValHisLeuValAlaThrSerAsnGlyGlnMetThrAlaThrThrAsnSer	671
1948	CCCCGGCGGAGAGGTGGTAAAGGCCCAATGCCACGCTGAAGGGCGCTGACGTACTGCGTC	2007
672	AlaGlyGlnAspValValArgSerSerSerAspIleLysAlaLeuThrTyrCysAsp	691
2008	CTGCAGTCTCTGCAGCTGGCTGGCTGCACGACAGCAGCTTGGCTGTATACCCGAGTTTGGC	2067
692	LeuLysCysIleHisMetGlyLysValGluValLeuValLeuArgLeuTyrProGluTyrGln	711

QY	2068	CCGCGCTTCAGTGTGGCTCCGAGGGGACCTCAGCTACAACCTGGGTGGTGCTGGGGAGGC	2121
Db	712	GlnGlnPheAlaAsnAspIleGlnHisAspLeuThrCysAsnLeuArgIleGluTyrglu	731
QY	2128	TCTGCAGAGTGGACACCAGC-----TCCCTGAGCGGCCGCAATAATCC	2169
Db	732	AsnGlnAspSerAspIleGlyProSerPheProLeuProSerIleSerGluAspAspGlu	751
QY	2170	CTTATGTCCACGCTGGAG-----GAGAAGGAGACAGATGGGGAGCAGGGC	2214
Db	752	AsnArggluGluAlaGluGluGlyGlyLysglyGluLysgluAsnglyGly-----Gly	769
QY	2215	CCC-----ACGGTCTCCCCAGCCCGCATGATGAGCCCTCC	2250
Db	770	ProProSerGlyAlaSerProLeuHisAsnIleSerAsnSerProLeuHisAlaThrArg	789
QY	2251	AGCCCCCTGTGTCTCCCTGGCTGCACCTCTCATCTCAGCTGCCAAGCTGTATCCCCA	2310
Db	790	SerProLeuLeuGlyMetGly-----SerPro	798
QY	2311	CGTGCAACAGCACCCCGGCTCTCTTAGTGGGAGGGAGGCCAGGCAGGGCAGGGGCT	2370
Db	799	Arg-----AsnGlnArgLeuHisGlnArgGly-----	807
QY	2371	TTGAAGGCTGAGGCTGGCCCTCTGCTCTCCGCCACGCGCCCTAGAGGGCTACGGCTGCC	2430
Db	808	-----ArgSerLeullethrLeuArg-----	814
QY	2431	CCCATGCCATGAAATGTGCCCCAGATCTGAGCCCCCAGGGTAGTAGATGCATTGAAGAC	2490
Db	815	-----GluThrAsnLysArgHisArgThrLeuAsnAla-----	825
QY	2491	GGCTGTGGCTCGGACAGCCCAAGTCTCTTCCGGCTGGGCCAGCTGCGCCCGGAATGT	2550
Db	826	AlaCysSerLeuAspArgGlySerPhe-----	834
QY	2551	AGCAGCAGCCCTCCCTCGACACAGAGGGCTGTCTACTGTCCCCATGGGCCCCAGC	2610
Db	835	--GluGluProGluProLeuGluGluGlu-----GlnSer	845
QY	2611	GAGCAAGGAACACAGACACTGGACAGCTTCGGCAGCGGTGACAGAGCTGTGCAGAG	2670
Db	846	SerGlyLysArgProSerLeuGluLysArgLeuAspSerGlnValSerThrLeuHisGln	865
QY	2671	CAGGTGTGCAGATCGGGAAGGACTGCAGTCTACTCGCCAGGCTGTGCAGTTGTCTGT	2730
Db	866	AspValalaglnLeuSerAlaGluValArgAsnAlaIleSerAlaLeuGlnGluMet---	884
QY	2731	CGCCCCACAGGGAGGTCCGTGCCCTCGGCATCGGGAGAGGGGGCGGTGCCCAGCCGAC	2790
Db	885	-----ThrPhe	886
QY	2791	ACCTCCGGGCTTCTGCAGCTCTGTGTGTGGACACTGGGCGATCCTCTACTGCCTGCAG	2850
Db	887	ThrSerAsnAlaMet-----ThrSerHisSerLeuLysPhe---	899
QY	2851	CCCCAGCTGGCTGTGC-----TTGAGTGGCACTTGGCCCCACCCCTCGTCGGGGCCCT	2904
Db	900	ProProAlaargSerIleProAsnIleSerGly--ValAlaGlyThrArgSerGlyVala	919
QY	2905	CCTCCCTCATGGACCTGGCCCTGGGGTCCCGAGCGTCTCAGAGTCCCCCTGGCCT	2964
Db	919	IaValGluHisGlyLeuMetGly---GlyValLeuAlaLaIaGluLeu--AlaAlaMe	937
QY	2965	CGAGCCACAGCTTCTGCAGCTCCACCT-----CAGACTCAGAGCCCTGCC	3012
Db	937	tGlnArgSerSerSerHisProProGluValTrpGlyArgAspValGlnLeuProThrSe	957
QY	3013	TCAGGAGACCTGTCTCTGAGCCGACGACCCCTGCCTCC	3052
Db	957	rAsnThrAlaSerSerLysAlaProSerProValGluPro	970


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QY 799 GCGTGGAGGTCTCTTCAATCCTTGACATGTGCTGAATTCGGTACCAATTCGTGCTC 858
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
460 IleValAspIleMetPheIleValAspIleLeuIleAsnPheArgThrThrValAsn 479
QY 859 AAGTCGGGCGAGTGTGCTTGGCCCAAGTCCATTGCTCCACTACCTCACCCTGG 918
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480 AlaAsnGluGluValValSerHisProGlyArgIleAlaValHisThrPheLysGlyTrp 499
QY 919 TTCCTCTCGATGTCATCGCAGCGCTGCCCTTTGACTGTCTACATGCTTCAAGTCAAC 978
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
500 PheLeuIleAspMetValAlaIleProPheAspLeuLeu----- 513
QY 979 GTGTACTTCGGGCC-----CATCTGCTGAAGACGGTGCCTGCTGCTG -020
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514 ---IlePheGlySerGlySerGluGluLeuIleGlyLeuLeuLysThrAlaArgLeuLeu 532
QY 1021 CGCTCTCGCTGCTTCCGGCGGTGGACCGGTACTCCAGTACAGCGCGTGTGCTG -080
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533 ArgLeuValArgValAlaArgLysLeuAspArgTyrSerGluTyrGlyAlaAlaValLeu 552
QY 1081 ACACTCTCATGCGCGTTCGCTGCTGCTGCGCACTGGGTGCGCTGCTGCTGTTTAC 1140
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553 PheLeuLeuMetCysThrPheAlaLeuIleAlaHisTrpLeuAlaCysIleTrpTyrAla 572
QY 1141 ATGGCCAGCGGAGATCGAGACGAGCAATCGAGCTGCTGAGATTGCTGCTGCTGCGAG 1200
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573 IleGlyAsnMetGluGlnProHisMetAspSer-----HisIleGlyTrpLeuHis 589
QY 1201 GAGTCGGCGCGGACTGTGAGACTCCCTACTACTGCTGTGGCGCGGAGCTGGAGGG 1260
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
590 AsnLeuGlyAspGlnIleGlyLysProTyr----- 599
QY 1261 AACAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGCAGGAGCCAAACGGGCGGCTG 1320
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600 AsnSerSerGly----- 603
QY 1321 GAGCTGCTGGCGCGCGCTGCTGCGAGCGGCTATCATACCTCCCTCTACTTCGCACTC 1380
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604 -----LeuGlyProSerIleLysAspLysTyrValThrAlaLeuTyrPheThrPhe 621
QY 1381 AGCAGCTCACAGCGTGGCTTGGCAGCGTCCGCAACACGACGACCGAGAGATC 1440
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622 SerSerLeuThrSerValGlyPheGlyAsnValSerProAsnThrAsnSerGluLysIle 641
QY 1441 TTCCTCATCTGCACCATGCTCATCGCGCGCTGATGACGCGGTGTGTGGGACGCTG 1500
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662 SerAlaIleIleGlnArgLeuTyrSerGlyThrAlaArgTyrHisThrMetLeuArg 681
QY 1561 CTGCGGAGTACATCCGATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGCTGGAG 1620
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682 ValArgGluPheIleArgPheHisGlnIleProAsnProLeuArgGlnArgLeuGlu 701
QY 1621 TACTTCCAGCCACCTGGCGGTGAACAAATGGATCGACACCGAGCTGTGTCAGAGC 1680
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702 TyrPheGlnHisAlaTrpSerTyrThrAsnGlyIleAspMetAsnAlaValLeuLysGly 721
QY 1681 CTCCTCTGAGAGTGGCGGACATCGCATCGCATCGCATCGCATCGCATCGCATCGCAT 1737
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722 PheProGluCysLeuGlnAlaAspIleCysLeuHisLeuAsnArgSerLeuLeuGlnHis 741
QY 1738 CTGCCACTGTTTGGCGGCGGCGGCTGCTGCGGCACTGTCTCTGCGCGCTGCGG 1797
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742 CysLysProPheArgGlyAlaThrLysGlyCysLeuArgAlaLeuAlaMetLysPheLys 761
QY 1798 CCGCGCTTTCAGCGCGGAGTACCTCATCCACAGCGGATGCTGCGAGCGCTC 1857
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762 ThrThrHisAlaProGlyAspThrLeuValHisAlaGlyAspLeuLeuThrAlaLeu 781
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Db      561 LeuAlaSerAspGlyCysLeuArgAlaLeuAlaMetHisPheGlnMetSerHisSerAla 580
QY      1813 CCGGGGAGTACCTCATCACCAGGCGATGCCCTGCAGGCCCTCTACTTGTCTGCTCT 872
Db      581 ProGlyAspLeuLeuThrHisThrGlyGluSerIleAspSerLeuCysPheIleValThr 600
QY      1873 GGTCTCATGAGTGTCTAAGGTTGGCACCGTCTCGCCATCTCTAGGAAGGCGACCTG 932
Db      601 GlySerLeuGluValIleGlnAspAspGluValValAlaIleLeuGlyLysGlyAspVal 620
QY      1933 ATCGCTGTGAGTCCCGCGGAGCAGTGTAAAGCCCAATGCCGACGTCAAGGG 1992
Db      621 PheGlyAspSerPheTrpLysAspSerAlaValGlyGlnSerAlaAlaSerValAla 640
QY      1993 CTACGCTACTGCTCTGAGTCTGTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2052
Db      641 LeuThrTyrCysAspLeuHisThrIleLysArgAspArgLeuLeuValLeuAspPhe 660
QY      2053 TACCCGAGTTTCCCGCGCTTTCAGTCTGTCGCTCGAGGAGGAGTCTAGCTACACCTG 2112
Db      661 TyrGlnAlaPheAlaAsnSerPheAlaArgAsnLeu-----ThrLeuThrTyrAsnLeu 678
QY      2113 GGTGCTGGGAGGCTCTGACAGGTGGACACGCTCCCTGAGCGCGACATACCTT 2172
Db      679 ArgHisArgLeuIlePheArgLysVal-----AlaAspValArgArgGluArgGluLeu 696
QY      2173 ATGTCC-----ACGCTGGAGAGAGAGGAGACAGAT----- 2202
Db      697 MetGluArgArgLysArgGluProGlnLeuGlnAlaGlnAspHisLeuValArgLys 716
QY      2203 -----GGGAGACAGGGGCCCAACGGTCTCCCGAGCCCGAGCTGATGAG 2244
Db      717 IlePheSerArgPheArgArgGluArgSerValAlaAlaAlaProAlaProAlaProAla 736
QY      2245 CCTTCAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2304
Db      737 ArgAlaSerPro-----AlaProProAlaThrAlaValAlaThrAlaAlaAlaPro 754
QY      2305 -----TCCCCACCTCGAACACGACACCCCGGCT-----CGTCTAGGT 2340
Db      755 ProAlaSerAspAlaGluArgGlyAspAlaProGlnProProProAlaValAlaAlaPro 774
QY      2341 GGCAGAGGAGGCGCAGCAGG-----GCGAGGCTTTGAAGGTGAGGCTGGGCCCC 2391
Db      775 AlaArgGlyLysTrpGlyArgLeuLeuAlaGlySerLeu-----AspAlaGlyGln 792
QY      2392 TCTGCTCCCGCCCGGCTGAGGGGCTAGGGGCTAGGGTGGCCCCCATGCTCATGGAATGCGCC 2451
Db      793 AlaAspThrProArgGlyAla-----PheSer 801
QY      2452 CCAGATCTGAGCCCGAGGCTAGTAGATGCGATTGAAGACGCGCTGTGCTCGGACGAGCC 2511
Db      802 ArgSerLeuSerAlaArg-----AspArgPro 810
QY      2512 AAGTTCTTTCGCGTGGGCGAGTCTGCGCGGAGTGTAGCAGCAGCCCTCC-----CCT 2568
Db      811 Pro-----ProSerGlyThrAspAlaThrAlaGlnAlaSerAlaAla 824
QY      2569 GGACACAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2628
Db      825 GlyAlaValThrSerAlaLeuSerLeuLysAlaSerPheAlaLysAlaArgSerAlaSer 844
QY      2629 ACCTG-----GACAAAGCTTCGGCAGCGGTGACAGAGTGTGACAGAGCAGGTG 2676
Db      845 AlaLeuGlyValGlyThrGlySerAlaArgGlnAspThrIleGlu----- 859
QY      2677 CTGAGATGGGAGAGACTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2736
Db      860 -----GluGluLeuGluGluArg-----ProPro 868
QY      2737 CACAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2793
Db      869 AlaLeuProAlaProProProValThrProAlaProThrProAlaProValSerThrHis 888

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QY      2794 TCCGGGCTTCTGAGCCTCTGTGTGTGGACACTGGGGGATCTCTCTACTGCTGCGAGCCC 2853
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QY      2854 CAGCTGGCTCTCTCTGAGT-----GGGACTTGGCCC 2886
Db      909 LysLeuGlyArgValGluLeuLeuLeuMetLeuAlaAlaArgLeuGlyAlaGluPro 928
QY      2887 CACCTCTGTCGGGGGCTCTCTCCCTCATGGCACCTGGCGCTGCGGCTGCGGCTGCT 2946
Db      929 GlyAspSerProGlyGlyAlaAla-----GlyAlaAlaSerAla 941
QY      2947 CAGAGCTCCCTGGCTCGAGCCACAGCTTCTGACCTTCTGACCTCCACCTCAGACTCAGAGCCC 3006
Db      942 AlaGlyAlaAspGluProArgAlaProAla-----AlaPro 953
QY      3007 CTGCTCTCAGAGACTCTGCTCTGAGCCAGCCACCTGCTGCTGCTGCTGCTGCTGCTGCTG 3066
Db      954 ProAla-----AspLeuAlaAlaLeuThrArgLysArgSerLysAlaArgSerLys 971
QY      3067 GAAGGGCTAGGACTGGGCGCGCAGAGCCTGTGAGCCAGGCTGAGGCTACGAGCTGGA 3126
Db      972 GlyAlaAlaProGlnAlaProThr-----ProThrThrProGlyAspAlaProSerSer 989
QY      3127 GAGCCCCCAGGCTCAGGGGCTGAGGCCCTGGCC 3156
Db      990 ---ProProGlyGlySerAlaGlyValAla 998

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RESULT 8

Q8JH78 PRELIMINARY; PRT; 1186 AA.

ID Q8JH78; AC Q8JH78; 01-OCT-2002 (T-EMBLrel. 22, Created)

DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)

DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)

DE Erg K+ channel.

GN ERG.

OS Brachydanio rerio (zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

OC NCBI_TaxID=7955;

RN [1]

RP SEQUENCE FROM N.A.

RA Langheinz U., Wagner T.;

RT "Zerg function in zebrafish."

RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.

DR GO; GO:0006812; P:cation transport; IEA.

DR GO; GO:0006813; P:potassium ion transport; IEA.

DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

DR GO; GO:0007165; P:signal transduction; IEA.

DR InterPro; IPR000595; cNMP binding.

DR InterPro; IPR003967; Erg channel.

DR InterPro; IPR005821; Ion trans.

DR InterPro; IPR001622; K+channel_pore.

DR InterPro; IPR005820; M-channel_nlg.

DR InterPro; IPR001610; PAC.

DR Pfam; PF00027; cNMP binding; 1.

DR Pfam; PF00520; ion trans; 1.

DR Pfam; PF00785; PAC; 1.

DR PRINTS; PR01470; ERGCHANNEL.

DR SMART; SM00100; cNMP; 1.

DR PROSITE; PS00042; cNMP BINDING_3; 1.

KW Ionic channel; Transmembrane.

SQ SEQUENCE 1186 AA; 132279 NW; BCF3F23551ABBD3 CRC64;

Alignment Scores: 2.36e-71 Length: 1186
Pred. No.: 1405.50 Matches: 396
Score:

Percent Similarity: 43.59% Conservative: 168
 Best Local Similarity: 30.60% Mismatches: 394
 Query Match: 23.08% Indels: 337
 DB: 13 Gaps: 36

US-09-965-830-1_COPY_6_3257 (1-3252) x Q8JH78 (1-1186)

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QY 1 ATGCCGGCCATGGGGCTCTCTGGCGCTCAGAACACCTTCTCTGACACCATCGCTACG 60
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QY 1 MetProValArgArgGlyHisValAlaLeuGlnAsnThrTyrLeuAspThrIleLeuArg 20
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QY 61 CGCTTCGACGCGACGACAGTACTTCGTGCTGGGCAAGCCCGACGCTGGCGGCTCTTC 120
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QY 21 LysPheAspGlyGlnAsnArgLysPheLeuIleAlaAsnAlaGlnMetLysAsnCys--- 39
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 CCGCTGGTCTACTGCTCTGATGGCTCTGACCTCAGCGGCTTCTCCGGGCTGAGGTC 180
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QY 40 GlyIleIleTyrCysAsnGlyPheCysGlnMetPheGlyPheSerArgAlaGluIle 59
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QY 181 ATGCAGCGGGGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
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QY 241 CAACAGATCCGACAGCCCTGACGACGACACAGGAGTTCAGGCTGAGCTGATCTGTAC 300
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QY 80 GlyGlnLeuAlaGlnAlaLeuLeuGlySerGluGluArgLysValGluIleLeuTyr 99
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QY 100 SerLysGluGlyThrCysArgProCysLeuIleAspValIleProValLysAsnGlu 119
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QY 361 GGGGAGGTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 417
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QY 120 GlyValValIleMetPheIleLeuAsnPheGlnGluLeuLeuAspProSerMetLysLys 139
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QY 418 GGGGCG-----CCGACAGATGAAAGAGACAGAGTGGTGGCGGCGCGCA 462
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QY 140 GlyGlyLeuLysGlnArgMetAlaAsnSerTyrLeuArgAlaGlyGlnArgArgMet 159
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QY 463 TATGCCGGGACGATCAAA-AGGCTTCAATGCCAACCGCG----- 503
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QY 160 HisLeuArgMetProSerLeuArgValLysArgGlnProSerLeuProLysAspHis 179
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 503 ----- 503
Db GluGlyValValAspTyrLeuGlnProSerHisGluGluValAlaLeuLysAspLeu 199
QY 503 ----- 503
Db GlnMetSerProAspSerCysLeuLysSerGluThrGlnAlaLeuIleGlnGlnThrPro 219
QY 504 -----GCGAGCGGGCGCGTCTACCATCTGTCGG 536
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 220 SerSerCysGluLeuSerProProSerArgProSerAspArgLeuGluPro-SerG 239
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 537 GCACCTGCAGAGCAGCCCAAGGCAAG-----CACAGCTCAATAAGGGG----- 582
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 239 yProLeuLeuLysHisSerHisSerArgGluSerMetHisSerLeuArgArgAlaSerSe 259
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 582 ----- 582
Db 259 rLeuHisAspIleAspGlyMetArgAspGlnTrpSerAspLeuLysProSerAsnLeuAs 279
QY 583 -----GTGTTTGGGGAACCAAC----- 603
Db 279 nSerThrSerAspSerAspLeuMetArgHisArgThrIleGlyArgIleProGlnValTh 299
QY 603 ----- 603
Db 299 rIleSerPheGlySerAspArgLeuArgProProSerProThrGluIleGluIleAl 319
QY 603 ----- 603

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Db 319 aProSerLysIleLysAspArgSerGlnAsnValSerGluLysValThrGlnValThrG 339
QY 604 -----TTGCTGTAGTACAAAGTAGCCGCCATCCGGAAGTC 638
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Db 339 nValLeuSerLeuGlyAlaAspValLeuProGluTyrLysLeuGlnAlaProArgIleHi 359
QY 639 GGCCTTTCATCTCTGCTGCTGCTGGGCACCTGAGAGCACCTGGATGGCTTCATCTGCT 698
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 359 sIysTrpThrIleLeuHisTyrSerProPheLysAlaValTrpAspTrpIleLeuLeu 379
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 699 CGCCACACTCTATGTGGCTGCTCACTGCTGCCCTACAGCGTGTGTGTGAGCACAGCAG 758
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 379 uLeuValLeuTyrThrAlaValPheThrProTyrSerAlaAlaPheLeuLeuAsnGlu 399
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 759 GGCAGTGGCGCGCGC-----GGCCCGCCCGAGCGTCTGTGACCT 797
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 399 nGluAspGluArgArgThrCysGlyTyrThrCysAsnProLeuAsnValValAspLe 419
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 798 GGCCTGGAGGCTCTCTCTCATCTTGCATCTGTGTGATTTCCGTACCATCTCTGCTC 857
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 419 uValValAspValMetPheIleAspIleLeuIleAsnPheArgThrThrTyrValAs 439
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 858 CAAGTCGGCCAGGTGTGTGTCGCCCAAGTCCATTTGCTCCACTAGCTCACACCTG 917
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 439 nHisAsnAspGluValValSerAsnProAlaArgIleAlaGlnHisTyrPheLysGly 459
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 918 GTTCTGTGTGATGTCATCGAGCGCTGCCCTTTCACCTGTGTGTGTGTGTGTGTGTGT 972
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 459 pPheLeuIleAspIleValAlaAlaIleProPheAspLeuLeu---IlePheArgSer 478
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 973 -----GTCAAGTGTACTTCTGGGCCCCCTGCTGTGAGACAGCGTGGCGCT 1016
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 478 ySerAspGluProGlnThrThrThrLeuIleGly-----LeuLeuLysThrAlaArg 496
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1017 GCTGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1076
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 496 uLeuArgLeuValArgValAlaArgLysLeuAspArgTyrSerGluTyrGlyAlaAla 516
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY 516 lLeuPheLeuLeuMetCysThrPheAlaLeuIleAlaHisTyrLeuAlaCysIleTrp 536
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Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 536 rAlaIleGlyAsnMetGlu---ArgThrSerSerAlaArgIleGlyGlyMetLysIle 555
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1191 CTGGCTGAGGAGTGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1250
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QY 555 yTrpLeuAspAsnLeuAlaAspGlnIle----- 564
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QY 1251 AGCTGGAGGAACAGCTCGCGCAGAGTGACAACCTGACAGCAGCAGCGGCGCAACGG 1310
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 565 -----GlyLysGlnTyrAsnAspSerAsnSer----- 573
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QY 1311 GACGGGCTGAGCTGCTGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1370
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 574 -----PheSerGlyProSerIleLysAspLysTyrValThrAlaLeuTy 588
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1371 CTTCGCACTCAGCAGCTCACCAGCGTGGCTTCGGCAACGTGTCGGCAACACCGCAC 1430
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QY 588 rPheThrPheSerSerLeuThrSerValGlyPheGlyAsnValSerProAsnThrAsnPr 608
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QY 608 oGluLysIlePheSerIleCysValMetLeuIleGlySerLeuMetTyrAlaSerIlePh 628
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QY 628 eGlyAsnValSerAlaIleIleGlnArgLeuTyrSerGlyThrAlaArgTyrHisThr 648
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QY 1551 CACGCGGACCTGCGGACATCATCCGATCCAGCGTATCCCAAGCCCTCAAGCAGCG 1610
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QY 648 nMetLeuArgValLysGluPheIleArgPheHisGlnIleProGlyGlyLeuArgGlnAr 668

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RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,	1042	CGGCTGGACCGGTACTCGCAGTACGCGCGTGTGTGACATGCTCATGCGCGTGTTC	1101
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,	Qy		
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,	Db		
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,	Qy		
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,	Db		
RA	de Pablo K., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,	Qy		
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,	Db		
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,	Qy		
RA	Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,	Db		
RA	Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,	Qy		
RA	Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,	Db		
RA	Hoslin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,	Qy		
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,	Db		
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,	Qy		
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang X., Lin X.,	Db		
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,	Qy		
RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,	Db		
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,	Qy		
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,	Db		
RA	Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,	Qy		
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,	Db		
RA	Shue B.C., Siden-Kimani I., Simpson M., Skupski M.P., Smith T.,	Qy		
RA	Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,	Db		
RA	Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,	Qy		
RA	Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,	Db		
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,	Qy		
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,	Db		
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,	Qy		
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;	Db		
RT	"The genome sequence of Drosophila melanogaster.";	Qy		
RL	Science 287:2185-2195 (2000).	Db		
DR	EMBL; AE003497; AAF48410.1; --	Qy		
DR	FlyBase; FBgn000535; eaq.	Db		
DR	GO; GO:0007619; P: courtship behavior; NAS.	Qy		
DR	GO; GO:0007611; P: learning and/or memory; NAS.	Db		
DR	GO; GO:0007608; P: olfaction; NAS.	Qy		
DR	GO; GO:0008016; P: regulation of heart rate; NAS.	Db		
DR	GO; GO:0045474; P: response to ether (sensu Insecta); NAS.	Qy		
DR	InterPro; IPR000595; CNMP binding.	Db		
DR	InterPro; IPR003967; Erg_channel.	Qy		
DR	InterPro; IPR005821; Ion_trans.	Db		
DR	InterPro; IPR001622; K+channel_pore.	Qy		
DR	InterPro; IPR005820; M+channel_nlg.	Db		
DR	InterPro; IPR001610; PAC.	Qy		
DR	InterPro; IPR000700; PAS-assoc.C.	Db		
DR	InterPro; IPR000014; PAS_domain.	Qy		
DR	Pfam; PF00027; CNMP_binding; 1.	Db		
DR	Pfam; PF00520; Ion_trans; 1.	Qy		
DR	Pfam; PF00785; PAC; 1.	Db		
DR	PRINTS; PR01470; ERGCHANNEL.	Qy		
DR	SMART; SM00100; CNMP; 1.	Db		
DR	SMART; SM00086; PAC; 1.	Qy		
DR	SMART; SM00091; PAS; 1.	Db		
DR	PROSITE; PS50042; CNMP_BINDING_3; 1.	Qy		
DR	PROSITE; PS50113; PAC; 1.	Db		
DR	PROSITE; PS50112; PAS; 1.	Qy		
KW	Ionic channel; Transmembrane.	Db		
SQ	SEQUENCE 1174 AA; 126370 MW; B8F86ACBB5627FD3 CRC64;	Qy		
Alignment Scores:				
Pred. No.:	2.62e-70	Length:	1174	
Score:	1387.00	Matches:	393	
Percent Similarity:	46.61%	Conservative:	192	
Best Local Similarity:	31.31%	Mismatches:	383	
Query Match:	22.78%	Indels:	288	
DB:	5	Gaps:	43	
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Db	1 MetProGlyGlyArgArgGlyLeuValAlaProGlnAsnThrPheLeuGluAsnIleIle 20			


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QY 2917 -----GCACCTGGCGCTGGGGTCCCGAGCGTCTCAGAGCTCCCC 2957
Db 1037 gArgSerLysSerArgLysAlaProAlaPro-----ProLysGlnThrLeuAlaSerTh 1055
QY 2958 CTGGCCTCGAGCCACAGCTTTC----- 2979
Db 1055 tAlaGlyThrAlaThrAlaAlaProAlaGlyValAlaGlySerGlyMetThrSerSerAl 1075
QY 2980 -----TGGACCTCCACCTCAGACTCAGACCCCTCGC 3011
Db 1075 aProAlaSerAlaAspGlnGlnGlnHisGlnSerThrAlaAspGlnSerProThrTh 1095
QY 3012 CTCAGGA-----GACCTCGCTCTGAGCCCGACACCCCTGCCTCCCC 3053
Db 1095 rProGlyAlaGluLeuLeuHisLeuArgLeuLeuGluGluAspPheThrAlaAlaGlnLe 1115
QY 3054 TCCTCTCTCTAGGAGGGCTAGACTGGGCCCGCAGAGCCTGTGAGCCAGGCTGAGGC 3113
Db 1115 uProSerThrSerSerGlyGlyAlaGlyGlyGlyGly-----SerGlySerGlyAl 1133
QY 3114 TACCAGCACTGAGAGCCCCCACCAGGCTCAGGGGGCTGGCTGGCCCTGGAGCCCCCA 3173
Db 1133 aThrProThrThrProProThrThrAlaGlyGly----- 1145
QY 3174 CAGCCTGGAGATGGTCTATTGGCTGCATGGCTCTGCACA 3216
Db 1146 -----SerGlySerGlyThr 1150

RESULT 10
Q8C035 PRELIMINARY; PRT; 988 AA.
AC Q8C035;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE EAG K+ channel.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10990;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK032438; BAC27869.1; --
DR PIR; PT0697.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0000155; F:two-component sensor molecule activity; IEA.
DR GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR GO; GO:0000160; P:two-component signal transduction system (p. .; IEA.
DR InterPro; IPR000595; cNMP_binding.
DR InterPro; IPR003967; Erg_channel.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000700; PAS-assoc.C.
DR InterPro; IPR000014; PAS_domain.
DR Pfam; PF00027; cNMP_binding; 1.
DR Pfam; PF00520; ion_trans; 1.
DR Pfam; PF00785; PAC; 1.
DR PRINTS; PR01470; ERGCHANNEL.
DR SMART; SM00100; cNMP; 1.
DR SMART; SM00086; PAC; 1.
DR TIGRFAMs; TIGR00229; sensory_box; 1.

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DR PROSITE; PS50042; CNMP_BINDING_3; 1.
DR PROSITE; PS50113; PAC; 1.
SQ SEQUENCE 988 AA; 111781 MW; 0EEELF577F5C18BB CRC64;

Alignment Scores:
Pred. No.: 8,32e-68 Length: 988
Score: -1342.50 Matches: 332
Percent Similarity: 50.55% Conservative: 178
Best local Similarity: 32.90% Mismatches: 314
Query Match: 22.05% Indels: 185
DB: 11 Gaps: 29

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Db 1 MetProGlyGlyLysArgGlyLeuValAlaProGlnAsnThrPheLeuGluAsnIleVal 20
QY 58 ACGGCTTCGACGGCAGCAGACAGTAACCTTCGTGTGGGCAAGCCCGACAGTGGCGGGCTC 117
Db 21 ArgArg-----SerSerGluSerSerPheLeuLeuGlyAsnAlaGlnIleValAsp--- 37
QY 118 TTCCTCGTGTACTGTCTGTGATGGCTTCTGTACCTCAGCGGCTTCTCCCGGCTGAG 177
Db 38 TrpProValValTyrSerAsnAspGlyPheCysLysLeuSerGlyTyrHisArgAlaasp 57
QY 178 GTCATGACGGGGCTGTGCTCTCTTCTTATGGCCAGACACACGAGTGCCTGTC 237
Db 58 ValMetGlnLysSerSerThrCysSerPheMetTyrGlyGluLeuThrAspLysLysThr 77
QY 238 CGCAACAGATCCGCAAGGCCCTGGAGCAGACAGGAGTTCAGGCTGAGTGATCGT 297
Db 78 IleGluLysValArgGlnThrPheAspAsnTyrGluSerAsnCysPheGluValLeuLeu 97
QY 298 TACCGAAGAGCGGGCTCCCGTCTCTGTGTCTCTCTGATGTACATACCCATAAAGATCAG 357
Db 98 TyrLysLysAsnArgThrProValTyrPheTyrMetGlnIleAlaProIleArgAsnGlu 117
QY 358 AAGGGGAGGTGGCTCTCTCTAGTCTCTCACAAGACATCAGCGCAACCAAGAACCGA 417
Db 118 HisGluLysValValLeuPheLeuLeuCysThrPheLysAspIleThrLeuPheLysGlnPro 137
QY 418 GGGGGCCCCGACAGATGGAAGGAGCAGGTGGTGGCGCGCCGATATATGGCGGGCAGCA 477
Db 138 IleGluAspAspSerThrLys-----GlyThrLysPheAlaArgLeuThr 153
QY 478 TCCAAAGCTTCAATGCAACCGCGGGGAGCGCGCTGTCTTACACCTGTTCGGG 537
Db 154 ArgAlaLeuThrAsn-----SerArgSerValLeuGlnGlnLeuThrPro 168
QY 538 CACCTGCAAGCAGCCAGGGCAAGCAC-----AAGCTCAAT 576
Db 169 MetAsnLysThrGluThrValHisLysHisSerArgLeuAlaGluValLeuGlnLeuGly 188
QY 577 AAGGGGTGTTGGGGAGAAACAACTTGCTCAGTACAAAGTAGCGCCATCGGGAAG 636
Db 189 SerAspIle-----LeuProGlnTyrLysGlnGluAlaProLysThr 202
QY 637 TCGCCCTTCATCTCTGTTCACCTGTGGGGCAGTCAGAGCCACCTGGGATGGCTTCTCTG 696
Db 203 ProProHisIleIleLeuHisTyrCysAlaPheLysThrThrTyrAspTyrValIleLeu 222
QY 697 CTGCCACACTATGTGGGTGTCTGTGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 756
Db 223 IleLeuThrPheTyrThrAlaIleMetValProTyrAsnValSerPheLysThrLysGln 242
QY 757 GAGCCAGTCCCGCGCGCGCCCGCCCTGTGTACCTGTGTACCTGGCCCTGGAGTCTCTTC 816
Db 243 AsnAsnIleAlaTrp-----LeuValLeuAspSerValValAspValIlePhe 258
QY 817 ATCCTTGACATTTGTGTAATTTCCGTACCACTTCTGTGTCCAGTCCGGCCAGGTGTGT 876
Db 259 LeuValAspIleValLeuAsnPheHisThrThrPheValGlyProGlyGlyGluValIle 278

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QY	877	TTTGCCCAAGTCCATTGTCCTCCACTAGCTACACCACTGGTCTCTGCTGGATGTCATC	936
Db	279	SerAspProLysLeuIleArgMetAsnTyrLeuIysThrTrpPheValIleAspLeuLeu	298
QY	937	GCAGCGCTGCCCTTTGACCTGCTACATCGCTTCAAG-----GTCAACGTG	981
Db	299	SerCysLeuProTyrAspIleIleAsnAlaPheGluAsnValAspGluGlyIleSerSer	318
QY	982	TACTTCGGGGCCCATCTGCTGAGACGGTGGCGCTGCTGGCGCTGCTGGCTGCTCCG	1041
Db	319	LeuPheSerSer-----LeuIysValValArgLeuLeuArgLeuGlyArgValAlaArg	336
QY	1042	CGCGTGCAGCGGTACTCGGACGACGCGCGCTGGCTGCACACTCTCTCATGCCGTGTC	1101
Db	337	LysLeuAspHisTyrLeuGluTyrGlyAlaAlaValLeuValLeuValCysValPhe	356
QY	1102	GCCTGCTCGGACGCTGGTGGCTGGCTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGG	1161
Db	357	GlyLeuValAlaHisTyrLeuAlaCysIleTyrTyrSerIleGlyAspTyrGluValIle	376
QY	1162	AGCAGCGAATCCGAGCTGCTGAGATT---GGCTGGCTGCAGAGCTGGCGCGCGACTG	1218
Db	377	AspGluValThrAsnThrIleGlnIleAspSerTrpLeuTyrGlnLeuAlaLeuSerIle	396
QY	1219	GAGACTCCCTACTACTGCTGGTGGCGGAGCCGAGCTGGAGGAAACAGCTCGCGCCAGAGT	1278
Db	397	GlyThrProTyrArgTyr-----AsnThrSerAlaGlyIleTrp	409
QY	1279	GACAACTGCAGCAGCAGCAGCGAGCCAAACGGGAGCGGCTGGAGCTGCTGGGGCGCG	1338
Db	410	Glu-----GlyGlyPro	413
QY	1339	TCGCTGGCAGCGCCTACATCACTCCCTCTACTTCGCACTCAGCAGCCTCACCAGCTG	1398
Db	414	SerLysAspSerLeuTyrValSerSerLeuTyrPheThrMetThrSerLeuThrThrIle	433
QY	1399	GGCTTCGGCAACTGTCGGCCACACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	1458
Db	434	GlyPheGlyAsnIleAlaProThrThrThrAspValGluLysMetPheSerValAlaMetMet	453
QY	1459	CTCACTCGCGCCCTGATGACCGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	1518
Db	454	MetValGlySerLeuLeuTyrAlaThrIlePheGlyAsnValThrThrIlePheGlnGln	473
QY	1519	ATGTACCGCCCGCGCTTTCTGTACACAGCGCGCAGCGCGCAGCTGCGGACTACATCCGC	1578
Db	474	MetTyrAlaAsnThrAsnArgTyrHisGluMetLeuAsnValArgAspPheLeuLys	493
QY	1579	ATCCACCGTATCCCAAGCCCTCAAGCAGCGCATCTCGAGTACTTCCAGCGCCACCTGG	1638
Db	494	LeuTyrGlnValProLysGlyLeuSerGluArgValMetAspTyrIleValSerThrTrp	513
QY	1639	CGCGTGAACATGGCATCGACACCGCGAGCTCTCGACAGCCTCCCTGACGAGCTGGCG	1698
Db	514	SerMetSerLysGlyIleAspThrGluLysValLeuSerIleCysProLysAspMetArg	533
QY	1699	GCAGACTGCCATGCACTGCACAGGAGTCTCTG---CAGCTGCCACTGTTTTCAGGCG	1755
Db	534	AlaAspIleCysValHisLeuAsnArgLysValPheAsnGlnHisProAlaPheGlnLeu	553
QY	1756	CCCAAGCGCGGCTCCCTGCGGCACTGCTCTCTGCGCCCTCGCGCCCTCTGCGACGCG	1815
Db	554	AlaSerAspGlyCysLeuArgAlaLeuAlaValGluPheGlnThrIleHisCysAlaPro	573
QY	1816	GGCAGATCACTCCACCAAGGGATGCGCTGAGGCGCTCTACTTTGCTGCTGCTGGC	1875
Db	574	GlyAspLeuIleTyrHisAlaGlyGluSerValAspAlaLeuCysPheValValSerGly	593
QY	1876	TCCATGAGGTGCTCAAGGGTGGCAGCGCTGCTGCGCATCTTACGGAAGCGGCACTGATC	1935

QY	1174	GAGCTGCTGAGATTGGCTGCGAGAGCTGGCCCGCGCTGAGAGCTCCCTACTAC	:233
Db	399	AlaLeuProAsp---GlyTrpLeuTrpLysLeuSerAsnAspLeuArgGlnHisTyr---	416
QY	1234	CTGGTGGCGGAGGCGACGTGGAGGAAACAGCTCGGCCAGAGTGCACACTGCACAGC	:293
Db	417	-----AsnIleProLeu	420
QY	1294	AGCAGCGAGCCAAACGGACGGGGCTGGAGCTGCTGGGGCGCCCGCTGCGCAGCGCC	:353
Db	421	SerAsnLysThr-----LeuValGlyProSerArgThrSerAla	435
QY	1354	TACATCACTCCCTACTTTCGACTCAGCAGCTCACCAGCTGGCTTCGGCAACGTG	:413
Db	436	TyrIleSerSerLeuTyrThrMetSerCysMetSerThrValGlyPheGlyAsnIle	455
QY	1414	TCGGCAACACGACACCGAGAGATCTTCTCATCTGCACATGCTCATCGCGCGCTG	:473
Db	456	AlaSerAsnThrAspAsnGluIlePheGlyValCysMetMetIleIleSerAlaLeu	475
QY	1474	ATCAGCGCGTGTGTTGGAAACGTGACGGCCATCATCCAGCGCATGTACGCCCGCCG	:533
Db	476	LeuTyrAlaAlaIlePheGlyHisMetThrThrIleIleGlnMetThrSerSerThr	495
QY	1534	TTTCTGTACACAGCGACCGCGACCTGCGGACTATATCCGATCCACCGTATCCC	:593
Db	496	ValArgTyrHisGluMetIleSerAsnValArgGluPheIleIleGlnMetThrSer	515
QY	1594	AGCCCTCAAGCAGCGCATGCTGGAGTACTTCCAGCCACCTGGCGGTGAACATGGC	:653
Db	516	LysGluLeuAlaGluArgValMetAspTyrValValSerThrTrpAlaMetThrLysGly	535
QY	1654	ATCGACACACCGAGCTGTCGAGCGCTCCCTGACGAGTGGCGCGCAGATCGCCATG	:1713
Db	536	IleAspThrAlaLysValLeuGlyTyrCysProLysAspMetLysAlaAspIleCysVal	555
QY	1714	CACCTGCACAGAGGTCCTG---CAGCTGCCACTGTTTGGCGGCGCAGCGCGGTGC	:770
Db	556	HisLeuAsnArgLysValPheAsnGluHisSerCysPheArgLeuAlaSerAspGlyCys	575
QY	1771	CTGGGCGACTGTCTGGCCCTCGCGCGCGCTTCTGCAGCGCGCGGAGTACTCATC	:1830
Db	576	LeuArgSerLeuAlaMetPheLeuGluLeuAsnHisAlaLaProGlyAspLeuLeuTyr	595
QY	1831	CACCAAGCGATGCTCGCGAGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	:1890
Db	596	HisThrGlyLysValAspAlaLeuTrpPheValSerGlySerLeuGluValIle	615
QY	1891	AAGGGTGGCACCGTGTGCGCATCTAGGAGGAGGCGACCTGATCGGCTGTGAGCTGCC	:950
Db	616	GlnAspAspGluValAlaIleLeuGlyLysGlyAspValPheGly-----	631
QY	1951	CGCGGAGCAGGTGGTAAGGCCAAT-----GCCGAGCTGAAG	:1989
Db	632	-----AspGluPheTrpLysAlaAsnGlySerThrGlyGlnSerAlaAlaAsnValArg	649
QY	1990	GGCTGAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	:2049
Db	650	AlaLeuThrTyrSerAspLeuHisMetIleLysLysAspLysLeuMetAspValLeuAsp	669
QY	2050	CTGTACCCCGAGTTTGGCCCGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	:2109
Db	670	PheTyrLysAlaPheAlaAsnSerPheAlaArgAsnMet-----ThrLeuThrTyrAsn	687
QY	2110	CTGGTGTGCGGGAGGCTCTGAGAGGTGGACACCATCTCCCTGAGCGGCGACATACC	:2169
Db	688	Leu-----ThrHisArgMetLysPheArgLys	696
QY	2170	CTTATGTCCAGCTGGAGGAGAGAGACAGATGGGGAGAG-----	:2211
Db	697	ValAlaAspValLysArgGluLysGluLeuAspAlaLysArgLysAsnGluLysLeuThr	716
QY	2212	-----GGCCCC	:2217

RESULT 12

O44164 ID O44164
AC O44164;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)

O44164 PRELIMINARY; PRT; 956 AA.

717 LeuProAsnAspHisProlleArgLysLeuLeuPheArgMetArgGluArgHisGlyPro 736
2218 ACGGTCTCCCGACGCCCA-----GCTGATGAGCCCTCCAGCCCTCGTGTCTCCCTGCTG 2271
737 ArgIlePheProSerProMetPheAlaAsp-----IleGluLysGly 750
2272 TGACCTCTCTATCTCTACGCTGCGAAGCTGTATCCCACTGCAAGACAGCAGCCCGGCT 2331
751 LeuLysLysSerThrGluIleSerArgIleSerSerSerLeuHisSerMetIle----- 767
2332 CGTCTAGGTGGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2391
768 -----AspGluThrGlyGlyGlySerSerTyrValLysSerProArg 782
2392 TCTGTCTCCCGACGCCCTAGAGGGCTACGCTGCCCGCCCATGCGATGGAATGTGCC 2451
783 SerLysProLysArg-----Pro 788
2452 CAGATCTGAGCCCGAGGTGTAGATGTCATTTGAGACGGCTGTGCTCGGACAGCAGC-- 2509
789 ProLeuMetLysArgGlnThrValAsp-----GluAsp-AlaLeuSerArgThrSerTr 806
2510 -----CCAAGTTCTCTTCCGCGTGGGCGAGCTGTGGCCCGGGAATGTAGCAGCAGCC 2562
806 pGlyMetAspLysLysAspArgGluTrpSerSerLeuSerAsn----- 820
2563 TCCCTGTGACAGAGCGGCTGCTCATGTTTCCCATGCGGCCCGAGGAGGAGGAGGAGGAG 2622
821 -----IleLysThrGluMe 825
2623 ACAGACACACTGACAAAGCTTCGCGAGCGG-----TGACAGAGCTGTACAGACAG 2673
825 LysSerLysPheAspIleIleGlyGluArgLeuThrIleIleGluIleAsnSerArg 845
2674 GTGCTGAGATCGGGAAGGAGTGCAGTCACTTCGCGAGGCTGTGAGCTTGTCTCGCG 2733
845 g-LeuAlaLeuLeuGluArgValLeuIleGlyAsnAsnGly----- 858
2734 CCCACAGGAGGAGTCCGTCCTCGCGCATCGGAGAGGCGGCGTCCCGACGAGCAGCACC 2793
859 -----GlyAlaAsnThrProSerThrMetProValGlySerPhe----- 871
2794 TCCGGGTTCTGAGCCCTGT 2853
872 -----SerAlaLeuAsnGluSerGlyAsn-----ArgLeuThrLeuAspAlaAlaP 887
2854 CAGCTGGCTCTGT 2913
887 roValAlaArgSerValSerTrp-----SerGluGlnHisGlnProH 901
2914 ATGSCACCTTGGCGCTGGGTCCCGAGCGTCTCAGAGTCTCCCTCGCTGCGAGCCACA 2973
901 iStrpGlnArgThrSerThrValProProLeuArgGluLeuGluAlaGlyLysTrpGlu- 920
2974 GCTTCTGGACCTCCACTCAGACTCAGAGCCCGCTGCTCAGAGAGCTCTGTCTCTGAG 3033
921 -----ProIleArgGluPro-ThrProAsn 929
3034 CCCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3093
930 ProSerThrSerSerSerArgValProHisIleGlnAsnAspGluAspGlyGluAlaArg 949
3094 CCT 3096
950 Pro 950

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN F16B3.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None.
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018 (1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Kemp K.; Wilson R.;
 RT "The sequence of C. elegans cosmid F16B3.";
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston K.;
 RT "Direct Submission.";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF036695; AAB88348.2; --
 DR PIR; T42394; T42394.
 DR WormPep; F16B3.1; CE24905.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004601; F:peroxidase activity; IEA.
 DR GO; GO:0000155; F:two-component sensor molecule activity; IEA.
 DR GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR GO; GO:0006813; P:potassium ion transport; IEA.
 DR GO; GO:0006979; P:response to oxidative stress; IEA.
 DR GO; GO:0000160; P:two-component signal transduction system (p. .; IEA.
 DR InterPro; IPR000595; cNMP binding.
 DR InterPro; IPR003967; Evg channel.
 DR InterPro; IPR005821; Ion_channel.
 DR InterPro; IPR001622; K+channel pore.
 DR InterPro; IPR001610; PAC.
 DR InterPro; IPR000700; PAS-assoc C.
 DR InterPro; IPR000014; PAS domain.
 DR InterPro; IPR002016; Peroxidase.
 DR Pfam; PF00027; cNMP_binding; 1.
 DR Pfam; PF00520; ion_trans; 1.
 DR Pfam; PF00785; PAC; 1.
 DR PRINTS; PR01470; ERGCHANNEL.
 DR SMART; SM00100; cNMP; 1.
 DR SMART; SM00086; PAC; 1.
 DR SMART; SM00091; PAS; 1.
 DR TIGRfams; TIGR00229; sensory_box; 1.
 DR PROSITE; PS50042; cNMP_BINDING_3; 1.
 DR PROSITE; PS50113; PAC; 1.
 DR PROSITE; PS50112; PAS; 1.
 DR PROSITE; PS00435; PEROXIDASE_1; 1.
 KW Hypothetical protein; Ionic channel; Transmembrane.
 SQ SEQUENCE 956 AA; 108090 MW; E998B7F2128054A8 CRC64;

 Alignment Scores:
 Pred. No.: 4.11e-63 Length: 956
 Score: 1259.50 Matches: 329
 Percent Similarity: 48.24% Conservative: 179
 Best Local Similarity: 31.24% Mismatches: 342
 Query Match: 20.68% Indels: 203
 DB: 5 Gaps: 35

 US-09-965-830-1_COPY_6_3257 (1-3252) x 044164 (1-956)
 QY 1 ATGCGG---GCCATGCGGGGCTCTCTGGCGCTCAGAACACCTTCTCTGGACACCATCGCT 57

1 MetProValGlyLysArgGlyLeuValAlaProGlnAsnThrPheLeuGluAsnValIle 20
 58 AGCGCTTCGACGGCAGCAGTAACCTCGTGGCAACGCCAGGTGGGGGCTC 117
 21 ArgArgCysAsnAlaAspThrSerPheIleLeuAlaAsnAlaGlnValValAsp--- 39
 118 TTCGGGTGGTCTACTGCTGATGGCTTCTGTGACCTCAGCGGCTTCTCCGGGCTGAG 177
 40 TyrProIleValTyrCysAsnAspGlyPheSerLysLeuValGlyTyrThrArgAlaGlu 59
 178 GTCATGACGCGGGCTGTGCTCTCTCTTTATGGCGCAGACACCATGAGCTCGTC 237
 60 IleMetGlnLysProCysSerLeuAlaPheMetHisGlyGluHisGlyGluValGlySer 79
 238 CGCCAACAGATCCGCAAGCGCTCGACGAGCAGCAGAGTTCACAGCTGAGCTGTCCTG 297
 80 LeuGlnLysMetGlnGluAlaLeuGluAsnAlaArgThrGluGlnAlaGluIleGlyLeu 99
 298 TACCGGAGAGGGGCTCCGCTTCTGTGCTCTCTGTGATGTATACCATTAAGATGAG 357
 100 CysLysLysAsnLysThrProIleThrLeuValHisLeuAlaProIleLysAsnHis 119
 358 AAAGGGAGGTGGCTCTCTCTAGTCTCTCACAGGACATCAGCGAAACCAAG----- 411
 120 LysAspAlaValLeuTyrLeuCysGlnPheLysAspIleThrProLeuLysGlnPro 139
 412 -----AACCGAGGGGGCCCGACAGATGGAAGGAGACAGAGTGTGGCGCGGCG 459
 140 LeuAspAspGluAsnAsnLysGlyLeuSerArgIleLeuGlnIleAla----- 155
 460 CGATATGGCGGGCAGCATCAAGGCTTCAATGCCAACCGCGCGGCGGAGCGGCGCGCTG 519
 156 ArgIleAlaLysSerLysGlnGln---PheAsnGlnIleGluThrLysAsp----- 171
 520 CTCTACCACCTGTCCGGGCACCTCGAAGACAGCGCCAGGCGGACAGCAAGCTCAATAAG 579
 172 -----LeuHisLysSerPro---GlyAsnThrSerSerAsn--- 182
 580 GGGGTGTTGGGGAGAACCAAC-----TTGCCTGAGTACAAAGTAGGCC 624
 183 -----PheAsnGlnValMetAsnLeuGlyGlyAspMetLeuProGlnTyrArgGlnGlu 200
 625 GCCATCCGGAAGTCCGCTTCATCTCTGTGACGTGGGGCAGCAGACCATCTGGAT 684
 201 ThrProLysThrSerProHisIleIleLeuHisTyrSerSerPheLysThrIleTyrAsp 220
 685 GGCTTCATCTCTCGCGCACCTCTATGTGCTGCTCACTGTGCTCTACAGCGTGTGT--- 741
 221 TrpSerIleLeuAlaLeuThrPheTyrThrAlaPheMetValProPheAsnIleAlaPhe 240
 742 -----GTGACACAGCAGCGGAGCCAGTGCAGCGCCGCG 774
 241 LysAsnSerLeuArgProPheTyrLeuIleSerSerArgGluAsnProGlyGlyGlyIle 260
 775 GGCGCGCGCGCTGTGACCTGGCGGTGGAGTCTCTTCATCTCATCTGACATTTGCTGT 834
 261 AspSerValAlaLeuMetAspSerIleValAspValIlePhePheAlaAspIleLeuLeu 280
 835 AATTTTCGTACCATTCGTGTCCAGTCCGCGCAGGTGTGTTGTCGCCCAAGTCCATT 894
 281 AsnPheHisThrThrPheValGlyProGlyGlyGluValIleGluProSerValIle 300
 895 TGCCTCCATCAGTACACCTGTTCTCTGCTGATGTCATCGCAGCGCTGCCCTTTGAC 954
 301 ArgGlnAsnTyrPheLysSerTrpPheLeuIleAspLeuLeuSerCysLeuProTyrAsp 320
 955 CTGCTACATGCCTTCAAG-----GTCAACGTGTACTTCGGGGGCCATCTG 999
 321 IlePheTyrMetPheLysArgAspGluArgIleGlySerLeuPheSerAla----- 338
 1000 CTGAAGACGTGCGCTGTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1059

638	IleCysValMetLeuIleGlySerLeuMetTyrAlaSerIlePheGlyAsnValSerAla	657
1507	ATCATCCAGCGCATGACGCCCGCGCTTCTACACAGCCGACGGCGGACCTGGCG	1566
658	IleIleGlnArgLeuTyrSerGlyThrAlaArgTyrHisMetGlnMetLeuArgValLys	677
1567	GACTACATCCGATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGCTGGAGTACTTC	1626
678	GluPheIleArgPheHisGlnIleProAsnProLeuArgGlnArgLeuGluGlnTyrPhe	697
1627	CAGGCCACCTGGGCGGTGAACATGTCATCGACACCGAGCTGCTGCAGAGCCTC	1683
698	GlnHisAlaTrpThrTyrThrAsnGlyIleAspMetAsnMetValCysMetSerVal	716

Search completed: September 1, 2004, 15:52:08
Job time : 462 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 1, 2004, 15:01:21; Search time 59 Seconds

(without alignments)

5740.073 Million cell updates/sec

Title: US-09-965-830-1_COPY_6_3257

Perfect score: 6089

Sequence: 1 atgcgggcacatcg9gggctc.....aagaagccacagggctctga 3252

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 283362

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model
-Q=/cgn2 1/USPTO spool p/US09965830/runat_01092004.160109.4795/app query.fasta_1.3399
-DB=SwissProt 42 -QFMT=fastan -SUFFIX=isp -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MAIRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09965830 @CGN 1 1 88 @runat_01092004.160109.4795 -NCPU=6 -ICPU=3
-NO_MMAP -LARGQUERY -NEG SCORE=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5704	93.7	1083	1 KCH3_HUMAN	Q9uld8 homo sapien
2	5428	89.1	1087	1 KCH3_RAT	O89047 rattus norv
3	5416	88.9	1087	1 KCH3_MOUSE	Q9wvj0 mus musculu
4	2529.5	41.5	1107	1 KCH8_HUMAN	Q96l42 homo sapien
5	2515	41.3	1102	1 KCH8_RAT	Q9gws8 rattus norv
6	2461.5	40.4	1017	1 KCH4_HUMAN	Q9uq05 homo sapien
7	2447.5	40.2	1017	1 KCH4_RAT	Q9rlt9 rattus norv
8	1778.5	29.2	876	1 KCH8_MOUSE	P59111 mus musculu
9	1551	25.5	1158	1 KCH2_CANFA	Q8t823 canis famil
10	1551	25.5	1159	1 KCH2_HUMAN	Q12809 homo sapien
11	1547	25.4	1162	1 KCH2_MOUSE	O35219 mus musculu
12	1537.5	25.3	1163	1 KCH2_RAT	O08962 rattus norv
13	1536	25.2	1161	1 KCH2_RABIT	Q8wny2 oryctolagus
14	1509.5	24.8	994	1 KCH6_HUMAN	Q9h252 homo sapien
15	1475	24.2	950	1 KCH6_RAT	O54853 rattus norv
16	1400.5	23.0	1195	1 KCH7_MOUSE	Q9er47 mus musculu
17	1395.5	22.9	1195	1 KCH7_RAT	O54852 rattus norv
18	1390	22.8	1174	1 CIKE_DROME	Q02280 drosophila

19	1384.5	22.7	1196	1 KCH7_HUMAN	Q9ns40 homo sapien
20	1380.5	22.7	962	1 KCH1_RAT	O63472 rattus norv
21	1371.5	22.5	989	1 KCH1_MOUSE	O60603 mus musculu
22	1367.5	22.5	987	1 KCH1_BOVIN	O18965 bos taurus
23	1358.5	22.3	989	1 KCH1_HUMAN	O95259 homo sapien
24	1337.5	22.0	988	1 KCH5_RAT	O9epi9 rattus norv
25	1332.5	21.9	988	1 KCH5_HUMAN	O8ncm2 homo sapien
26	1035.5	17.0	526	1 KCH2_CHICK	O9p84 gallus gall
27	580	9.5	1186	1 HCN4_MOUSE	O70507 mus musculu
28	577	9.5	1198	1 HCN4_RAT	O9jka7 rattus norv
29	566	9.3	1203	1 HCN4_HUMAN	O9jka7 rattus norv
30	562.5	9.2	1175	1 HCN4_RABIT	O9t66 oryctolagus
31	527	8.7	889	1 HCN2_HUMAN	O9ul51 homo sapien
32	513	8.4	863	1 HCN2_MOUSE	O88703 mus musculu
33	496	8.1	834	1 HCN2_RAT	O9jka8 rattus norv
34	495	8.1	910	1 HCN1_MOUSE	O88704 mus musculu
35	487	8.0	779	1 HCN3_MOUSE	O88705 mus musculu
36	486	8.0	822	1 HCN1_RABIT	O9mzsl oryctolagus
37	485	8.0	910	1 HCN1_RAT	Q9jkb0 rattus norv
38	484.5	8.0	780	1 HCN3_RAT	O9jka8 rattus norv
39	480	7.9	890	1 HCN1_HUMAN	O60741 homo sapien
40	475.5	7.8	774	1 HCN3_HUMAN	O9pl23 homo sapien
41	439	7.2	706	1 HCN3_BOVIN	O29441 bos taurus
42	429.5	7.1	683	1 CNG1_RAT	O62827 r comp-gate
43	424.5	7.0	694	1 CNG3_HUMAN	Q16281 homo sapien
44	423.5	7.0	735	1 CNG1_CHICK	Q90805 gallus gall
45	422.5	6.9	631	1 CNG3_MOUSE	Q9jjz8 mus musculu

ALIGNMENTS

RESULT 1

KCH3_HUMAN					
ID	KCH3_HUMAN	STANDARD;	PRT;	1083 AA.	
AC	Q9ULD8; Q9UQ06;				
DT	28-FEB-2003 (Rel. 41, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last sequence update)				
DT	15-MAR-2004 (Rel. 43, Last annotation update)				
DE	Potassium voltage-gated channel subfamily H member 3 (Ether-a-go-go-like potassium channel 2) (ELK channel 2) (ELK2) (Brain-specific eag-like channel 1) (BEC1).				
GN	KCNH3 OR KIAA1282.				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RC	SEQUENCE FROM N.A.				
RP	TISSUE=Brain;				
RX	MEDLINE=99386988; PubMed=10455180;				
RA	Miyake A., Mochizuki S., Yokoi H., Kohda M., Furuichi K.;				
RT	"New ether-a-go-go K+ channel family members localized in human telencephalon.";				
RL	J. Biol. Chem. 274:25018-25025(1999).				
[2]					
RN	[2]				
RC	SEQUENCE FROM N.A.				
RP	TISSUE=Brain;				
RX	MEDLINE=20039619; PubMed=10574462;				
RA	Nagase T., Ishikawa K.-I., Kikuno R., Hirose M., Nomura N., Ohara O.;				
RT	"Prediction of the coding sequences of unidentified human genes. XV. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";				
RL	DNA Res. 6:337-345(1999).				
CC	-I- FUNCTION: Pore-forming (alpha) subunit of voltage-gated potassium channel. Elicits an outward current with fast inactivation.				
CC	Channel properties may be modulated by cAMP and subunit assembly.				
CC	-I- SUBUNIT: The potassium channel is probably composed of a homo- or heterotetrameric complex of pore-forming alpha subunits that can associate with modulating beta subunits.				
CC	-I- SUBCELLULAR LOCATION: Integral membrane protein.				
CC	-I- TISSUE SPECIFICITY: Detected only in brain, in particular in the telencephalon. Detected in the cerebral cortex, occipital pole,				

CC frontal and temporal lobe, putamen, amygdala, hippocampus and
 CC caudate nucleus.
 CC -!- DOMAIN: The segment S4 is probably the voltage-sensor and is
 CC characterized by a series of positively charged amino acids at
 CC every third position.
 CC -!- SIMILARITY: Belongs to the potassium channel family. H (Eag)
 CC subfamily.
 CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
 CC -!- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.
 CC -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL; AB022696; BAA83590.1; -;
 CC EMBL; AB033108; BAA86596.1; ALT_INIT.
 CC Genew; HGNC:6252; KCHN3.
 CC MIM; 604527; -;
 CC GO; GO:0016021; F:integral to membrane; NAS.
 CC GO; GO:0005249; F:voltage-gated potassium channel activity; TAS.
 CC GO; GO:0006813; P:potassium ion transport; TAS.
 CC InterPro; IPR000595; cNMP binding.
 CC InterPro; IPR003967; Erg_channel.
 CC InterPro; IPR005821; Ion_trans.
 CC InterPro; IPR001622; K+channel_pore.
 CC InterPro; IPR005820; M+channel_nlg.
 CC InterPro; IPR001610; PAC.
 CC InterPro; IPR000700; PAS-assoc_C.
 CC InterPro; IPR000014; PAS_domain.
 CC Pfam; PF00027; cNMP_binding; 1.
 CC Pfam; PF00520; ion_trans; 1.
 CC Pfam; PF00785; PAC; 1.
 CC PRINTS; PR01470; ERGCHANNEL.
 CC SMART; SM00100; cNMP; 1.
 CC SMART; SM00086; PAC; 1.
 CC TIGRfams; TIGR00229; sensory_box; 1.
 CC PROSITE; PS00888; cNMP_BINDING_1; FALSE_NEG.
 CC PROSITE; PS00889; cNMP_BINDING_2; FALSE_NEG.
 CC PROSITE; PS0042; cNMP_BINDING_3; 1.
 CC PROSITE; PS50112; PAS; 1.
 CC PROSITE; PS50113; PAC; 1.
 CC Transprot; Ion transport; Ionic channel; Voltage-gated channel;
 CC Potassium channel; Potassium; Potassium transport; Transmembrane;
 CC Glycoprotein; Multigene family.
 CC FT DOMAIN 1 228 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 229 249 SEGMENT S1 (POTENTIAL).
 CC FT TRANSMEM 260 280 SEGMENT S2 (POTENTIAL).
 CC FT DOMAIN 281 302 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 303 323 SEGMENT S3 (POTENTIAL).
 CC FT TRANSMEM 332 352 SEGMENT S4 (POTENTIAL).
 CC FT DOMAIN 353 361 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 362 382 SEGMENT S5 (POTENTIAL).
 CC FT DOMAIN 454 474 SEGMENT H5 (PORE-FORMING) (POTENTIAL).
 CC FT TRANSMEM 480 500 SEGMENT S6 (POTENTIAL).
 CC FT DOMAIN 501 1083 CYTOPLASMIC (POTENTIAL).
 CC FT DOMAIN 18 90 PAC.
 CC FT DOMAIN 93 145 PRO-RICH.
 CC FT NP_BIND 951 1057 cNMP.
 CC FT CARBOHYD 421 421 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 428 428 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 436 436 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SQ SEQUENCE 1083 AA; 117128 MW; EF35C8968D7418CC CRC64;

Alignment Scores:
 Pred. No.: 1,13e-244 Length: 1083
 Score: 5704.00 Matches: 1083
 Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 93.68% Indels: 0
 DB: 1 Gaps: 0
 US-09-965-830-1_COPY_6_3257 (1-3252) x KCH3_HUMAN (1-1083)
 QY 1 ATGCGCGCCATGCGGGCTCTGCGCTCAGAACACCTTCTGACACCATCGCTAGC 60
 DB 1 MetProAlaMetArgGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20
 QY 61 CGCTTCGACGCGACGACAGTAACCTTCGTGCTGGGCAACGCCAGGTGGCGGGCTCTTC 120
 DB 21 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnValAlaGlyLeuPhe 40
 QY 121 CCGGTGCTTACTGCTCTCATGGCTTCTGTGACCTCACGGGCTTCTCCGGGTGAGTCC 180
 DB 41 ProValValTyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal 60
 QY 181 ATGCGCGGGCTGCTGCTCTCTTCTTCTTATGGGCGACACACAGTGTGAGTCTCGCCG 240
 DB 61 MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArg 80
 QY 241 CAACAGATCCGCAAGGCCCTTGACGACGACCAAGAGTTCAGGCTGAGTGTCTGTATC 300
 DB 81 GlnGlnIleArgLysAlaLeuAspGluHisLysGluPheLysAlaGluLeuIleLeuTyr 100
 QY 301 CGAAGAGCGGGCTCCGCTTCTGCTGCTCTGATGTGATACCCATAAAGATGAGAAA 360
 DB 101 ArgLysSerGlyLeuProPheTrpCysLeuLeuAspValIleProIleLysAsnGluLys 120
 QY 361 GGGGAGGTGCTCTCTTCTTCTTCTTCTCAAGGACATCAGCGAAACCAAGAACCGAGGG 420
 DB 121 GlyGluValAlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGly 140
 QY 421 GGGCGCGACAGATGGAAGAGAGACAGTGTGTGGCGCGCCGATATGCGCGGGCGAGTCC 480
 DB 141 GlyProAspArgTrpLysGluThrGlyGlyArgArgArgTyrGlyArgAlaArgSer 160
 QY 481 AAAGCTTCAATGCAACCGCGCGCGCGCGCTCTTCTTCTTCTTCTTCTTCTTCTTCTT 540
 DB 161 LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis 180
 QY 541 CTGCAGAGCAGCCCAAGGGCAACACAGTCTCAATAGGGGTGTGTTGGGGAGAAACCA 600
 DB 181 LeuGlnLysGlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyGluLysPro 200
 QY 601 AACTTGGCTCAGTACAAAGTAGCCCATCCGGAAGTGGCGCTTCTTCTTCTTCTTCTTCT 660
 DB 201 AsnLeuProGluTyrLysValAlaAlaIleArgLysSerProPheIleLeuLeuHisCys 220
 QY 661 GGGCAGCTGAGAGCCACCTGGGATGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 720
 DB 221 GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal 240
 QY 721 ACTGTGCCCTACAGCTGTGTGAGACAGCAGCGGAGCCAGTGCCTCCCGCGCGCGCG 780
 DB 241 ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro 260
 QY 781 CCCAGCGTCTGTGACCTGGCGCTGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 840
 DB 261 ProSerValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPhe 280
 QY 841 CGTACCACATTCGTCTCCAGTCCGCGCGCGGCTGTTGTTGTTGTTGTTGTTGTTGTTGTT 900
 DB 281 ArgThrThrPheValSerLysSerGlyGlnValValPheAlaProLysSerIleCysLeu 300
 QY 901 CACTACGTCACACCTGGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 960
 DB 301 HisTyrValThrThrTrpPheLeuLeuAspValIleAlaLeuProPheAspLeuLeu 320
 QY 961 CATGCTTCAAGGTCAAGTGTACTTTCGGGGCGCCATCTCTCTGAGACGCTGCGCTGCTG 1020
 DB 321 HisAlaPheLysValAsnValTyrPheGlyAlaHisLeuLeuLysThrValArgLeuLeu 340

QY	1021	CGCTGCTCGGCTGCTTCGGCGCTGGACCGGTACTCGCAGTACAGCGCGGTGGTCTG	1080
Db	341	ArgLeuLeuArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValValLeu	360
QY	1081	ACACTGCTCATGGCGGTGGTTCGGCTGCTCGGCATCGGTGCGCTGCTGTTTAC	1140
Db	361	ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr	380
QY	1141	ATTGGCCAGCGGAGATCGAGAGCAGCAATCCGAGTCCCTGAGATTGGCTGGCTGAG	1200
Db	381	IleGlyGlnArgGluLeuGlnSerSerGlnSerGluLeuProGluLeuGlyTrpLeuGln	400
QY	1201	GAGTGGCCCGCGCATGGAGATCTCCCTACTCTGCTGGCGCGGAGCGCAGCTGGAGG	1260
Db	401	GluLeuAlaArgArgLeuGluThrProTyrTyrLeuValGlyArgArgProAlaGlyGly	420
QY	1261	AACAGTCCGGCCAGAGTCAACATGTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	1320
Db	421	AsnSerSerGlyGlnSerAspAsnCysSerSerSerSerGluAlaAsnGlyThrGlyLeu	440
QY	1321	GAGCTGCTGGGGCGCGCTGCGCAGCGCTCATCACTCCCTCTACTCTGCTGCTGCTG	1380
Db	441	GluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeu	460
QY	1381	AGCAGCTCACAGCGTGGGCTTCGGCAACGTGTCCGCCAACACAGCAGCAGCAGCAGC	1440
Db	461	SerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGluLeuVal	480
QY	1441	TTCCTCATCTGCACCATGCTCATCGCGCGCTGATGACGCGGTGGTTCGGGAACGTG	1500
Db	481	PheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValValPheGlyAsnVal	500
QY	1501	ACGGCATCATCCAGCATGATACCGCGCGCTTCTCTACCAAGCGCGCAGCGCGCAG	1560
Db	501	ThrAlaIleIleGlnArgMetTyrAlaArgArgPheLeuTyrHisSerArgThrArgAsp	520
QY	1561	CTGGCGACTACATCCGCATCCACGTATCCCAAGCGCGCTTCTCTACCAAGCGCGCAG	1620
Db	521	LeuArgAspTyrIleArgIleHisArgIleProLysProLeuLysGlnArgMetLeuGlu	540
QY	1621	TACTTCAGGCGCCTGGCGGTGAACATGTCATCGACACACCGAGCTGTCGAGAGC	1680
Db	541	TyrPheGlnAlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeuGlnSer	560
QY	1681	CTCCCTGACGAGCTCGCGCAGACATCCCATGACCTGCACAGGAGGTCTCGAGCTG	1740
Db	561	LeuProAspGluLeuArgAlaAspIleAlaMetHisLeuHisLysGluValLeuGlnLeu	580
QY	1741	CCACTGTTTGAGCGCGCAGCGCGGTGCTGCGGGCACTGTCTCTGCGCTGCGGCCC	1800
Db	581	ProLeuPheGluAlaAlaSerArgGlyCysLeuArgAlaLeuSerLeuAlaLeuArgPro	600
QY	1801	GCCTTCGACGCGCGCGAGTACTCATCCACAGCGGATGCGCTGCGAGCGCTCTAC	1860
Db	601	AlaPheCysThrProGlyGlyLeuIleHisGlnGlyAspAlaLeuGlnAlaLeuTyr	620
QY	1861	TTTCTGCTGCTGCTCCATGAGGTGCTCAAGGTGCGCCGCTGCGCTGCGCTGCGCTG	1920
Db	621	PheValCysSerGlySerMetGluValLeuLysGlyGlyThrValLeuAlaIleLeuGly	640
QY	1921	AAGGGCACTGATCGGCTGTGAGTGTCCCGCGGGAGCAGGTGGTAAAGGCCAATGCC	1980
Db	641	LysGlyAspLeuIleGlyCysGluLeuProArgArgGluGlnValValLysAlaAsnAla	660
QY	1981	GACGTGAGGGCTGAGTACTGCTGCTGAGTGTCTGAGTGTCTGAGTGTCTGAGTGTCT	2040
Db	661	AspValLysGlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGlyLeuHisAsp	680
QY	2041	AGCTTCGCTGTACCCGAGTTTGGCGGCTTCAGTCTGCTGCGCTCCGAGGGGAGCTC	2100
Db	681	SerLeuAlaLeuTyrProGluPheAlaProArgPheSerArgGlyLeuArgGlyGluLeu	700

QY	2101	AGCTACAACTCGGTGCTGGGGAGGCTCTGCAGAGGTGACACACAGCTCCCTGAGCGGC	2160
Db	701	SerTyrAsnLeuGlyAlaGlyGlySerAlaGluValAspThrSerSerLeuSerGly	720
QY	2161	GACAAATACCTTATGTCCACGCTGGAGGAGAGAGACAGATGGGAGCAGGCGCCACG	2220
Db	721	AspAsnThrLeuMetSerThrLeuGluGluLysGluThrAspGlyGluGlnGlyProThr	740
QY	2221	GTCTCCCGAGCCCGAGCTGATGAGCCCTCCAGCCCTGCTGTCTGCTGCTGCTGCTGCT	2280
Db	741	ValSerProAlaProAlaAspGluProSerSerProLeuLeuSerProGlyCysThrSer	760
QY	2281	TCATCTCAGCTGCCAAGCTGTATCCCGACCTCGAACAGCAGCAGCAGCAGCTGTAGGT	2340
Db	761	SerSerSerAlaAlaLysLeuLeuSerProArgArgThrAlaProArgProArgLeuGly	780
QY	2341	GGCAGAGGAGGAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2400
Db	781	GlyArgGlyArgProGlyArgAlaGlyAlaLeuLysAlaGluAlaGlyProSerAlaPro	800
QY	2401	CCAGCGGCGCTAGAGGGGCTACGGCTGCGCCCGCATGCGCATGGAATGTGCCCGCATCTG	2460
Db	801	ProArgAlaLeuGluGlyLeuArgLeuProProMetProTrpAsnValProProAspLeu	820
QY	2461	AGCCCCAGGAGTGTAGTGGCATTCGAAGCAGCTGTGGCTCGGACCGAGCCCAAGTCTCT	2520
Db	821	SerProArgValValAspGlyIleGluAspGlyCysGlySerAspGlnProLysPheSer	840
QY	2521	TTCCCGCTGGGCGAGCTGGCGCGGAAATGTAGCAGCAGCCCTCCCTCGACACAGAGC	2580
Db	841	PheArgValGlyGlnSerGlyProGluCysSerSerProSerProGlyProGluSer	860
QY	2581	GGCTGTCTACTGTTCCTCCATGGGCGCCAGCGAGGCAAGAAACACACACACTGGACAG	2640
Db	861	GlyLeuLeuThrValProHisGlyProSerGluAlaArgAsnThrAspThrLeuAspLys	880
QY	2641	CTTCGGAGGCGGTACAGAGCTGTACAGCAGGTGTGTCAGATCGGAGGAGCTGAG	2700
Db	881	LeuArgGlnAlaValThrGluLeuSerGluGlnValLeuGlnMetArgGluGlyLeuGln	900
QY	2701	TCACTTCGCCAGGCTGTGAGCTGTCTGCGCGCCACAGGAGGCTCCGTCCTCGG	2760
Db	901	SerLeuArgGlnAlaValGlnLeuValLeuAlaProHisArgGluGlyProCysProArg	920
QY	2761	GCATCGGAGAGGCGCGTGCAGCCAGCACCTCCGGGCTTCTGACGCTCTGTGTGTG	2820
Db	921	AlaSerGlyGlyProCysProAlaSerThrSerGlyLeuLeuGlnProLeuCysVal	940
QY	2821	GACACTGGGCGATCTCTACTGCTGCGAGCCCGAGCTGCTGTCTTGTAGTGGGACT	2880
Db	941	AspThrGlyAlaSerSerTyrCysLeuGlnProProAlaGlySerValLeuSerGlyThr	960
QY	2881	TGGCCCGACCTCTCCGCGGCGCTCTCCCTCATGTCAGCCCTCGGCTGGGCTCCCGCA	2940
Db	961	TrpProHisProArgProGlyProProProLeuMetAlaProTrpProTrpGlyProPro	980
QY	2941	CGCTCTCAGAGTCCCTCGCTGCGAGCCAGCACAGCTTCTTGACCTCCACTCAGACTCA	3000
Db	981	AlaSerGlnSerSerProTrpProArgAlaThrAlaPheTrpThrSerThrSerAspSer	1000
QY	3001	GAGCCCGCTCGCTCAGGAGCTGCTGCTGAGCCCGAGCCCGCTGCTGCTGCTGCTGCT	3060
Db	1001	GluProProAlaSerGlyAspLeuCysSerGluProSerThrProAlaSerProProPro	1020
QY	3061	TCTGAGGAGGCGGTAGGACTGGGCGCGCAGAGCCTGTGAGCCAGGCTGAGGCTACCGC	3120
Db	1021	SerGluGluGlyAlaArgThrGlyProAlaGluProValSerGlnAlaGluAlaThrSer	1040
QY	3121	ACTGGAGAGCCCCACAGGCTGAGGGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3180
Db	1041	ThrGlyGluProProProGlySerGlyLeuAlaLeuProTrpAspProHisSerLeu	1060
QY	3181	GAGATGGTGTATTGGCTGCCATGGCTGTGGCACAGTCCAGTGGAGCCCGAGGAGAGGC	3240

-- SIMILARITY: Contains 1 PAS (PRR-ARNT-SIM) dimerization domain.
-- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.

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CC	EMBL; AJ007627; CA007586.1; --
CC	EMBL; AB022697; BAA83591.1; --
CC	EMBL; AF073892; AAC61522.1; --
CC	PIR; T31100; T31100.
CC	InterPro; IPR000595; cNMP binding.
CC	InterPro; IPR003967; Erg channel.
CC	InterPro; IPR005821; Ion trans.
CC	InterPro; IPR001622; K+channel_pore.
CC	InterPro; IPR005820; M+channel_nlg.
CC	InterPro; IPR001610; PAC.
CC	InterPro; IPR000700; PAS-assoc C.
CC	InterPro; IPR000014; PAS domain.
CC	Pfam; PF00027; cNMP_binding; 1.
CC	Pfam; PF00520; ion_trans; 1.
CC	Pfam; PF00785; PAC; 1.
CC	PRINTS; PR01470; ERGCHANNEL.
CC	SMART; SM00100; cNMP; 1.
CC	SMART; SM00086; PAC; 1.
CC	SMART; SM00091; PAS; 1.
CC	TIGRFAMS; TIGR00229; sensory_box; 1.
CC	PROSITE; PS00888; cNMP_BINDING_1; FALSE_NEG.
CC	PROSITE; PS00889; cNMP_BINDING_2; FALSE_NEG.
CC	PROSITE; PS00442; cNMP_BINDING_3; 1.
CC	PROSITE; PS01112; PAS; 1.
CC	PROSITE; PS01113; PAC; 1.

KW Transport; Ion transport; Ionic channel; Voltage-gated channel;
KW Potassium channel; Potassium; Potassium transport; Transmembrane;
KW Glycoprotein; Multigene family.

KW	DOMAIN	1	228	CYTOPLASMIC (POTENTIAL).
FT	FT	229	249	SEGMENT S1 (POTENTIAL).
FT	TRANSMEM	260	280	SEGMENT S2 (POTENTIAL).
FT	DOMAIN	281	302	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	303	323	SEGMENT S3 (POTENTIAL).
FT	TRANSMEM	332	352	SEGMENT S4 (POTENTIAL).
FT	DOMAIN	353	361	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	362	382	SEGMENT S5 (POTENTIAL).
FT	DOMAIN	457	477	SEGMENT H5 (PORE-FORMING) (POTENTIAL).
FT	TRANSMEM	483	503	SEGMENT S6 (POTENTIAL).
FT	DOMAIN	504	1087	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	18	90	PAS.
FT	DOMAIN	93	145	PRO-RICH.
FT	DOMAIN	954	1061	cNMP.
FT	NP_BIND	585	700	.
FT	CARBOHYD	421	421	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	428	428	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	439	439	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	1087 AA;	117579 MW;	16B5AFFC3B0A405B CRC64;

Alignment Scores:
Pred. No.: 1.66e-232 Length: 1087
Score: 5428.00 Matches: 1039
Percent Similarity: 96.60% Conservative: 11
Best Local Similarity: 95.58% Mismatches: 33
Query Match: 89.14% Indels: 4
DB: 1 Gaps: 2

US-09-965-830-1_COPY_6_3257 (1-3252) x KCH3_RAT (1-1087)

Oy 1 ATGCCGGCATCGCGGCCTCTGTGCGCTCAGAACACTTCCTGGACACCATCGCTAGC 60
|||
Db 1 MetProAlaMetArgGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20
|||

Db 1061 GluMetValLeuIleGlyCysHisGlySerGlyThrValGlnTrpThrGlnGluGly :080
QY 3241 ACAGGGGTC 3249
Db 1081 ThrGlyVal 1083
RESULT 2
KCH3 RAT
ID KCH3 RAT STANDARD; PRT; 1087 AA.
AC 089047;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Potassium voltage-gated channel subfamily H member 3 (Ether-a-go-go-
DE like potassium channel 2) (ELK channel 2) (rElk2) (Brain-specific eag-
DE like channel 1) (BEC1).
DE KCNH3 OR ELK2.
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain cortex;
RX MEDLINE=99043952; PubMed=9824707;
RA Engeland B., Neu A., Ludwig J., Koepfer J., Pongs O.;
RT "Cloning and functional expression of rat ether-a-go-go-like K+
RT channel genes.";
RL J. Physiol. (Lond) 513:647-654 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99386988; PubMed=10455180;
RA Miyake A., Mochizuki S., Yokoi H., Kohda M., Furuichi K.;
RT "New ether-a-go-go K+ channel family members localized in human
RT telencephalon.";
RL J. Biol. Chem. 274:25018-25025 (1999).
RN [3]
RP SEQUENCE OF 120-273 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98382545; PubMed=9714851;
RA Shi W., Wang H.-S., Pan Z., Wymore R.S., Cohen I.S., McKinnon D.,
RA Dixon J.E.;
RT "Cloning of a mammalian elk potassium channel gene and EAG mRNA
RT distribution in rat sympathetic ganglia.";
RL J. Physiol. (Lond) 511:675-682 (1998).
RN [4]
RP TISSUE SPECIFICITY.
RX MEDLINE=20163472; PubMed=10718922;
RA Wulfsen I., Hauber H.P., Schiemann D., Bauer C.K., Schwarz J.R.;
RT "Expression of mRNA for voltage-dependent and inward-rectifying K
RT channels in GH3/B6 cells and rat pituitary.";
RL J. Neuroendocrinol. 12:263-272 (2000).
CC -!- FUNCTION: Pore-forming (alpha) subunit of voltage-gated potassium
CC channel. Elicits an outward current with fast inactivation.
CC Channel properties may be modulated by cAMP and subunit assembly.
CC -!- SUBUNIT: The potassium channel is probably composed of a homo- or
CC heterotetrameric complex of pore-forming alpha subunits that can
CC associate with modulating beta subunits.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Highly expressed in adult and embryonic brain,
CC in particular in cerebellum, brain stem, hippocampus, cortex and
CC striatum. Detected at slightly lower levels in heart, spinal cord,
CC olfactory bulb, pituitary and medulla. In the hippocampus
CC expression is strongest in the pyramidal cell body layers of the
CC dentate gyrus. Also found in pituitary.
CC -!- DOMAIN: The segment S4 is probably the voltage-sensor and is
CC characterized by a series of positively charged amino acids at
CC every third position.
CC -!- SIMILARITY: Belongs to the potassium channel family. H (Eag)
CC subfamily.
CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.

QY 61 CGCTTCGACGGGACGACAGTAACTCTGCTGGGCAACGCCAGGTGGCGGCTCTTC 120
Db 21 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnValAlaGlyLeuPhe 40
QY 121 CCCTGCTCTACTGCTCTGATGCTCTGTGACCTCACGGCTTCTCCCGGCTGAGGTC 180
Db 41 ProValValTyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal 60
QY 181 ATGACGGGGGCTGTGCTCTCTCTCTCTTTATGGCCAGACACCAAGTGTGAGCTGCTCCG 240
Db 61 MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGlnLeuValArg 80
QY 241 CAACAGATCCGCAAGCCCTGGACAGCACAAGAGCTTCAAGGCTGAGCTGATCTCTGTAC 300
Db 81 GlnGlnIleArgGlyAlaLeuAspGluHisGlyPheLysAlaGluLeuIleLeuTyr 100
QY 301 CGAAGAGCGGCTCCCGTCTGCTGCTCTCTCTGATGTATATCCCAATAAGATGAGAAA 360
Db 101 ArgLysSerGlyLeuProPheTrpCysLeuLeuAspValIleProIleLysAsnGluLys 120
QY 361 GGGAGGTGGCT 420
Db 121 GlyGluValAlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGly 140
QY 421 GSCCCGACAGATGAAGAGACAGGTGTGGCCGCGCCGATATGGCCGCGCACGATCC 480
Db 141 GlyProAspAsnTrpLysGluArgGlyGlyArgArgGlyArgGlyArgGlyArgGly 160
QY 481 AAGGCTTCAATGCCCAACCGCGGCGGAGCCGCGGCTCTCTCTCTCTCTCTCTCTCTCT 540
Db 161 LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis 180
QY 541 CTGCAGAAGACGCCAAGCAAGCACAGCTCAATTAAGGGGTGTGGGAGAGAAACA 600
Db 181 LeuGlnLysGlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyGlnLysPro 200
QY 601 AACTGCTCTGAGTACAAAGTAGCCGCATCCGGAAGTCGCCCTTCTCTCTCTCTCTCTCT 660
Db 201 AsnLeuProGluTyrLysValAlaAlaIleArgLysSerProPheIleLeuHisCys 220
QY 661 GGGCACTGAGAGCCACCTGGGATGGCTTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
Db 221 GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal 240
QY 721 ACTGTGCCCTACAGCGTGTGTGAGCACAGCAGCGGAGCCAGTCCGCGCCGCGCGCG 780
Db 241 ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro 260
QY 781 CCCAGCTCTGTGACCTGGCGGTGAGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
Db 261 ProSerValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPhe 280
QY 841 CGTACCACTCTGTCTCAAGTCGGCGGAGGTGTGGTTCGCCCAAGTCTCATTTGCTC 900
Db 281 ArgThrThrPheValSerLysSerGlyGlnValPheAlaProLysSerIleCysLeu 300
QY 901 CACTACGTCAACACCTGTTCTCTGTGATGTCATCGCAGCGCTGCCCTTTGACTGCTGTA 960
Db 301 HisTyrValThrTrpPheLeuLeuAspValIleAlaLeuProPheAspLeuLeu 320
QY 961 CATGCCCTCAAGTCAACGTGTACTTCGGGCCCATCTGTGGAAGCGGTGCGCTGTGCT 1020
Db 321 HisAlaPheLysValAsnValTyrValGlyAlaHisLeuLeuLysThrValArgLeuLeu 340
QY 1021 CGCCTGTGCGCGCTCTCGCGCTGGACCGGTACTCTCGAGTACAGCGCGCTGGTGTG 1080
Db 341 ArgLeuLeuArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValValLeu 360
QY 1081 ACATGCTCATGGCGGTGTTCCGCTCTCTCGCGCACTGGGTGCGCTGCTGCTGCTTTTAC 1140
Db 361 ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr 380
QY 1141 ATGGCCAGCGGAGATCGAGAGCAGCGAATTCGAGCTGCTGAGATTGGCTGCTGCAG 1200

Db 381 IleGlyGlnGlnIleGluAsnSerGluSerGluLeuProGluIleGlyTrpLeuGln 400
QY 1201 GAGCTGCCCGCCGACATGGAGACTCCCTACTACTCTGTGGCGCGGAGCCAGCTGAGGG 1260
Db 401 GluLeuAlaArgLeuGluThrProTyrTyrLeuValSerArgSerProAspGlyGly 420
QY 1261 AACAGCTCCGGCCAGAGTGCACAACTGCAGAGCAGC-----AGCGAGGCCAACGGG 1311
Db 421 AsnSerSerGlyGlnSerGluAsnCysSerSerSerGlyGlyGlySerGluAlaAsnGly 440
QY 1312 ACGGGCTCGAGCTGTGGCGCGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 1371
Db 441 ThrGlyLeuGluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyr 460
QY 1372 TTCGCACTCAGCAGCCTCAACGCGTGGCTTTCGCAACGTGTCTGTCTGTCTGTCTGTCT 1431
Db 461 PheAlaLeuSerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThr 480
QY 1432 GAGAAGATCTTCTCCATCTGCACCATGCTCATCGCGCGCTGTATGCACCGGTGTGT 1491
Db 481 GluLysIlePheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValPhe 500
QY 1492 GGGAACTGACCGCCATCATCCAGCGCATGTAGCGCGCGCTTCTGTCTGTCTGTCTGTCT 1551
Db 501 GlyAsnValThrAlaIleIleGlnArgMetTyrAlaArgArgPheLeuTyrHisSerArg 520
QY 1552 ACGCGCGACTTCCGCGACTACATCCGCATCCACCGCTATCTCCCAAGCCCTCAAGAGCGC 1611
Db 521 ThrArgAspLeuArgAspTyrIleArgIleHisArgIleProLysProLeuLysGlnArg 540
QY 1612 ATGCTGGAGTACTTCCAGGCCACCTGGCGGTGAAACAATGGCATCGACACCCAGCTG 1671
Db 541 MetLeuGluTyrPheGlnAlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeu 560
QY 1672 CTGCAGAGCCTCCCTGACGAGCTGCGCGCAGACATCGCCATCGCCTCTGTCTGTCTGTCT 1731
Db 561 LeuGlnSerLeuProAspGluLeuArgAlaAspIleAlaMetHisLeuHisGluVal 580
QY 1732 CTGCAGCTGCCACTGTTTGTAGCGCGCAGCGCGCTGCTGCGGGCACTGTCTCTGGCC 1791
Db 581 LeuGlnLeuProLeuPheGluAlaAlaSerArgGlyCysLeuArgAlaLeuSerLeuAla 600
QY 1792 CTGGCGCGCGCTTCTGCACCGCGCGCGAGTACTTATCCACCAAGCGATGCCCTGCAG 1851
Db 601 LeuArgProAlaPheCysThrProGlyGluTyrLeuIleHisGlnGlyAspAlaLeuGln 620
QY 1852 GCCCTCTACTTGTCTGCTCTGGCTCCATGGAGGTGCTCAAGGTGGCACCGTGTCTGCC 1911
Db 621 AlaLeuTyrPheValCysSerGlySerMetGluValLeuLysGlyGlyThrValLeuAla 640
QY 1912 ATCTAGGGAAGGCGACCTGATCGGCTGTGAGCTGCGCGCGCGGAGCAGGTGTAAG 1971
Db 641 IleLeuGlyLysGlyAspLeuIleGlyCysGluLeuProGlnArgGluGlnValValLys 660
QY 1972 GCCAATCCGACGTGAAGGGCTGACGTACTGCTCTGTGAGTGTCTGTGAGTGGCTGGC 2031
Db 661 AlaAsnAlaAspValLysGlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGly 680
QY 2032 CTGCACGACAGCCTTGGCTGTACCCGAGTTTGGCGCGCTTCACTGTGGCTGCGCTCGA 2091
Db 681 LeuHisGluSerLeuAlaLeuTyrProGluPheAlaProArgPheSerArgGlyLeuArg 700
QY 2092 GGGAGCTCAGCTACACCTGGGTGTGGGGAGGCTCTGTGAGAGTGGACACCGAGTCC 2151
Db 701 GlyGluLeuSerTyrAsnLeuGlyAlaGlyGlyValSerAlaGluValAspThrSerSer 720
QY 2152 CTGAGCGGCACAAATACCTTATGTCCACGCTGGAGAGAGAGACAGATGGGAGCAG 2211
Db 721 LeuSerGlyAspAsnThrLeuMetSerThrLeuGluLysGluThrAspGlyGluGln 740
QY 2212 GGGCCACGCTCTCCCGAGCCCGCAGCTGTAGCCCTCCAGCCCTGTCTGTCTCTCTCT 2271

FT TRANSMEM 303 323 SEGMENT S3 (POTENTIAL).
 FT TRANSMEM 332 352 SEGMENT S4 (POTENTIAL).
 FT DOMAIN 353 361 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 362 382 SEGMENT S5 (POTENTIAL).
 FT DOMAIN 457 477 SEGMENT H5 (PORE-FORMING) (POTENTIAL).
 FT TRANSMEM 483 503 SEGMENT S6 (POTENTIAL).
 FT DOMAIN 504 1087 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 18 90 PAS.
 FT DOMAIN 93 145 PAC.
 FT DOMAIN 954 1061 PRO-RICH.
 FT NP BIND 585 700 CNMP.
 FT CARBOHYD 421 421 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 428 428 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 439 439 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 1087 AA; 117537 MW; EB5DB6B78BA851F8 CRC64;

Alignment Scores:
 Pred. No.: 5,62e-232 Length: 1087
 Score: 5416.00 Matches: 1037
 Percent Similarity: 96.41% Conservative: 11
 Best Local Similarity: 95.40% Mismatches: 35
 Query Match: 88.95% Indels: 4
 DB: 1 Gaps: 2

US-09-965-830-1_COPY_6_3257 (1-3252) x KCH3_MOUSE (1-1087)

QY 1 ATCGCGGCATCGCGGCTCTCTGCGCTCAGAACACCTCTCGACACCATCGCTACG 60
 DB 1 MetProAlaMetProGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20

QY 61 CGCTTCGACGGACCCACAGTAACCTGCTGGTGGCAACGCCAGGTGGCGGGCTCTTC 120
 DB 21 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnValAlaGlyLeuPhe 40

QY 121 CCCGTGCTACTGCTCTGATGGCTTCTGTACCTACCTACCGGGTCTTCCGGGCTGAGTC 180
 DB 41 ProValValTyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal 60

QY 181 ATGACGCGGGGTGTGCTGCTCTCTCTCTTATGGCGCAGACACCGAGTGTCTCCGCG 240
 DB 61 MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArg 80

QY 241 CAACAGATCCGACGGCCTCGACGACGACAGGAGTTCAAGGCTGAGCTGATCCTGTAC 300
 DB 81 GlnGlnIleArgLysAlaLeuAspGluHisLysGluPheLysAlaGluLeuLeuTyr 100

QY 301 CGGAAGACGGGCTCCGCTCTGCTGCTCTGCTGATGATACCCATAAAGATGAGAAA 360
 DB 101 ArgLysSerGlyLeuProPheTrpCysLeuLeuAspValIleProIleLysAsnGluLys 120

QY 361 GGGGAGGTGGCTCTCTCTCTCTCTCTCTCACAGGACATCAGCAAAACCAAGACCGAGGG 420
 DB 121 GlyGluValAlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGly 140

QY 421 GGGCCCGACAGATGAGAGACAGTGTGTGGCGCGCCGATATGGCGGGCGACATCC 480
 DB 141 GlyProAspAsnTrpLysGluArgGlyGlyArgArgArgTyrGlyArgAlaGlySer 160

QY 481 AAAGGCTTCATGCAACCGCGCGGAGCGCGCGCTGTCTACACCTGTCCGGGCAC 540
 DB 161 LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis 180

QY 541 CTGCAGAGCAGCCCAAGGGCAAGCACAGTCTCAATGAAGGGGTGTTGGGGAGAACCA 600
 DB 181 LeuGlnLysGlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyGluLysPro 200

QY 601 AACTTGCTGAGTCAAGTAGCCGCCATCCGGAAGTCGCCCTTCACTCTGTCGACTGT 660
 DB 201 AsnLeuProGluTyrLysValAlaAlaIleArgLysSerProPheIleLeuLeuHisCys 220

QY 661 GGGGCACTGAGACCACTGGATGGCTTCACTCTGCTCGGCCACACTCTATGTGGCTGTC 720
 DB 221 GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal 240

QY 721 ACTGTGCCCTACAGCGTGTGTGTGACACAGACGGAGCCAGTCCCGCCCGCGGCCG 780
 DB 241 ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro 260

QY 781 CCCAGCGTGTGACCTGGCCCTGGAGGTCTCTTCATCTTGACATTGTGCTGAATTTC 840
 DB 261 ProSerValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPhe 280

QY 841 CQTACACATTCGTGTCCAAAGTCGGGCCAGGTGGTGTGTTGCCCCCAAGTCCATTCCCTC 900
 DB 281 ArgThrThrPheValSerLysSerGlyGlnValValPheAlaProLysSerIleCysLeu 300

QY 901 CACTACGTCACACCTGCTGCTGCTGATGATCATCGACGCGCTGCCCTTTCACCTGCTA 960
 DB 301 HisTyrValThrThrPheLeuLeuAspValIleAlaAlaLeuProPheAspLeuLeu 320

QY 961 CATGCTTCAAGGTCAACGTGTACTTTCGGGGCCCATCTGCTGAAGACGTGCGCTGCTG 1020
 DB 321 HisAlaPheLysValAsnValTyrValGlyAlaHisLeuLeuLysThrValArgLeuLeu 340

QY 1021 CGCTGTGCGGCTGCTTCCGGCGCTGACCGGTACTCGCAGTACAGCGCCCTGGTGTG 1080
 DB 341 ArgLeuLeuArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValValLeu 360

QY 1081 ACACGTCTCATGGCGCTGCTCGCCCTGCTCGCGCACTGGTCCGCTGCTGCTGTTTAC 1140
 DB 361 ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr 380

QY 1141 ATTGCCACCGGGAGATCGAGACGAGCAATCCAGTGCCTGAGATTGGTGGCTGCAG 1200
 DB 381 IleGlyGlnGlnGluIleGluAsnSerGluSerGluLeuProGluIleGlyTrpLeuGln 400

QY 1201 GAGTGGCCCGCGACTCGAGACTCCCTACTACCTGTGGTGGCGCGAGCCAGTGGAGGG 1260
 DB 401 GluLeuAlaArgArgLeuGluThrProTyrTyrLeuValSerArgSerProAspGlyGly 420

QY 1261 AACAGCTCCGCGCCAGAGTGACACTGCGAGCAGCAGC-----AGCAGCGCCAACGG 1311
 DB 421 AsnSerSerGlyGlnSerGluAsnCysSerSerSerGlyGlyGlySerGluAlaAsnGly 440

QY 1312 ACGGGCTGAGTGTGCTGGGGCGCGCTGCTGGCGAGCGCTACATCACCTCCCTCTAC 1371
 DB 441 ThrGlyLeuGluLeuLeuGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyr 460

QY 1372 TTCGCACTACAGACCTCACCGCGTGGCTTCGGCAACGTGTCCGCCAACACCGACACC 1431
 DB 461 PheAlaLeuSerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThr 480

QY 1432 GAGAAGATCTCTCATCTGCACCATCTCATCGCGCCCTGTATGACCGCGTGTGTTT 1491
 DB 481 GluLysIlePheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValValPhe 500

QY 1492 GGGAACTGACGGCCATCATCCAGCGATGTACCGCGCCCTTCTCTAGCACAGCGCG 1551
 DB 501 GlyAsnValThrAlaIleIleGlnArgMetTyrAlaArgArgPheLeuTyrHisSerArg 520

QY 1552 ACGCGCACTGCGCACTACATCCGATCCACCGTATCCCAAGCCCTTCAAGCAGCGCG 1611
 DB 521 ThrArgAspLeuArgAspTyrIleArgIleHisArgIleProLysProLeuLysGlnArg 540

QY 1612 ATGCTGAGTACTTCCAGGCGCCTGGCGGTGAACTGGCATGCGACACCGCAGCTG 1671
 DB 541 MetLeuGluTyrPheGlnAlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeu 560

QY 1672 CTGCAGAGCTCTCTGACGAGTGCAGCATCGCCATCGCCATCGACCTGCACAGGAGTCT 1731
 DB 561 LeuGlnSerLeuProAspGluLeuArgAlaAspIleAlaMetHisLeuHisLysGluVal 580

QY 1732 CTGCAGCTGCCACTGTTTGAAGCGCGCAGCGCGCTGCGCTGCGGGCACTGTCTCTGCC 1791
 DB 581 LeuGlnLeuProLeuPheGluAlaAlaAspArgGlyCysLeuArgAlaLeuSerLeuAla 600

1792 CTGCGCGCCGCTTCTGACGCGCGGAGTACCTCATCCACCAAGCGCATCCCTGCGAG :851
Db LeuArgProAlaPheCysThrProGlyGluTyrLeuIleHisGlnGlyAspAlaLeuGln :620
1852 GGCCTTACTTGTCTGCTCTGCTCCATGAGAGTCTCAAGGTGGCACCCTGCTCGCC :911
Db AlaLeuTyrPheValCysSerGlySerMetGluValLeuLysGlyGlyThrValLeuAla :640
1912 ATCTTAGGAGAGGCGACCTGATCGGCTGTGAGTCCCGCGGAGGAGGTGGTAAAG :971
Db IleLeuGlyLysGlyAspLeuIleGlyCysGluLeuProGlnValValLys :660
1972 GCCAATGCCACGTGAAGGGCTGACGTACTGCGTCTCTGAGTGTCTGACGTGGCTGGC :2031
Db AlaAsnAlaAspValLysGlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGly :680
2032 CTGACGACGAGCTTGGCTGTATCCCGAGTTTGGCCCGGCTTCAAGTGGCTCCGAC :2091
Db LeuHisGluSerLeuAlaLeuTyrProGluPheAlaProArgPheSerArgGlyLeuArg :700
2092 GGGGAGCTACGCTACAACTGGTGTGGGGAGGCTCTGACAGGTGGACACAGCTCC :2151
Db GlyGluLeuSerTyrAsnLeuGlyAlaGlyValSerAlaGluValAspThrSerSer :720
2152 CTGAGCGGCGACATACCTTATGTCACGCTGGAGGAGAGGACAGATGGGAGCAG :2211
Db LeuSerGlyAspAsnThrLeuMetSerThrLeuGluGluLysGluThrAspGlyGluGln :740
2212 GGCCCGACGCTCTCCCGAGCCGACGTATGAGGCTTCCAGCCCTGCTGTCTCCCTGGC :2271
Db GlyHisThrIleSerProAlaProAlaAspGluProSerSerProLeuLeuSerProGly :760
2272 TGCACTCTCTCCTCAGCTGCGCAAGCTGCTATCCCGAGTCCGAAAGCAGCACCCGCGCT :2331
Db CysThrSerSerSerAlaAlaLysLeuLeuSerProArgArgThrAlaProArgPro :780
2332 CGTCTAGTGGCAGAGGAGCCAGGCGAGCGGCTTTGAAGGTGAGGCTGGCGCC :2391
Db ArgLeuGlyGlyArgGlyArgProSerArgAlaGlyValLeuLysProGluAlaGlyPro :800
2392 TGTGCTCCCGACGCGGCTAGAGGCTACGGCTGCGCCCGCATGCGCATGATGATGCGCC :2451
Db SerAlaHisProArgThrLeuAspGlyLeuGlnLeuProMetProTyrAsnValPro :820
2452 CCAGATCTGAGCCCGCAGGTAGTATGATGATGATGATGATGATGATGATGATGATGAT :2511
Db ProAspLeuSerProArgValValAspGlyIleGluAspGlyCysGlySerAspGlnHis :840
2512 AAGTTCTCTTCCGCTGGCGCAGTCTGGCGCGGAAATGTAGCAGCAGCCCTCCCTGGGA :2571
Db LysPheSerPheArgValGlyGlnSerGlyProGluCysSerSerProSerProGly :860
2572 CCAGAGAGCGCTGCTCAGTGTTCCTCCATGGGCGCCAGGAGGCAAGGACACAGACACA :2631
Db ThrGluSerGlyLeuLeuThrValProLeuValProSerGluAlaArgAsnThrAspThr :880
2632 CTGACACAGCTTCCGCGAGCGCTGACAGAGTGTGACAGAGTGTGACAGTCCGAGAA :2691
Db LeuAspLysLeuArgGlnAlaValThrGluLeuSerGluGlnValLeuGlnMetArgGlu :900
2692 GGACTGAGTCACTTGGCGAGGCTGTGAGTGTGCTGCGCGCGCCACAGGAGGAGTCCG :2751
Db GlyLeuGlnSerLeuArgGlnAlaValGlnLeuIleValLeuValProGlnGlyGln :920
2752 TGCCCTGGGCGATCGGAGAGGCGCGGCGCGCAGCAGCAGCTCCGCGCTCTGCGAGCT :2811
Db CysProArgValSerGlyGluGlyProCysProAlaThrAlaCysGlyLeuLeuGlnPro :940
2812 CTGTGTGTGGACACTGGGGCGATCTCTCTACTGCTGACGCGCCCGAGCTGCTGTCTGTG :2871
Db LeuArgValAspThrGlyAlaSerSerTyrCysLeuGlnProProAlaGlySerValLeu :960
2872 AGTGGGACTTGGCCCGCCACCTGCTCGCGGG---CCTCTCTCCCTCATGCGACCCCTGGCC :2928

961 SerGlyThrTrpProHisProArgProGlyHisProProProLeuMetAlaProTyrPro :980
2929 TGGGGTCCCGCAGCGCTCTCAGAGCTCCCGCTCGAGCCACAGCTTTCTGGACCTCC :2988
Db TrpGlyProProAlaSerGlnSerProTyrProArgAlaThrAlaLeuThrThrSer :1000
2989 ACCTCAGACTCAGAGCCCGCTCGCTCAGAGACCTCTGCTGAGCCGACGACCCCTGCC :3048
Db ThrSerAspSerGluProProGlySerGlyAspLeuCysSerGluProSerThrProAla :1020
3049 TCCCTCTCTCTCTCAGAGAGGGCTAGACTGGGCCCGCAGAGGCTGTGAGCCAGGCT :3108
Db TCCCTCTCTCTCTCAGAGAGGGCTAGACTGGGCCCGCAGAGGCTGTGAGCCAGGCT :3108
3109 GAGGCTTACGACACTCGAGAGCCCGCCACAGGCTCAGGGGCTCGCTTGGCTTGGGAC :3168
Db GluAlaThrSerThrGlyGluProProProGlySerGlyGlyArgAlaLeuProTyrAsp :1060
3169 CCCACAGCTGAGAGTGTGCTTATGCTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG :3228
Db ProHisSerLeuGluMetValLeuIleGlyCysHisGlyProGlySerValGlnThr :1080
3229 CAGGAGAGGACACAGCGGTC 3249
1081 GlnGluGluGlyThrGlyVal 1087
RESULT 4
KCH8 HUMAN
ID KCH8 HUMAN STANDARD; PRT; 1107 AA.
AC Q96L42; 2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Potassium voltage-gated channel subfamily H member 8 (Ether-a-go-go-like potassium channel 3) (ELK channel 3) (ELK3) (ELK1) (hElk1).
GN KCNH8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Baxter D.F., Kirk M., Garcia A.F., Raimondi A., Holmgvist M.H., Flint K.K., Bojanic D., DiStefano P.S., Curtis R., Xie Y.;
RT "A novel membrane potential-sensitive fluorescent dye improves cell-based assays for ion channels.";
RL J. Biomol. Screen. 7:79-85(2002).
CC -!- FUNCTION: Pore-forming (alpha) subunit of voltage-gated potassium channel. Elicits a slowly activating, outward rectifying current. Channel properties may be modulated by cAMP and subunit assembly.
CC -!- SUBUNIT: The potassium channel is probably composed of a homo- or heterotetrameric complex of pore-forming alpha subunits that can associate with modulating beta subunits.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- DOMAIN: The segment S4 is probably the voltage-sensor and is characterized by a series of positively charged amino acids at every third position.
CC -!- SIMILARITY: Belongs to the potassium channel family. H (Eag) subfamily.
CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
CC -!- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.
CC -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

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CC EMBL; AY053503; AAL15429.1; -.
DR Genew; HGNC:18864; KCNHB.
DR InterPro; IPR000595; cNMP binding.
DR InterPro; IPR003967; Erg_Channel.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000700; PAS-assoc_C.
DR InterPro; IPR000014; PAS_domain.
DR Pfam; PF00027; cNMP_binding; 1.
DR Pfam; PF00520; ion_trans; 1.
DR Pfam; PF00785; PAC; 1.
DR PRINTS; PR01470; ERGCHANNEL.
DR SMART; SM00100; cNMP; 1.
DR SMART; SM0086; PAC; 1.
DR TIGRfam; TIGR00229; sensory_box; 1.
DR PROSITE; PS00888; cNMP_BINDING_1; FALSE_NEG.
DR PROSITE; PS00889; cNMP_BINDING_2; FALSE_NEG.
DR PROSITE; PS0042; cNMP_BINDING_3; 1.
DR PROSITE; PS0113; PAC; 1.
DR PROSITE; PS0112; PAS; FALSE_NEG.
KW Transport; Ion transport; Ionic channel; Voltage-gated channel;
KW Potassium channel; Potassium; Potassium transport; Transmembrane;
KW Glycoprotein; Multigene family.
FT DOMAIN 1 225
FT TRANSMEM 226 246 SEGMENT S1 (POTENTIAL).
FT TRANSMEM 256 276 SEGMENT S2 (POTENTIAL).
FT DOMAIN 277 298 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 299 319 SEGMENT S3 (POTENTIAL).
FT TRANSMEM 328 348 SEGMENT S4 (POTENTIAL).
FT DOMAIN 349 357 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 358 378 SEGMENT S5 (POTENTIAL).
FT DOMAIN 420 440 SEGMENT H5 (PORE-FORMING) (POTENTIAL).
FT TRANSMEM 449 469 SEGMENT S6 (POTENTIAL).
FT DOMAIN 470 1107 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 18 90 PAC.
FT DOMAIN 93 145 SER-RICH.
FT DOMAIN 951 1064 POLY-GLU.
FT NP_BIND 711 723 cNMP.
FT CARBOHYD 551 668 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 320 320 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1107 AA; 123832 MW; 4DC93F85B674905 CRC64;

Alignment Scores:
Pred No.: 9,87e-105 Length: 1107
Score: 2529.50 Matches: 559
Percent Similarity: 60.24% Conservative: 150
Best Local Similarity: 47.49% Mismatches: 267
Query Match: 41.54% Indels: 201
DB: 1 Gaps: 27

US-09-965-830-1_COPY_6_3257 (1-3252) x KCH8_HUMAN (1-1107)
QY 1 ATGCGGCCATCGGGGCTCTCTGGCGCTCAGAACACCTTCTCTGGACACCATCGCTACG 60
Db 1 MetProValMetLysGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20
QY 61 CGCTTCACGGCAGCGACAGTAATTCGTGCTGGGCAACGCCAGGTGGGGGCTCTTC 120
Db 21 ArgPheAspGlyThrHisSerAsnPheIleLeuAlaAsnAlaGlnValAlaLysGlyPhe 40
QY 121 CCGGTGCTCTACTGCTCTGCTTCTCTCTTATGGGCGACACCATGAGCTGCTCCGC 180
Db 41 ProlleValTyrCysSerAspGlyPheCysGluLeuAlaGlyPheAlaArgThrGluVal 60
QY 181 ATGCGAGCGGGCTGTGCTGCTCTCTCTCTCTTATGGGCGACACCATGAGCTGCTCCGC 240
Db 61 MetGlnLysSerCysSerCysLysPhePheGlyValGluThrAsnGluGlnLeuMet 80
QY 241 CAACAGATCCGCAAGGCCCTGGACGACACAGGAGTTCAAGGTGAGCTGATCCTGTAC 300

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81 LeuGlnIleGluLysSerLeuGluGluLysThrGluPheLysGlyGluIleMetPheTyr 100
301 CGGAAGAGCGGCTCCCGTTCTGTGTCTCTCTGGATGTATACCCATAAGAAATGAGAAA 360
101 LysLysAsnGlySerProPheTrpCysLeuLeuLeuAspIleValProIleLysAsnGluLys 120
361 GGGGAGGTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
121 GlyAspValValLeuPheLeuAlaSerPheLysAspIleThrAspThrLysValLysIle 140
421 GCGCCGACAGATGGAAGGAGACAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
141 ThrProGluAspLysLysGluAsp-----LysValLysGlyLysArgSerArgAla 156
481 ---AAAGGCTTCAATGCCAACCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 537
157 GlyThrHisPheAspSerAlaArgArgSerArgAlaValLeuTyrHisIleSerGly 176
538 CACCTGCAAGACGACCCCAAGGCAAGCAAGCTCAATAAGGGGGTGTGTGGGAGAAA 597
177 HisLeuGlnArgGluGlyLysAsnLysLeuLysIleAsnAsnValPheValAspLys 196
598 CCAAACCTTGTCTGAGTACAAAGTAGCCGCCATCCGGAGTCCGCCCTCATCTGTGTGAC 657
197 ProAlaPheProGluTyrLysValSerAspAlaLysLysSerLysPheIleLeuHis 216
658 TGTGGGCACTGAGGACACCTGGATGGCTTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 717
217 PheSerThrPheLysAlaGlyTrpAspTrpLeuIleLeuLeuAlaThrPheTyrValAla 236
718 GTCACTGTGCTTACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 777
237 ValThrValProTyrAsnValCysPheIleGlyAsnAspAspLeuSerThrThrArgSer 256
778 CCGCCACAGCTGTGACCTGCGGTGGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 837
257 ---ThrThrValSerAspIleAlaValGluLeuPheIleAspIleLeuAsn 275
838 TTCGTACCACTTCGTGTCCAAGTCCGGGCGGAGGTGTGTGTGTGTGTGTGTGTGTGTGT 897
276 PheArgThrThrTyrValSerLysSerGlyGlnValIlePheGluAlaArgSerIleCys 295
898 CTCACACTGTCACACCTGTTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 957
296 IleHisTyrValThrThrTrpPheIleLeuAspLeuIleAlaLeuProPheAspLeu 315
958 CTACATGCTTCAAGGTCAAGCTGTACTTCGGGGCCCATCTCTGTAAGACGGTGGCGCTG 1017
316 LeuTyrAlaPheAsnValThrValValSerLeuValHisLeuLeuLysThrValArgLeu 335
1018 CTGCGCTGTGCGCTGCTTCCGCGGTGTCTCGGAGTCTCTGAGTACAGCGCGCTGTGTG 1077
336 LeuArgLeuLeuArgLeuLeuGlnLysLeuAspArgTyrSerGlnHisSerThrIleVal 355
1078 CTGACACTGTCATGGCGGTGTGCGCTGCTGCGCACTGGGTGCGCTGCGCTGCGTGTGT 1137
356 LeuThrLeuLeuMetSerMetPheAlaLeuLeuAlaHisTrpMetAlaCysIleTrpTyr 375
1138 TACATTGGCCGCGGAGATCGAGACGAGCATCCGAGCTGCTGAGATGGCTGGCTGGCTG 1197
376 ValIleGlyLysMetGluArgGluAspAsnSerLeuLeuLysTrpGluValGlyTrpLeu 395
1198 CAGGAGTGGCCCGGCGACTGAGACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1257
396 HisGluLeuGlyLysArgLeuGluSerProTyrTyr----- 407
1258 GGAACAGCTCCCGCCAGAGTGACAACTGTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1317
408 GlyAsnAsnThr----- 411
1318 CTGAGAGTGTGGGCGCGCTGCTGCGCGCGCTTACATCATCTCCCTCTCTCTCTCTCTCT 1377

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Db	412	-----LeuGlyGlyProSerIleArgSerAlaTyrIleAlaAlaLeuTyrPheThr	428
QY	1378	CTCAGAGCTCACCAGCTGGCTTCGCGACAGTGTCCGCAACACGACACCGAGAG	1437
Db	429	LeuSerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspAlaGluLys	448
QY	1438	ATCTCTCTCCATCTGCACCATGCTCATCGCGCGCTGATCAGCGCGTGTGTGGAAAC	1497
Db	449	IlePheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaLeuValPheGlyAsn	468
QY	1498	GTGACGGCCATCATCAGCGCATGTACGCCCGCGCTTCTGTACACAGCGCGCAGCGC	1557
Db	469	ValThrAlaIleIleGlnArgMetTyrSerArgTyrSerLeuTyrHisThrArgThrLys	488
QY	1558	GACCTCGGACTACATCCGATCCACCGTATCCCAAGCCCTCAAGAGGAGCGATGCTG	1617
Db	489	AspLeuLysAspPheIleArgValHisLeuProGlnGlnLeuLysGlnArgMetLeu	508
QY	1618	GAGTACTTCCAGGCCACCTGGCGGTGAACAATGGCATCGACACCGAGCTGTGTCAG	1677
Db	509	GluTyrPheGlnThrThrTyrSerValAsnAsnGlyIleAspSerAsnGluLeuLys	528
QY	1678	AGCTCTCCCTGACAGTGGCGGAGCATGCGCCATGACCTGACACAGAGGTCCTGCGAG	1737
Db	529	AspPheProAspGluLeuArgSerAspIleThrMetHisLeuAsnLysGluIleLeuGln	548
QY	1738	CTGCCACTGTTTGGCGGCGCAGCGCGTGTGCGGCACTGTCTCTGCGCCCTGCGG	1797
Db	549	LeuSerLeuPheGluCysAlaSerArgGlyCysLeuArgSerLeuSerLeuHisLys	568
QY	1798	CCGCGCTTCTGACGCGCGGCGAGTACTCATCCACCAAGCGCATGCGTGCAGGCGCTC	1857
Db	569	ThrSerPheCysAlaProGlyGluTyrLeuLeuArgGlnGlyAspAlaLeuGlnAlaIle	588
QY	1858	TACTTTGTCTGCTCTCCAGTGTCTGAGTGTCTGAGTGTCTGAGTGTCTGAGTGTCTG	1917
Db	589	TyrPheValCysSerGlySerMetGluValLeuLysAspSerMetValLeuAlaIleLeu	608
QY	1918	GGGAGGCGCAGCTGATCGCTGTGAGCTGCCCGCGGAGGAGTGTGTAAAGGCCAAT	1977
Db	609	GlyLysGlyAspLeuIleGlyAlaAsnLeuSerIleLysAspGlnValIleLysThrAsn	628
QY	1978	GCCGACCTGAAGGGCTGACGTACTGCTGTCTGAGTGTCTGAGTGTCTGAGTGTCTG	2037
Db	629	AlaAspValLysAlaLeuThrTyrCysAspLeuGlnCysIleLeuLysGlyLeuPhe	648
QY	2038	GACAGCTTGTGCTGTACCGGATGTGCGCGCTTGTGCTGCTGCTGCTGCTGCTGCTG	2097
Db	649	GluValLeuAspLeuTyrProGluTyrAlaHisLysPheValGluAspIleGlnHisAsp	668
QY	2098	CTCAGCTACACCTGGGTGCTGGG-----GGAGGCTCT	2130
Db	669	LeuThrTyrAsnLeuArgGlyHisGluSerAspValIleSerArgLeuSerAsnLys	688
QY	2131	GCAGAGTGGACACAGCTCCCTGAGCGGCGACAAATACCTTATGTCCACGCTG-----	2184
Db	689	SerMetValSerGlnSerGluProLysGlyAsnGlyAsnIleAsnLysArgLeuProSer	708
QY	2185	-----GAGGAGAGGACAGACATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2232
Db	709	IleValGluAspGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu	726
QY	2233	CCAGCTGATGACCTCCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2292
Db	727	-----LeuSerProIleCysThrArgGlySerSerSer	737
QY	2293	GCCAGCTGCTATCCCACTGCAACAGCACCGCGCTGCTGTAGTGTGGCAGAGGAGG	2352
Db	738	-----Arg	738
QY	2353	CCAGGAGGCGAGGGCTTTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG	2397
Db	739	AsnLysLysValGlySerAsnLysAlaTyrLeuGlyLeuSerLeuLysGlnLeuAlaSer	758
QY	2397	-----	2397
Db	759	GlyThrValProPheHisSerProIleArgValSerArgSerAsnSerProLysThrLys	778
QY	2398	-----CCGCCA-----CGGGCCCTAGAGGGGCTACGGCTGCGCCCGC	2433
Db	779	GlnGluIleAspProProAsnHisAsnLysArgLysGlyLysAsnLeuLysLeuGlnLeu	798
QY	2434	ATGCCATGGAAT-----GTGCCCCAGATCTGAGCCCGAGGGTAGTAGATGATGAA	2487
Db	799	SerThrLeuAsnAsnAlaGlyProProAspLeuSerProArgIleValAspGlyIleGlu	818
QY	2488	GACGGCTGTGGTTCGAGCCAGCCCAAG-----TTCTCTTTTCGGCTGGCCAGCTG	2544
Db	819	AspGlyAsnSerSerGluGluSerGlnThrPheAspPheGlySerGluArgIleArgSer	838
QY	2545	GAATGTAGCAGCAGCCCTCCCTCGA-----CCAGAGAGCGGCTGTCTACTGTCTCC	2601
Db	839	GluProArgIleSerProProLeuGlyAspProGluIleGlyAlaAlaValLeuPheIle	858
QY	2602	GGGCCCCAGCGAGGAGAACACAGACACACTGGCAAGCTTCGGCAGCGGTGACAGAG	2661
Db	859	LysAlaGluGluThrLys-----GlnGlnIleAsnLysLeuAsnSerGluValThr	876
QY	2662	CTGTCTAGCAGAGTGTCTGAGATCGCGGAGGAGTGTGAGTGTGAGTGTGAGTGTG	2721
Db	877	LeuThrGlnGluValSerGlnLeuGlyLysAspMetArgAsnValIleArgLeuLeuGlu	896
QY	2722	CTTGCTCTGCGGCC-----CACAGGAGGGTCTCGGTGC	2754
Db	897	AsnValLeuSerProGlnGlnProSerArgPheCysSerLeuHisSerThrSerValCys	916
QY	2755	CTTCGGGCA-----TCGGAGAGGGCGCTGCCCGAGC	2787
Db	917	ProSerArgGluSerLeuGlnThrArgThrSerTyrSerAlaHisGlnProCys-----	934
QY	2788	AGCACCTCCGGGCTTCTGAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2844
Db	935	-----LeuHisLeuGlnThrGlyGlyAlaIleTyrThrGln	946
QY	2845	CTCAGCGCCCGAGTGTCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2904
Db	947	AlaGlnLeuCysSerSerAsnIleThrSerAspIleTyrSer-----	960
QY	2905	CTCCTCCCTCATGGCACCCCTGGCGCTGCGGGTCCCGCCAGCTGTACAGCTCCCTCC	2964
Db	961	-----ValAspProSerSerValGlySerSer---Pro	970
QY	2965	CGAGCCACAGCTTCTGTGACCTCCACTCAGACTCAGAGCCCTGCTCAGGAGACCTC	3024
Db	971	GlnArgThrGly-----AlaHisGluGlnAsnProAlaAspSerGluLeu	985
QY	3025	TGCTCTGAGCGCCAGCACCCCTGCTGCTCCCT-----	3054
Db	986	TyrHisSerProSerLeuAspTyrSerProSerHisTyrGlnValGlnGluGlyHis	1005
QY	3055	-----CCTCCTTCTGAGGAGGGGTAGGACTGGGCGCCGCGCAGAG	3093
Db	1006	LeuGlnPheLeuArgCysIleSerProHisSerAspSerThrLeuThr---ProLeuGln	1024
QY	3094	CCTGTGAGCGAGGTGAGGTACAGGACTGAGGAGGAGGAGGAGGAGGAGGAGGAGG	3153
Db	1025	SerIleSerAlaThrLeuSerSerSerValCysSerSerSerGluThrSerLeuHisLeu	1044
QY	3154	GCTTGTGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	3213
Db	1045	ValLeuPro-----SerArgSerGluGlu-----GlySerPheSerGlnGly	1058
QY	3214	ACAGTC-----CAGTGGACCCAGGAA	3234
Db	1059	ThrValSerSerPheSerLeuGluAsnLeuProGlySerTrpAsnGlnGlu	1075

Db 61 MetGlnLysSerCysSerCysLysPheLeuPheGlyValGluThrAsnGluGlnLeuMet 80
 QY 241 CAACAGATCCGAGCCCTGACAGACACAGAGGTTCAAGGCTGAGTGTCTGTAC 300
 Db 81 LeuGlnIleGluLysSerLeuGluGlnLysValGluPheLysGlyGluIleMetPheTyr 100
 QY 301 CGGAGAGCGGCTCCGCTTCTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
 Db 101 LysLysAsnGlyAlaProPheTyrCysLeuLeuLeuLeuLeuLeuLeuLeuLeu 120
 QY 361 GGGAGGCTGGCT 417
 Db 121 GlyAspValValLeuPheLeuAlaSerPheLysAspIleThrAspThrLysValLysIle 140
 QY 418 GGGGGCCCGACAGATGGAGAGACAGGTGGTGGCGCGCGCGATGATGCGCGGACGA 477
 Db 141 ThrSerGluAspLysGluAspArgAlaLysGlyArgSerArgAlaGly----- 57
 QY 478 TCCAAAGGCTTCAATGCCAACCGCGCGGAGCGCGGCTGTCTTACCACTGTCTCGG 537
 Db 158 ---SerHisPheAspSerAlaArgArgSerArgAlaValLeuTyrHisIleSerGly 176
 QY 538 CACTCGAGAGCAGCCCAAGGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 597
 Db 177 HisLeuGlnArgArgGluLysAsnLysLeuLysIleAsnAsnValPheValAspLys 196
 QY 598 CAAACTGCTGCTACAGAGTACAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCG 657
 Db 197 ProAlaPheProGluTyrLysValSerAspAlaLysLysSerLysPheIleLeuLeuHis 216
 QY 658 TGTGGGCACTGAGGACCTGGATGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 717
 Db 217 PheSerThrPheLysAlaGlyTyrAspTyrLeuLeuLeuLeuLeuLeuLeuLeu 236
 QY 718 GTCACTGTGCTTACAGCGTGTGTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 777
 Db 237 ValThrValProTyrAsnValCysPheIleGlyAsnGluAspLeuSerThrThrArgSer 256
 QY 778 CCGCCAGCTCTGAGCTGGCGGCGGAGTCTCTCTCTCTCTCTCTCTCTCTCTCT 837
 Db 257 ---ThrThrValSerAspIleAlaValGluLeuLeuPheIleAspIleLeuLeuAsn 275
 QY 838 TTCGCTACCACTTCTGCTCAAGTGGCGGCGGAGTGGTGGTGGTGGTGGTGGTGG 897
 Db 276 PheArgThrThrTyrValSerLysSerGlyGlnValIlePheGluAlaArgSerIleCys 295
 QY 898 CTCACATGCTACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 957
 Db 296 IleHisTyrValThrThrTyrPheIleAspLeuIleAlaLeuProPheAspLeu 315
 QY 958 CTACATGCTTCAAGGTCAAGTCTTCTGCGGCGGCGGCGGCGGCGGCGGCGGCG 1017
 Db 316 LeuTyrAlaPheAsnValThrValValSerLeuValHisLeuLeuLysThrValArgLeu 335
 QY 1018 CTGCGCTGTGCTGCTGCTTCCGCGGCTGACCGGTACTCGAGTACAGCGCGCTGGT 1077
 Db 336 LeuArgLeuLeuArgLeuLeuGlnLysLeuAspArgTyrSerGlnHisSerThrIleVal 355
 QY 1078 CTGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1137
 Db 356 LeuThrLeuLeuMetSerMetPheAlaLeuLeuAlaHisTrpMetAlaCysIleTyrTyr 375
 QY 1138 TACATTGGCAGCGGAGATCGAGAGCAGCAATCCGAGTGCCTGAGATTGGCTGGCTG 1197
 Db 376 ValIleGlyLysMetGluArgGluAsnSerLeuLeuLysTyrTrpGluValGlyTrpLeu 395
 QY 1198 CAGGAGCTGGCGCGGCTGAGACTCCCTACTACTGCTGGTGGCGGCGGAGCCACTGGA 1257
 Db 396 HisGluLeuGlyLysArgLeuGluSerProTyrTyr----- 407
 QY 1258 GGAACAGCTCGGCGGAGGTGACAACTGCACAGCAGCAGCAGCAGCAGCAGCAGCAG 1317
 Db 408 GlyAsnAsnThr----- 411

QY 1318 CTGAGCTGCTGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1377
 Db 412 -----LeuGlyGlyProSerIleArgSerAlaTyrIleAlaAlaLeuTyrPheThr 428
 QY 1378 CTCAGCAGCTCACCAGCGTGGCTTCCGCAACGTTGTCGCAACACGACGACCGAGAAG 1437
 Db 429 LeuSerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspAlaGluLys 448
 QY 1438 ATCTTCTCCATCTGACCATGCTCATCGCGCGCTGATGACGCGGTGTGTGTGGGAAC 1497
 Db 449 IlePheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaLeuValPheGlyAsn 468
 QY 1498 GTGACGCGCATCATCAGCGCATGACGCGCGCTTCTGTACACAGCGCGCAGCGCG 1557
 Db 469 ValThrAlaIleIleGlnArgMetTyrSerArgTyrPheSerLeuTyrHisThrArgThrLys 488
 QY 1558 GACCTCGCGACTACATCGCATCCACCGCTATCCCAAGCCCTCAAGCAGCGCATGCTG 1617
 Db 489 AspLeuLysAspPheIleArgValHisHisLeuProGlnGlnLeuLysGlnArgMetLeu 508
 QY 1618 GAGTACTTCCAGGCCACCTGGCGGTGAACAATGATCGACACACCGAGCTGCTGCAG 1677
 Db 509 GluTyrPheGlnThrThrTyrSerValAsnAsnGlyIleAspSerAsnGluLeuLys 528
 QY 1678 AGCCTCCTGACAGCTGCGCGCAGCATCGCCATCGACCTGACACAGGAGTCTGCAG 1737
 Db 529 AspPheProAspGluLeuArgSerAspIleThrMetHisLeuAsnLysGluIleLeuGln 548
 QY 1738 CTCGCCATGTTTCAGCGCGCGCGCTGCTGCGGCGCTGCTGCGGCGCTGCTGCGG 1797
 Db 549 LeuSerLeuPheGluCysAlaSerArgGlyCysLeuArgSerLeuSerLeuHisIleLys 568
 QY 1798 CCGCGCTTCTGACGCGCGGCTGCTGCGGCGCTGCTGCGGCGCTGCTGCGGCGCT 1857
 Db 569 ThrSerPheCysAlaProGlyGluTyrLeuLeuArgGlnGlyAspAlaLeuGlnAlaIle 588
 QY 1858 TACTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1917
 Db 589 TyrPheValCysSerGlySerMetGluValLeuLysAspSerMetValLeuAlaIleLeu 608
 QY 1918 GGGAGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1977
 Db 609 GlyLysGlyAspLeuIleGlyAlaAsnLeuSerIleLysAspGlnValIleLysThrAsn 628
 QY 1978 GCGCAGCTGAAGGCGCTGACGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2037
 Db 629 AlaAspValLysAlaLeuThrTyrCysAspLeuGlnCysIleIleLeuLysGlyLeuPhe 648
 QY 2038 GACAGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2097
 Db 649 GluValLeuGlyLeuTyrProGluTyrAlaHisLysPheValGluAspIleGlnHisAsp 668
 QY 2098 CTCAGCTACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2130
 Db 669 LeuThrTyrAsnLeuArgGluGlyHisLeuSerAspValIleSerArgLeuSerAsnLys 688
 QY 2131 GCAGAGGTGGACACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2184
 Db 689 SerThrValProGlnAlaGluProLysGlyAsnGlySerIleLysLysArgLeuProSer 708
 QY 2185 -----GAGGAGAGGACAGATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2235
 Db 709 IleValGluAspGluGluGluGluValGluGluGluGluGluGluGluGluGlu 728
 QY 2236 GCTGATGAGCCCTCAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2295
 Db 729 IleTyrThrArgGlySerSerValSerHisSerLysLysThrGlySerSerLysSerTyr 748
 QY 2296 AAGCTGCTATCCCACTGCA-----ACAGCAGC-----CGGCT---CGT 2334
 Db 749 LeuGlyLeuSerLeuLysGlnLeuThrSerGlyThrValProPheHisSerProIleArg 768

QY 2335 CTAGTGGCAGAGGAGGCCAGGCGGCGGCTTTGAAGCTGAGGCTGGCCCTCT 2394
 Db : : : : :
 769 ValSerSerAlaAsnSerPro-----LysThrLysGlnGluAlaAspProPro 784
 QY 2395 GCTCCCGCCAGGCGCCCTAGAG-----GGCTACGGCTGCCCGCCATGCCATGAAT 2445
 Db : : : : :
 785 AsnHisGlyThrArgLysGluLysAsnLeuLysValGlnLeuCysSerLeuGlyThrAla 804
 QY 2446 GTGCCCGCATGTGAGCCCGGAGTGTAGATTCGATTCGACGAGCTGTGCTCGGAC 2505
 Db : : : : :
 805 GlyThrProGluLeuSerProArgLysValAspGlyLeuGluAspGlyAsnSerSerGlu 824
 QY 2506 CAGCCCAAG--TTCTCTTCCCGCGGCGGCGGCTGTGCGCGGAGTGTAGCAGACGCC 2562
 Db : : : : :
 825 GluThrGlnThrPheAspPheGlySerGluGlnLeuArgProGluProArgLysSerPro 844
 QY 2563 TCCCTCGGACCCAGAG-----ACGCGCTCTCCTACTGTTCCTCCCATGGCCCGCCAGG 2613
 Db : : : : :
 845 SerLeuGlyGluSerGluLeuGlyAlaAlaPheLeuPheile-----Lys 859
 QY 2614 GCAAGGAACACA---GACACTGGACAACTTCGCGAGCGGTGACAGAGCTGTCCAG 2670
 Db : : : : :
 860 AlaGluGluThrLysGlnGlnLeuAsnLysLeuAsnSerGluValThrThrLeuThrGln 879
 QY 2671 CAGTCTGCTGCATCGGGAAGAGTGTAGTCACTTCGCGAGGCTGTGCGAGTGTCTCTG 2730
 Db : : : : :
 880 GluValSerGlnLeuGlyLysAspMetArgSerLysMetGlnLeuLeuGluAsnLeu 899
 QY 2731 GCGCCCGCCAGGAGGCTCGGCGCTCGGCGATCGGAGAGGCGGCTGCGCCAGCCAGC 2790
 Db : : : : :
 900 SerProGlnGlnProSerGlnPheCysSerLeuHisProThrSerLysCysProSerArg 919
 QY 2791 ACCTCGGCGCTTGCAGCGCTGTGTGTGACACTGGCGGCGATCTCTCTACTGCTCGTGCAG 2850
 Db : : : : :
 920 GluSerPheGlnThrArg-----ValSerTrpSerAlaHisGlnProCysLeuHis 936
 QY 2851 CCCCAGCT-----GGCTCTGCTTGAAGTGGAGCTTGGCCCGCCAG 2889
 Db : : : : :
 937 LeuGlnAlaAsnGlyAlaHisLeuThrHisGlyAsnValThrSerAspLeuTrp----- 954
 QY 2890 CTTCTCGCGGCGCTCTCCCTCATGTCACCTGCGCTGGCTGGCTGCGCCAGCGTCTCAG 2949
 Db : : : : :
 955 -----SerValAspProSerLeuValGlySerAsnProGlnArgThrGluAlaHisGlu 972
 QY 2950 AGCTCCCGC----- 2958
 Db : : : : :
 973 GlnSerProValAspSerGluLeuHisHisSerProAsnLeuAlaThrSerProSerHis 992
 QY 2959 -----TGGCTCGAGCCACCA 2973
 Db : : : : :
 993 CysGlnValIleGlnGluGlyHisLeuGlnPheLeuArgCysLysSerProHisSerAsp 1012
 QY 2974 GCTTCTCGACCTCCACCTCAGACTCAGAGCCCGCTGCTCAGAGACCTGCTCTGAG 3033
 Db : : : : :
 1013 ThrThrLeuThrProLeuGlnSerLysAlaThrLeuSerSerValCysSerSer 1032
 QY 3034 CCCAGCACCCCT-----GCCTCCCTCTCTCTGAGGAGGCGCTAGGACT-- 3081
 Db : : : : :
 1033 SerGluThrSerLeuHisLeuValLeuProSerArgSerGluGluGlySerLysThrHis 1052
 QY 3082 GGGCCCGCAGAGCTGTGAGCGAGCTGAGCTACCGAGCTGAGAGCCCGCCAGCCAGGG 3141
 Db : : : : :
 1053 GlyProValSerSerPheSerLeu-----GluAsnLeuProGly 1065
 QY 3142 TCAGGGGCGCTGGCTTGGCTGGGAC 3168
 Db : : : : :
 1066 Ser-----TrpAsp 1068
 Db : : : : :
 RESULT 6
 KCH4 HUMAN
 ID KCH4 HUMAN
 AC Q9U005;
 DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Potassium voltage-gated channel subfamily H member 4 (Ether-a-go-go-
 DE like potassium channel 1) (ELK channel 1) (ELK1) (Brain-specific eag-
 DE like channel 2) (BEC2).
 GN KCNH4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=99386988; PubMed=10455180;
 RA Miyake A., Mochizuki S., Yokoi H., Kohda M., Furuichi K.;
 RT "New ether-a-go-go K+ channel family members localized in human
 RT telencephalon."
 RL J. Biol. Chem. 274:25018-25025(1999).
 CC -!- FUNCTION: Pore-forming (alpha) subunit of voltage-gated potassium
 CC channel. Elicits an outward current, but shows no inactivation.
 CC Channel properties may be modulated by cAMP and subunit assembly.
 CC -!- SUBUNIT: The potassium channel is probably composed of a homo- or
 CC heterotetrameric complex of pore-forming alpha subunits that can
 CC associate with modulating beta subunits.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Detected only in brain, in particular in the
 CC telencephalon. Detected in putamen and caudate nucleus, and at
 CC lower levels in cerebral cortex, occipital and hippocampus.
 CC -!- DOMAIN: The segment S4 is probably the voltage-sensor and is
 CC characterized by a series of positively charged amino acids at
 CC every third position.
 CC -!- SIMILARITY: Belongs to the potassium channel family. H (Bag)
 CC subfamily.
 CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
 CC -!- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.
 CC -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
 CC -----
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 CC -----
 DR EMBL; AB022698; BAAR3592.1; -;
 DR Genbank; HGNC:6253; KCNH4.
 DR MIN; 604528; -;
 DR GO; GO:0008076; C:voltage-gated potassium channel complex; TAS.
 DR GO; GO:0005249; F:voltage-gated potassium channel activity; TAS.
 DR GO; GO:0006813; P:potassium ion transport; TAS.
 DR InterPro; IPR000595; CNMP binding.
 DR InterPro; IPR003967; Efg channel.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR01622; K-channel_pore.
 DR InterPro; IPR005820; M-channel_nlg.
 DR InterPro; IPR001610; PAC.
 DR InterPro; IPR000700; PAS-assoc.C.
 DR InterPro; IPR000114; PAS domain.
 DR Pfam; PF00027; CNMP binding; 1.
 DR Pfam; PF00520; ion_trans; 1.
 DR Pfam; PF00785; PAC; 1.
 DR PRINTS; PR01470; ERGCHANNEL.
 DR SMART; SM00100; CNMP; 1.
 DR SMART; SM00086; PAC; 1.
 DR SMART; SM00091; PAS; 1.
 DR TIGRFAMs; TIGR00229; sensory_box; 1.
 DR PROSITE; PS00888; CNMP_BINDING_1; FALSE_NEG.
 DR PROSITE; PS00889; CNMP_BINDING_2; FALSE_NEG.
 DR PROSITE; PS50042; CNMP_BINDING_3; 1.
 DR PROSITE; PS50112; PAS; 1.
 DR PROSITE; PS50113; PAC; 1.
 DR Transport; Ion transport; Ionic channel; Voltage-gated channel;

J. Neurosci. 21:4609-4624 (2001).

-!- FUNCTION: Pore-forming (alpha) subunit of voltage-gated potassium channel. Elicits an outward current, but shows no inactivation. Channel properties may be modulated by cAMP and subunit assembly.

-!- SUBUNIT: The potassium channel is probably composed of a homo- or heterotetrameric complex of pore-forming alpha subunits that can associate with modulating beta subunits.

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- TISSUE SPECIFICITY: Highly expressed in adult testis, and in adult and embryonic brain. In adult brain found in piriform cortex, olfactory tubercle, cerebral cortex, hippocampus pyramidal cells and dentate gyrus and basal ganglia of caudate/putamen and accumbens nucleus. Detected at intermediate levels in lung, spinal cord, and pituitary.

-!- DEVELOPMENTAL STAGE: Expressed at day E18 in embryonic brain.

-!- DOMAIN: The segment S4 is probably the voltage-sensor and is characterized by a series of positively charged amino acids at every third position.

-!- SIMILARITY: Belongs to the potassium channel family. H (Bag) subfamily.

-!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.

-!- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.

-!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.

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EMBL; AJ007628; CAA07587.1; -
 EMBL; AB022699; BAA83593.1; -
 PIR; T31354; T31354.
 InterPro; IPR000595; CNMP binding.
 InterPro; IPR003967; Exg channel.
 InterPro; IPR005821; Ion trans.
 InterPro; IPR001622; K-channel pore.
 InterPro; IPR005820; M-channel_n19.
 InterPro; IPR001610; PAC.
 InterPro; IPR000700; PAS-assoc C.
 InterPro; IPR000014; PAS domain.
 Pfam; PF00027; CNMP binding; 1.
 Pfam; PF00520; ion_trans; 1.
 Pfam; PF00785; PAC; 1.
 PRINTS; PR01470; ERGCHANNEL.
 SMART; SM00100; CNMP; 1.
 SMART; SM00086; PAC; 1.
 SMART; SM00091; PAS; 1.
 TIGRFAMs; TIGR00229; sensory box; 1.
 PROSITE; PS00888; CNMP_BINDING_1; FALSE_NEG.
 PROSITE; PS00889; CNMP_BINDING_2; FALSE_NEG.
 PROSITE; PS00442; CNMP_BINDING_3; 1.
 PROSITE; PS01112; PAS; 1.
 PROSITE; PS01113; PAC; 1.
 PROSITE; PS01113; PAC; 1.
 TransProt; Ion transport; Ionic channel; Voltage-gated channel;
 Potassium channel; Potassium; Potassium transport; Transmembrane;
 Glycoprotein; Multigene family.
 KW DOMAIN 1 232 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 233 253 SEGMENT S1 (POTENTIAL).
 FT TRANSMEM 263 283 SEGMENT S2 (POTENTIAL).
 FT TRANSMEM 284 305 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 306 326 SEGMENT S3 (POTENTIAL).
 FT TRANSMEM 335 355 SEGMENT S4 (POTENTIAL).
 FT TRANSMEM 356 364 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 365 385 SEGMENT S5 (POTENTIAL).
 FT TRANSMEM 428 448 SEGMENT H5 (PORE-FORMING) (POTENTIAL).
 FT TRANSMEM 455 475 SEGMENT S6 (POTENTIAL).
 FT TRANSMEM 476 1017 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 14 90 PAS.
 FT DOMAIN 93 145 PAC.
 FT NP_BIND 557 672 CNMP.

FT CARBOHYD 415 415 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CONFLICT 825 825 R -> W (IN REF. 1).
 SQ SEQUENCE 1017 AA; 111403 MW; BFDHOFIB35437C9F CRC64;
 Alignment Scores:
 Pred. No.: 4,04e-101 Length: 1017
 Score: 2447.50 Matches: 533
 Percent Similarity: 60.09% Conservative: 131
 Best Local Similarity: 48.24% Mismatches: 243
 Query Match: 40.20% Indels: 198
 DB: 1 Gaps: 23
 US-09-965-830-1_COPY_6_3257 (1-3252) x KCHA_RAT (1-1017)
 QY 1 ATGCCGCCATCGGGGCTCTGGCGCTCAGACACCTCTCTGACACCATCGCTACG 60
 Db 1 MetProValMetTysGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20
 QY 61 CGCTTCGACGGCAGCAGCAGTAACTTCGTCTGGCAAGCCGAGGTGGCGGGCTCTTC 120
 Db 21 ArgPheAspGlyThrHisSerAsnPheLeuLeuAlaAsnAlaGlnGlyProArgGlyPhe 40
 QY 121 CCCGTGCTCTACTGCTCTGATGGCTTCTGTGACTCAGGGCTTCTCCGGGCTGAGTTC 180
 Db 41 ProIleValTyrCysSerAspGlyPheCysGluLeuThrGlyTyrGlyArgThrGluVal 60
 QY 181 ATGCAGCGGGCTGCTGCTCTCTCTTCTTATGGCCACACACCATGAGTCTCGTCCGC 240
 Db 61 MetGlnTysThrCysSerCysArgPheLeuTyrGlyProGluThrSerGluProAlaLeu 80
 QY 241 CACAGATCCGCAAGGCTCTGACGACGACCAAGGAGTTCAAGGCTGAGTCTCTCTATC 300
 Db 81 GlnArgLeuGlnTysAlaLeuGluGlyHisGlnGluHisArgAlaGluIleCysPheTyr 100
 QY 301 CGGAAGAGCGGGCTCCCGTCTCTGTGTCTCTGTGATGTATGCCATTAAGAAATGAGAA 360
 Db 101 ArgLysAspGlySerAlaPheTyrCysLeuLeuAspMetMetProIleLysAsnGluLeu 120
 QY 361 GGGGAGTGGCTCTCTCTCTAGTCTCTCAGAGGACATCAGCGAAACCAAGAACCGAGG 420
 Db 121 GlyGluValValLeuPheLeuPheSerPheLysAspIleSerGlnSerGlyGlyProGly 140
 QY 421 -----GGCCCCCAGACAGATGGAAGGAGAGACAGGTGGTGGCGGCGGC 459
 Db 141 LeuGlySerProGlyIleHisGlyAspAsnAsnHisGluAsnSerLeuGlyArg--- 159
 QY 460 CGATATGGCGGCGACGATCCAAAGGCTTCAATGCCAACCGCGCGGCGAGCGGCGCTG 519
 Db 160 -----ArgGlyAlaSerSerArgLeuArgSerThrArgArgGlnAsnArgThrVal 176
 QY 520 CTCTACACCTGTCCGGGCACCTGCAGAGCAGCCCAAGGCGCAAGCACAAGCTCAATAAG 579
 Db 177 LeuHisArgLeuThrGlyHisPheGlyArgArgAspGlnGlySerValLysAlaAsnSer 196
 QY 580 GGGGTGTTTGGGAGAAACCAAACTGTGCTGAGTACAAAGTAGCCGATCCGGAAGTCG 639
 Db 197 AsnValPheGluProLysProSerValProGluTyrLysValAlaSerValGlyGlySer 216
 QY 640 CCCTTCATCTCTGCTGCTGGGACCTGAGAGCCACTGGGATGGCTTCACTCTCTCTC 699
 Db 217 ArgCysLeuLeuLeuHisTyrSerIleProLysAlaValTrpAspGlyLeuLeuLeu 236
 QY 700 GCCACACTCTATGCTGCTCACTGTGCGCTGACGCTGTGTGTGTGAGCAGCAGCGGAG 759
 Db 237 AlaThrPheTyrValAlaValThrValProTyrAsnValCysPheAlaGlyAspAsp 256
 QY 760 CCCAGTGGCGCGCGCGCGCGCGCGCTGTGCTGACCTGGCGGTGAGTCTCTCTCAATC 819
 Db 257 ThrProIleThrSerArgHisThrLeuValSerAspIleAlaValGluMetLeuPhe 276
 QY 820 CTGTGACATTGTGCTGAATTTCCGTATCCACCATTCGTGTCGAGTCGCGGCGAGTGGT 879
 Db 277 LeuAspIleLeuAsnPheArgThrThrTyrValSerGlnSerGlyGlnValSer 296

QY	880	GCCCCAAGTCCATTGGCTCCACTACGTCACCACTGGTTCCTGCTGGATGTCATCGCA	933
Db	297	AlaProArgSerIleGlyLeuHisTyrIleuAlaThrPhePheValAspLeuAla	316
QY	940	GGCTGCCCTTTGAACTGCTACATCCCTTCAAGGTCAAAGTGTACTTCGGGGCCCATCTG	999
Db	317	AlaLeuProPheAspLeuLeuTyrValPheAsnIleThrValThrSerLeuValHisLeu	336
QY	1000	CTGAAGAGCGGTGCGCTGCTGGCTGGCTGGCTGGCTTCGCGGGCTGGACCGGTACTCG	1059
Db	337	LeuIysThrValArgLeuLeuArgLeuLeuArgLeuGlnIysLeuGluArgTyrSer	356
QY	1060	CAGTACAGCGCGTGGTGTGTGACACTGTCTATGGCGGTGTCGGCTGCTCGCGCACTGG	1119
Db	357	GlnCysSerAlaValValLeuThrLeuLeuMetSerValPheAlaLeuLeuAlaHisIleP	376
QY	1120	GTGCGCTCGGTCTGGTTTATCATTTGGCCAGCGGAGATCGAGACGACGGAATCCGAGCTG	1179
Db	377	MetAlaCysValTrpTyrValIleGlyArgGluMetGluAlaAsnAspProLeuLeu	396
QY	1180	CTGTAGATTGGTGGCTGCAGAGCTGCGCCGCGACTGGAGACTCCCTACTACCTGGTG	1239
Db	397	TrpAspIleGlyTrpLeuHisGluLeuGlyLysArgLeuGluGluProTyr	413
QY	1240	GGCGGAGCGCAGCTGGAGGAAAGACTCGCGCCAGAGTGACAACTGCACAGCAGCAGC	1299
Db	413	-----	413
QY	1300	GAGGCCAACGGACGGGGCTGGAGCTGCTGGGCGGCCGTGCTGGCAGCGCTATCATC	1359
Db	414	---ValAsnGlySerAla-----GlyGlyProSerArgArgSerAlaTyrIle	428
QY	1360	ACCTCCCTCTACTTTGCGACTCAGCAGCTCACCAGCGTGGGCTTCGCAACGTGTCGCC	1419
Db	429	AlaAlaLeuTyrPheThrLeuSerSerLeuThrSerValGlyPheGlyAsnValCysAla	448
QY	1420	AACACGACACCGAGAAGATCTTCTCCATCTGCACCATGCTCATCGCGCGCCGTATGCC	1479
Db	449	AsnThrAspAlaGluIysIlePheSerIleCysThrMetLeuIleGlyAlaLeuMetHis	468
QY	1480	GCGTGTGTGTTGGGAACGTGAACGGCCATCATCCAGCGCATGTACGCCCGCCCTTTCTG	1539
Db	469	AlaValValPheGlyAsnValThrAlaIleIleGlnArgMetTyrSerArgArgSerLeu	488
QY	1540	TACCACAGCGCACGCGCGACCTGCGGACTACATCGCATCCACCGTATCCCAAGCCC	1599
Db	489	TyrHisSerArgMetIysAspLeuIysAspPheIleArgValHisArgLeuProArgPro	508
QY	1600	CTCAAGCAGCGCATGTGTGAGTAGTCTTCAGCGCCACTGGGCGGTGAACATGCATCGAC	1659
Db	509	LeuIysGlnArgMetLeuGluTyrPheGlnThrThrTipAlaValAsnSerGlyIleAsp	528
QY	1660	ACACCGAGTGTGACAGCCTCCCTGACGAGCTGGCGCGACATCCGCTATGCACCTG	1719
Db	529	AlaAsnGlnLeuLeuArgAspPheProAspGluLeuArgAlaAspIleAlaMetHisLeu	548
QY	1720	CACAAGGAGTCTGCAGCTGCCACTGTTTGAGCGGCCAGCGCGGCTGCCTGGCGGCA	1779
Db	549	AsnArgGluLeuLeuGlnLeuProLeuPheGlyAlaAlaSerArgGlyCysLeuArgAla	568
QY	1780	CTGTCTGTGCGCCCTGGCGCCGCTTCTGTCAGCGCGGCGAGTAGTCTCATCCACCAAGC	1839
Db	569	LeuSerLeuHisIleIysThrSerPheCysAlaProGlyGluPheLeuLeuArgArgGly	588
QY	1840	GATGCCCTGACGGCCTCTACTTTGTGTCTGCTCCATGGAGTGTCTCAAGGGTGGC	1899
Db	589	AspAlaLeuGlnAlaHisTyrTyrValCysSerGlySerLeuGluValLeuArgAspAsn	608
QY	1900	ACCGTGTCTGCCATCTCAGGAGGAGCGACCTCATCGGCTGTGAGCTGCCCGCGGGAG	1959
Db	609	ThrValLeuAlaLeuGlyIysGlyAspLeuIleGlyAlaAspIleProGluLeuGly	628

QY	1960	CAG	-----GTGTAAAGGCCAATGCCAGCTGTAAGGGGCTG	1995
Db	629	GlnGluProGlyAlaGlyAlaGlyCysValLeuIysThrSerAlaAspValIysAlaLeu	648	
QY	1996	ACGTACTGCTGCTCAGCTGCTCAGCTGGCTGGCTGCACGACGCTTGCCTGCTAC	2055	
Db	649	ThrTyrCysGlyLeuGlnGlnLeuSerArgGlyLeuAlaGluValLeuArgLeuTyr	668	
QY	2056	CCCGAGTTTGGCCCGCTCAGTCGTGGCTCCGAGGGGAGCTCAGCTACAACCTGGT	2115	
Db	669	ProGluTyrValAlaAlaPheArgAlaGlyLeuProArgAspLeuThrPheAsnLeuArg	688	
QY	2116	GCTGGGGGA-----GGCTCTGCA	2133	
Db	689	GlnGlySerGluAsnAsnGlyLeuGlyArgPheSerArgSerProArgLeuSerGlnAla	708	
QY	2134	GAGGTGGACACGAGCTCCCTCAGCGGGCACAATACCTTATGTCACGCTGGAGGAGAAG	2193	
Db	709	ArgSerAspThrLeuGlySerSerSerAspIysThrLeuProSerIle-----Thr	725	
QY	2194	GAGACAGATGGGGACGAGGGCCACACGCTCTCCCGAGCCCGAGCTGATGAGCCCTCCAGC	2253	
Db	726	GluThrGluGly-----GlyMetGluProGlyAlaGlySerIysProArgArg	741	
QY	2254	CCCCTGCTGCTCCCTGGCTGCACCTCTCATCTCAGCTGCCAAGCTG-----	2301	
Db	742	ProLeuLeuLeuProAsnLeuSerProAlaArgProArgGlySerLeuValSerLeuLeu	761	
QY	2302	-----CTATCCCCACGTCA	2316	
Db	762	GlyGluGluLeuProPheSerAlaLeuValSerSerProSerLeuSerPro-----	779	
QY	2317	ACAGCACCCCGGCTCTAGTGGCAGAGGAGGAGCGAGGCGAGGCGGGCTTTGAAG	2376	
Db	780	--ThrProSerProAlaLeuAlaGlyArgGly-----	789	
QY	2377	GCTCAGGCTGGCCCTCT-----GCTCCCCACGGGCCCTAGAGGG-----	2418	
Db	790	-----SerSerProSerLeuHisGlyProProArgGlySerAlaAlaTrpLysProPro	807	
QY	2419	---CTACGGCTGCCCCCATGCCATGGAATGTCGCCCGCAGATCTGAGCCCGAGGTAGTA	2475	
Db	808	GlnLeuLeuThrProProLeuGlyThrPheGlyProProAspLeuSerProArgIleVal	827	
QY	2476	GATGGCAATTGAACACGGCTGGC-----TCGGACACGCCCAAGTCTCTTCCGCGTGGGC	2532	
Db	828	AspGlyIleGluAspSerSerAsnThrAlaGluAlaProThrPheArgPhe-----	844	
QY	2533	CAGTCTGGCCGGAATGTAGCAGACGCCCTCCCTGGACCCAGAGCGGCTGTCTACT	2592	
Db	845	SerIysArgProGluProThrArgThrArgSerGlnAlaProLeuSer-----	860	
QY	2593	GTCCCCATGGGCCCCAGCGACGACAGAC-----ACAGACACTGGAACAGCTCGG	2646	
Db	861	-----GlyProArgLeuSerArgGluLeuAlaThrGluAlaAlaGluGluValIys	877	
QY	2647	CAGCGCGTCACAGCTGTCCAGACAGGTGCTGCAGATGCGCGGAAGGACTGCAGTCACTT	2706	
Db	878	GluIysValCysArgLeuAsnGlnGluIleSerArgLeuAsnGlnGluValSerGlnLeu	897	
QY	2707	CGCCAGGCTGTGAGCTTCTCTGGCGGCCACAGAGGAGGGTCCGTGCCCTCGGCGATCG	2766	
Db	898	SerArgGluLeuArgGlnValMet-----	905	
QY	2767	GGAGAGGGCCGTGCCACCGACGACCTCGGGCTTCTGCAGCCTCTGTGTGGACACT	2826	
Db	906	-----GlyLeuLeuGlnAlaArg-----	911	
QY	2827	GGGGCATCTCTACTGCTGCAGCCCCCAGCTGCTCTGTCTTTCAGTGGGACTTGGCCC	2886	
Db	912	-----LeuGlyProProSer-----	916	
QY	2887	CACCTCTGTCGGGGCTCTCTCCCTCATGGCACCTCGCCCTGGGGTCCCGCCAGCGTCT	2946	

Db 101 valHisLeuLeuLysThrValArgLeuLeuArgLeuLeuLeuGlnLysLeuAsp 120
QY 1051 CGGTACTCGCAGTACAGCGCGGTGCTGCTCACACTGCTCATGCCGCTGTCGCGCTC 1110
Db 121 ArgTyrSerGlnHisSerThrIleValLeuThrLeuLeuMetSerMetPheAlaLeuLeu 140
QY 1111 GCGCATGGTCCGCTCGCTGCTGTTTACATTGGCCAGCGGAGATCGAGAGCGCAA 1170
Db 141 AlaHisTrpMetAlaCysIleTrpTyrValIleGlyMetGluArgGluAspAsnSer 160
QY 1171 TCCGAGCTGCTCAGATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1230
Db 161 LeuLeuLysTrpGluValGlyTrpLeuHisGluLeuGlyLysArgLeuGluSerProTyr 180
QY 1231 TACCTGGTGGCGCGGAGCGCTGCGAGGAAAGCTGCGGCGCAGAGTGACACTGACG 1290
Db 181 Tyr-----GlyAsnAsnThr----- 185
QY 1291 AGCAGCAGCGAGGCCAACCGGAGCGGGCTGGAGCTGCTGGGCGGCCGCTGCGCAGC 1350
Db 186 -----LeuGlyGlyProSerIleArgSer 193
QY 1351 GCCTACATCACCTCCTCTACTTCGACCTCAGCAGCTCAGCAGCTGCGGCTTGGCAAC 1410
Db 194 AlaTyrIleAlaAlaLeuThrPheThrLeuSerSerLeuThrSerValGlyPheGlyAsn 213
QY 1411 GTGTCGCGCAACACGACGACCGAGAAAGATCTTCTCCATCTGCACCATGCTCATCGCGCC 1470
Db 214 ValSerAlaAsnThrAspAlaGluLysIlePheSerIleCysThrMetLeuIleGlyAla 233
QY 1471 CTGATGCAGCGGTGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1530
Db 234 LeuMetHisAlaLeuValPheGlyAsnValThrAlaIleGlnArgMetTyrSerArg 253
QY 1531 CGCTTCTGTACACAGCG 1590
Db 254 TrpSerLeuTyrHisThrArgThrLysAspLeuLysAspPheIleArgValHisLeu 273
QY 1591 CCCAAGCCCTCAAGCAGCGCTGCTGGAGTACTTCCAGCGCCACTGGCGGTGAACAT 1650
Db 274 ProGlnGlnLeuLysGlnArgMetLeuGluTyrPheGlnThrThrTrpSerValAsnAsn 293
QY 1651 GGCATCGACACACGAGCTGTGAGAGCTCTCCAGCAGCTCCCTGAGCGCGCGAGCATCGCC 1710
Db 294 GlyIleAspSerAsnGluLeuLysAspPheProAspGluLeuArgSerAspIleThr 313
QY 1711 ATGCACCTGCACAGGAGCTCTGAGCTGCCACTGTTTGGCGCGCGCGCGCGCGCGCTG 1770
Db 314 MetHisLeuAsnLysGluIleGlnLeuSerLeuPheGluCysAlaSerArgGlyCys 333
QY 1771 CTGCGGCGACTGTCTGTGGCCCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1830
Db 334 LeuArgSerLeuSerLeuHisIleLysThrSerPheCysAlaProGlyGluTyrLeuLeu 353
QY 1831 CACCAAGCGATGCTGCGAGCGCTCTACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1890
Db 354 ArgGlnGlyAspAlaLeuGlnAlaIleTyrPheValCysSerGlySerMetGluValLeu 373
QY 1891 AAGGTGGCACCGCTCGCCATCTAGGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1950
Db 374 LysAspSerMetValLeuAlaIleLeuGlyLysGlyAspLeuIleGlyAlaAsnLeuSer 393
QY 1951 CGCGGAGCAGGTGGTAAAGCGCAATGCCAGCTGAAGGGCTGAGCTACTGCTGCTGCTG 2010
Db 394 IleLysAspGlnValIleLysThrAsnAlaAspValLysAlaLeuThrTyrCysAspLeu 413
QY 2011 CAGTGTCTGAGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2070
Db 414 GlnCysIleIleLeuLysGlyLeuPheGluValLeuGlyLeuTyrProGluTyrAlaHis 433
QY 2071 CGCTTCAGTGTGCGCTCCGAGGGAGCTCAGCTACAACTGGGTGGTGGTGGTGGTGGT 2121
Db 434 LysPheValGluAspIleGlnHisAspLeuThrTyrAsnLeuArgGluGlyHisGluSer 453

QY 2122 -----GGAGCTCTGCAGAGTGGACACACAGCTCCTCCTGAGCGCGAC 2163
Db 454 AspValIleSerArgLeuSerAsnLysSerThrValSerGlnAlaGluProLysGlyAsn 473
QY 2164 AATACCTTATGTCACGCTG-----GAGGAGAGGACAGACAGATGGGAG 2208
Db 474 GlySerIleAsnLysArgLeuProSerIleValGluAspGluGluGluValGlu 493
QY 2209 CAGGCGCCACAGCTCTCCCGAGCGCGCTGATGAGCCCTCCAGCCCTGCTGCTGCTGCT 2268
Db 494 GluGluGluThrThrSerLeuSerProIleTyrThrArgGlySerSerValSerHisSer 513
QY 2269 GGTGTCACCTCTCATCTCAGCTGCCAAGCTGCTATCCCGACGTGCGAACAGCACCCCGG 2328
Db 514 LysLysThrGlySerAsnLysThrTyrLeuGlyLeuSerLeuLysGlnLeuAlaSerGly 533
QY 2329 CCT-----CGTCTAGTGGCAGAGGAGCGCGCGCGCGCGCGCGCGCGCGG 2367
Db 534 ThrValProPheHisSerProIleArgValSerSerAlaAsnSerPro----- 549
QY 2368 GCTTTGAAGGCTGAGGCTGGCGCTCTGCTCCCGACGCGCGCTAGAG-----GGG 2418
Db 550 LysThrLysGlnGluAlaAspProProAsnHisGlyArgLysGlnLysAsnLeuLys 569
QY 2419 CTACGCTGCCCGCCCATGTCATGGAATGTCGCCCGACATCTGAGCCCGAGGTAGTAGAT 2478
Db 570 ValGlnLeuSerSerLysSerAlaGlyThrProGluLeuSerProArgIleValAsp 589
QY 2479 GGCATTGAAGCGGTGGCTGGCGACCGACCGCAAG-----TTCTCTTCCGCTGGCGCAG 2535
Db 590 GlyIleGluAspGlyAsnSerAsnGluGluThrGlnThrPheAspPheGlySerGluGln 609
QY 2536 TGTGCGCGCGAATGTAGCAGCAGCGCCCTCCCTGCGACGAGCGCGCTGCTCACTGTT 2595
Db 610 IleArgProGluProArgIleSerPro---ProLeuAlaGluSerGluIle----- 625
QY 2596 CCCCATGGCGCCAGC-----GAGCAAGGAACACACA---GACACACTGGACAG 2640
Db 626 -----GlyAlaAlaPheLeuPheIleLysAlaGluGluThrLysGlnGlnIleAsnLys 643
QY 2641 CTTCGCGCGCGGTGACAGAGCTGTGACAGAGGTGTGAGATGCGGGAGAGGATCGAG 2700
Db 644 LeuAsnSerGluValThrThrLeuThrGlnGluValSerGlnLeuGlyArgAspMetArg 663
QY 2701 TCATCTCGCAGGCTGTGCTGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 2748
Db 664 SerIleMetGlnLeuLeuGluAsnIleLeuSerProGlnGlnProSerGlnPheCysSer 683
QY 2749 -----CGTGCCTCGGCGCATCGGAGAGGCGCGCTGCCAGCGACCGCTCGCGGCTT 2802
Db 684 LeuHisProThrProMet-----CysProSerArgGluSer----- 695
QY 2803 CTGCGAGCTCTGTGTGAGACACTGGGCGCATCTCTCTACTGCTGCGAGCGCGCGAGCT 2859
Db 696 LeuGlnThrArg---ValSerTrpSerAlaHisGlnProCysLeuHisLeuGlnAlaGly 714
QY 2860 -----GGCTCTGCTGTGAGTGGGACTTGGCCCGCGCGCGCGCGCGCGCGCGCGG 2901
Db 715 GlyAlaHisLeuTyrHisGlyAsnValAlaSerGlyIleTrp-----SerVal 730
QY 2902 CTTCTCTCCCTCATGGCACCTGGCGCTGGGGTCCCGACGCTCTCAGAGCTCCCC--- 2958
Db 731 AspProSerLeuValGlySerSerProGlnArgThrGluAlaHisGluGlnAsnProAla 750
QY 2958 ----- 2958
Db 751 AspSerGluLeuHisSerProAsnLeuAspTyrSerProSerHisCysGlnValIle 770
QY 2959 -----TGGCTCGAGCGCACAGCTTTCGAGCC 2985
Db 771 GlnGluGlyHisLeuGlnPheLeuArgCysIleSerProHisSerAspThrThrLeuThr 790


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1  MetProValArgArgGlyHisValAlaProGlnAsnThrPheLeuAspThrIleArg 20
  |||||  |||||  ::|||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
61  CGCTTCAGCGGACGACAGTAACCTCGTGTGGCAACCGCCAGGTCGGGGCTCTTC 120
  ::|||  ::|||  |||||  ::|||  ::|||  ::|||  ::|||  ::|||  ::|||  ::|||
21  LysPheGluGlyGlnSerArgLysPheIleAlaAsnAlaArgValGluAsnCys--- 39
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
121  CCCTGTCTACTCTGTGATGGCTTCGTGACCTACCGGGCTTCCTCCGGGCTGAGTC 180
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
40  AlaValIleTyrCysAsnAspGlyPheCysGluLeuCysGlyTyrSerArgAlaGluVal 59
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
181  ATCAGCGGGCTGTGCTCTCTCTCTTATGGCCACACACAGTCGTCGCCG 240
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
60  MetGlnArgProCysThrCysAspPheLeuHisGlyProArgThrGlnArgArgAlaAla 79
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
241  CAACAGATCCGAGGCCCTGGACGACCAAGAGTTCAGGCTGAGCTGATCCTGTAC 300
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
80  AlaGlnIleAlaGlnAlaLeuLeuGlyAlaGluGluArgLysValGluIleAlaPheTyr 99
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
301  CGGAAGAGCGGCTCCGGTCTCGGTCTCTCGTGTATGATACCCATAAAGATGAGAAA 360
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
100  ArgLysAspGlySerCysPheLeuCysLeuValAspValValProValLysAsnGluAsp 119
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
361  GGGGAGGTGGCTCTCTCTCTA-----GTCTCTCACAAAGACATC----- 399
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
120  GlyAlaValIleMetPheIleLeuAsnPheGluValValMetGluLysAspMetValGly 139
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
400  -----AGCCAAACCAAGAACCGAGGGGCCGACAGATGGAAGGAGACAGT--- 447
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
140  SerProThrHisAspThrAsnHisArgGlyProProThrSerTyrLeuAlaProGlyArg 159
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
447  ----- 447
160  AlaLysThrPheArgLeuLysLeuProAlaLeuLeuAlaLeuThrArgGluSerSer 179
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
447  ----- 447
180  AlaArgProGlyGlyValGlySerAlaGlyAlaProGlyAlaValValAspValAsp 199
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
447  ----- 447
200  LeuSerProAlaValProSerArgGluSerLeuAlaLeuAspGluValThrAlaMetAsp 219
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
447  ----- 447
220  AsnHisValAlaGlyLeuGlyProMetGluGlnArgAlaLeuValGlySerSerSer 239
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
447  ----- 447
240  ProProAlaGlyAlaProGluProLeuProSerProArgAlaHisSerLeuAsnProAsp 259
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
448  -----GGTGGCCGGCCGATATGGCGGCGACGATCCAAAGGCTTCAATGCCAACCGG 501
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
260  AlaSerGlySerCysSerLeuAlaArgThrArgSerArgGluSerCysAlaSerVal 279
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
502  CGCGGG----- 507
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
280  ArgArgAlaSerSerAlaAspAspIleGluAlaMetArgAlaGlyLeuProProProPro 299
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
508  -----AGCCGGGCGGCTCTACACCTGTCGGGACCTCGCAGAACGAG- 552
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
300  ArgHisAlaSerThrGlyAlaMetHisProLeuArgGlyGlyLeuLeuAsnSerThrSer 319
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
552  ----- 552
320  AspSerAspLeuValArgTyrArgThrIleSerLysIleProGlnIleThrLeuAsnPhe 339
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
552  ----- 552
340  ValAspLeuLysGlyAspProPheLeuAlaSerProThrSerAspArgGluIleAla 359
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
553  CCCAAGGGCAGACAGCTCAATAAGGGGTGTTGGGAGAGAAACCAAC----- 603
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

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360  ProlLysIleLysGluArgThrHisAsn-----ValThrGluLysValThrGlnValLeu 377
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
604  -----TTGCCCTGAGTACAAAGTAGCCGCCCATCCGGAAGTCGCCCTTC 645
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
378  SerLeuGlyAlaAspValLeuProGluTyrLysLeuGlnAlaProArgIleHisArgTyr 397
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
646  ATCCTGTTCACATGTGGGACCTGAGAGCCACCTGGGATGGCTTCATCTCTGCTGCCACA 705
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
398  ThrIleLeuHisTyrSerProPheLysAlaValTyrAspTyrLeuIleLeuLeuVal 417
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
706  CTCTATGTGGCTCTACTGTGCCCTACAGCGCTGTGTGTG-----ACCACAGCACGG 756
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
418  IleTyrThrAlaValPheThrProTyrSerAlaAlaPheLeuLeuLysGluThrGluGlu 437
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
757  GAGCCACAGTGCC-----GCCCGCGCCCGCCAGCTGTGTGACCTGGCC 801
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
438  GlyProProAlaProAspCysGlyTyrAlaCysGlnProLeuAlaValValAspPheIle 457
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
802  GTGGAGCTCTCTTCATCTTCATCTTCACATTGTGCGAATTCGGTACACATTCGTGTCCAAG 861
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
458  ValAspIleMetPheIleValAspIleLeuIleAsnPheArgThrThrTyrValAsnAla 477
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
862  TCGGGCAGCTGGTGTTCGCCCAAGTCCATTGTCTCCACTAGCTACACCACTGGTTC 921
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478  AsnGluGluValValSerHisProGlyArgIleAlaValHisTyrPheLysGlyTyrPhe 497
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
922  CTGCTGGATGTCTCGACGCTGCTTCCTTACCTTACCTGCTACATGCTTCAAGGTCAACGTG 981
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
498  LeuIleAspMetValAlaIleProPheAspLeuLeu----- 510
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
982  TACTTCCGGGGCC-----CATCTGTGAAGACGGTGGCTGTGGCC 1023
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
511  IlePheGlySerGlySerGluGluLeuIleGlyLeuLeuLysThrAlaArgLeuLeuArg 530
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
1024  CTGCTGCGCTCTTCCCGGCTGACCGGTACTCGCAGTACAGCGCGTGGTGGTGCAC 1083
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
531  LeuValArgValAlaArgLysLeuAspArgTyrSerGluTyrGlyAlaAlaValLeuPhe 550
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
1084  CTGCTCATGGCGGTTCGCTCGCTCGCAGTCTGGGTGCGCTGCTGTGTTTACATT 1143
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
551  LeuLeuMetCysThrPheAlaLeuIleAlaHisTrpLeuAlaCysIleTyrTyrAlaIle 570
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
1144  GCCCAGCGGGAGATCGAGAGCAGCGAATCCAGCTGCTGAGATTGGCTGGCTGCAGGAG 1203
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571  GlyAsnMetGluGlnProHisMetAspSer-----ArgIleGlyTyrLeuHisAsn 587
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
1204  CTGCGCCCGCAGCTGAGACTCCCTACTACCTGTGGCGGAGGCCAGCTGGAGGAG 1263
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588  LeuGlyAspGlnIleGlyLysProTyr-----Asn 597
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
1264  AGCTCCCGCCAGAGTGACAACTGCAGCAGCAGCAGGACGAGGACGGGCTGGAG 1323
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598  SerSerGly----- 600
  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
1324  CTGCTGGCGCGCGCTGCTGCGCAGCGCTACATACCTCCCTCTACTTCGCACTCAGC 1383
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601  ---LeuGlyGlyProSerIleLysAspLysTyrValThrAlaLeuTyrPheThrPheSer 619
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620  SerLeuThrSerValGlyPheGlyAsnValSerProAsnThrAsnSerGluLysIlePhe 639
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1444  TCCATCTGCACCATGTCTATCGCGGCTGATCGACGCGTGGTGTGGTGGAACTGACG 1503
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660  AlaIleIleGlnArgLeuTyrSerGlyThrAlaArgTyrHisThrGlnMetLeuArgVal 679
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1564  CGCAGCTACATCCGATCCACCGTATCCCCAAGCCCTCAAGCAGCGCATCTGGAGTAC 1623
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680  ArgGluPheIleArgPheHisGlnIleProAsnProLeuArgGlnArgLeuGluGluTyr 699
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[illegible]

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[5]
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RA Crociani O., Guasti L., Balzi M., Becchetti A., Wanke E., Olivetto M.,
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RT cells.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
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RP SEQUENCE OF 1-376 FROM N.A. (ISOFORM 2).
RC TISSUE=Heart;
EX MEDLINE=98012815; PubMed=9351462;
RA London B., Trudeau M.C., Newton K.P., Beyer A.K., Copeland N.G.,
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RP SEQUENCE OF 27-1159 FROM N.A. (ISOFORM 1).
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RC TISSUE=Brain;
EX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
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RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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RX MEDLINE=97373956; PubMed=9230439;
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[14]
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RX MEDLINE=99235979; PubMed=10219239;
RA Abbott G.W., Sesti F., Splawski I., Buck M.E., Lehmann M.H.,
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[15]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 1-135, AND MUTAGENESIS OF
RP PHE-29 AND TYR-43.
RX MEDLINE=99059500; PubMed=9845367;
RA Morais Cabral J.H., Lee A., Cohen S.L., Chait B.T., Li M.,
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RT channel N terminus: a eukaryotic PAS domain.";
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[16]
RP VARIANTS LQT2 ASP-470; VAL-561 AND SER-628.
RX MEDLINE=95196272; PubMed=7889573;
RA Curran M.E., Splawski I., Timothy K.W., Vincent G.M., Green E.D.,
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RP VARIANT LQT2 MET-822.
RX MEDLINE=97071892; PubMed=8914737;
RA Sattler C.A., Walsh E.P., Vesely M.R., Plummer M.H., Ginsburg G.S.,
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[18]
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RX MEDLINE=96259954; PubMed=8635257;
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RP VARIANT LQT2 THR-561.
RX MEDLINE=97031865; PubMed=8877771;
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RP VARIANTS LQT2 ILE-474; HIS-611; VAL-614 AND LEU-630.
RX MEDLINE=97176600; PubMed=9024139;
RA Tanaka T., Nagai R., Tomoike H., Takata S., Yano K., Yabuta K.,
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RL Circulation 95:565-567 (1997).
 RN [21]
 RP VARIANTS LOT2 CYS-572; ASP-588; VAL-614 AND ALA-630.
 RX MEDLINE=98360095; PubMed=9693036;
 RA Splawski I., Shen J., Timothy K.W., Vincent G.M., Lehmann M.H.,
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 RT "Genomic structure of three long QT syndrome genes: KVLQT1, HERG, and
 RT KCNE1";
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 RN [22]
 RP VARIANTS LOT2 LEU-612; VAL-614; ASP-629; SER-629 AND SER-633.

Alignment Scores:
 Pred. No.: 1,356-61 Length: 1159
 Score: 1551.00 Matches: 424
 Percent Similarity: 44.86% Conservative: 143
 Best Local Similarity: 33.54% Mismatches: 337
 Query Match: 25.47% Indels: 360
 DB: 1 Gaps: 38

US-09-965-830-1_COPY_6_3257 (1-3252) x KCH2_HUMAN (1-1159)

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 QY 61 CGCTTCGAGCGGACGACAGTAACTTCGTCTGGCAACGCCAGGTGGCGGGCTCTTC 120
 Db 21 LysPheGlnGlyGlnSerArgLysPheIleAlaAsnAlaArgValGluAsnCys--- 39
 QY 121 CCGTGTCTACTCTCTGTGCTTCTGTGACTCAGCGGCTTCCTCCGGCTGAGTTC 180
 Db 40 AlaValIleTyrCysAsnAspGlyPheCysGluLeuCysGlyTyrSerArgAlaGluVal 59
 QY 181 ATGAGCGGGCTGTGCTCTCTCTTATGGGCGACACACCATGAGTCTGCTCCG 240
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 QY 241 CACAGATCCGAGCGCTGGACGACAGAGTTCAGGCTGAGCTGATCTCTATC 300
 Db 80 AlaGlnIleAlaGlnAlaLeuLeuGlyAlaGluGlyValGluIleAlaPheTyr 99
 QY 301 CGGAAGAGCGGCTCCGCTTCTGTGCTGTGATGATACCCATAAGATGAGAAA 360
 Db 100 ArgLysAspGlySerCysPheLeuCysLeuValAspValProValLysAsnGluAsp 119
 QY 361 GGGAGTGGCTCTCTCTCTA-----GTCCTCACAGGACATC----- 399
 Db 120 GlyAlaValIleMetPheIleLeuAsnPheGluValValMetGluLysAspMetValGly 139
 QY 400 -----AGCGAAACCAAGAACCGAGGGGGCGCCGACAGATGG----- 435
 Db 140 SerProAlaHisAspThrAsnHisArgGlyProProThrSerTrpLeuAlaProGlyArg 159
 QY 435 ----- 435
 Db 160 AlaLysThrPheArgLeuLysLeuProAlaLeuLeuAlaLeuThrAlaArgGluSerSer 179
 QY 436 ---AAGGAGACAGTGTGGCGCGCGCGATATGGCGGCG---ACGATCCAAAGGCTTC 489
 Db 180 ValArgSerGlyGlyAlaGly-GlyAlaGlyAla-ProGlyAlaValValAspValAla 199
 QY 490 AATGCCAACCGCGCG----- 503
 Db 199 spLeuThrProAlaAlaProSerSerGluSerLeuAlaLeuAspGluValThrAlaMetAla 219
 QY 504 -----GGGAGCGCGCGCGTCTCTA----- 524
 Db 219 spAsnHisValAlaGlyLeuGlyProAlaGluGluArgAlaLeuValGlyProGly 239
 QY 525 ---CCACTGTCCGGCAGTGCAGAGGAGCGAGGCGCAAG---CACAGTCTCAAT--- 576
 Db 239 erProProArgSerAlaProGlyGlnLeu-ProSerProArgAlaHisSerLeuAsnPro 258

QY 576 ----- 576
 Db 259 AspAlaSerGlySerSerCysSerLeuAlaArgThrArgSerArgGluSerCysAlaSer 278
 QY 577 -----AAGGGGTGTGTTGGGAG 594
 Db 279 ValArgArgAlaSerSerAlaAspAspIleGluAlaMetArgAlaGlyValLeuProPro 298
 QY 595 AAACCAAC----- 603
 Db 299 ProProArgHisAlaSerThrGlyAlaMetHisProLeuArgSerGlyLeuLeuAsnSer 318
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 Db 439 GlyProAlaThrGluCysGlyTyrAlaCysGlnProLeuAlaValValAspLeuIle 458
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 Db 552 LeuLeuMetCysThrPheAlaLeuIleAlaHisIleAlaCysIleTyrAlaIle 571
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 QY 1204 CTGCGCCCGCAGCTGGAGACTCCCTACTACCTGCTGGCGCGGAGGCGAGCTGGAGG 1263
 Db 589 LeuGlyAspGlnIleGlyLysProTyr-----Asn 598

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Db 602 ---LeuGlyGlyProSerIleLysAspLysIleValThrAlaLeuTyrPheThrPheSer 620

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Db 621 SerLeuThrSerValGlyPheGlyAsnValSerProAsnThrAsnSerGlnLysIlePhe 640

QY 1444 TCCATCTGCACATCTCATCGCGCCCTGATGACGCGGTGTGTTGGGAACGTGACG 1503
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QY 2203 GGGAGCAGGGCCCCCAGGTCCTCCCGAGCCCGAGCTGATGAGCCCTCCAGCCCTGCTG 2262
Db 899 ThrGluGln----- 901

QY 2263 TCCCTTGGCTGACCTCTCATCTCTCAGTGTCCCAAGTGTATCCCACTCGAAGCA 2322
Db 902 ---ProGlyGluValSerAla-----LeuGlyProGlyArgAlaGly 914

QY 2323 CCCCAGGCTCTAGTGTGCGAGAGGAGGAGCGGAGCGGAGGCTTTGAAGGCTGAG 2382

```

RESULT 11

KCH2 MOUSE

```

ID KCH2_MOUSE STANDARD; PRT; 1162 AA.
AC O35219; O35220; O35221; O35989;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Potassium voltage-gated channel subfamily H member 2 (Ether-a-go-go
DE related gene potassium channel 1) (ERGL) (MERG) (Mergl) (ether-a-go-
GN KCN2 OR ERG OR MERG1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

```

NCBI_TaxID=10090;
 [1] SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3), AND VARIANTS ARG-186;
 RP THR-455; ITR-752 AND ASN-1006; TISSUE=Heart;
 RC STRAIN=129/SV, and BALB/c; TISSUE=Heart;
 RX MEDLINE=98012815; PubMed=9351462;
 RA London B., Trudeau M.C., Newton K.P., Beyer A.K., Copeland N.G.,
 RA Gilbert D.J., Jenkins N.A., Slatyer C.A., Robertson G.A.;
 RT "Two isoforms of the mouse ether-a-go-go-related gene coassemble to
 RT form channels with properties similar to the rapidly activating
 RT component of the cardiac delayed rectifier K⁺ current.";
 RL Circ. Res. 81:870-878(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).
 RC TISSUE=atrial tumor;
 RX MEDLINE=98012799; PubMed=9351446;
 RA Lees-Miller J.P., Kondo C., Wang L., Duff H.J.;
 RT "Electrophysiological characterization of an alternatively processed
 RT ERG K⁺ channel in mouse and human hearts.";
 RL Circ. Res. 81:719-726(1997).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT ARG-186.
 RC TISSUE=Colon smooth muscle;
 RA Shoen F., Malykhina A., Akbarali H.I.;
 RT "Smooth muscle KCNH2 erg potassium channel.";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Pore-forming (alpha) subunit of voltage-gated inwardly
 CC rectifying potassium channel. Channel properties are modulated by
 CC CAMP and subunit assembly. Mediates the rapidly activating
 CC component of the delayed rectifying potassium current in heart
 CC (IKr) (By similarity).
 CC -1- SUBUNIT: The potassium channel is probably composed of a homo- or
 CC heterotrimeric complex of pore-forming alpha subunits that can
 CC associate with modulating beta subunits. Heteromultimer with
 CC KCNH6/ERG2, KCNH7/ERG3, KCNE1 and KCNE2 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Comment=Experimental confirmation may be lacking for some
 CC isoforms;
 CC Name=1; Synonyms=1A, A;
 CC IsoId=O35219-1; Sequence=Displayed;
 CC Name=2; Synonyms=1A';
 CC IsoId=O35219-2; Sequence=VSP_000969;
 CC Name=3; Synonyms=1B, B;
 CC IsoId=O35219-3; Sequence=VSP_000970;
 CC -1- TISSUE SPECIFICITY: Isoform 1 is expressed in heart, brain and
 CC testis and at low levels in lung. Isoform 3 is expressed
 CC predominantly in heart. The expression of isoform 2 is low in all
 CC tissues tested.
 CC -1- DOMAIN: The segment S4 is probably the voltage-sensor and is
 CC characterized by a series of positively charged amino acids at
 CC their third position.
 CC -1- PTM: Phosphorylated on serine and threonine residues (By
 CC similarity).
 CC -1- SIMILARITY: Belongs to the potassium channel family. H (Eag)
 CC subfamily.
 CC -1- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
 CC -1- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.
 CC -1- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
 CC -1- CAUTION: Ref.3 sequence was originally reported as deriving from
 CC rabbit.
 CC -1- CAUTION: Ref.3 sequence differs from that shown due to a
 CC frameshift in position 1057.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC

DR EMBL; AF012868; AAC53418.1; --
 DR EMBL; AF012869; AAC53419.1; --
 DR EMBL; AF012871; AAC53420.1; --
 DR EMBL; AF012870; AAC53420.1; JOINED.
 DR EMBL; AF012871; AAC53421.1; --
 DR EMBL; AF012871; AAC53422.1; --
 DR EMBL; AF012870; AAC53422.1; JOINED.
 DR EMBL; AF012870; AAC53422.1; --
 DR EMBL; AF034762; AAB87571.1; --
 DR EMBL; AF493342; AAL35327.2; ALT_FRAME.
 DR MGD; MGI:1341722; Kcnh2.
 DR InterPro; IPR000595; cNMP binding.
 DR InterPro; IPR003967; Erg Channel.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR001622; K+channel_pore.
 DR InterPro; IPR005820; M+channel_nlg.
 DR InterPro; IPR001610; PAC.
 DR InterPro; IPR007000; PAS-assoc C.
 DR InterPro; IPR000014; PAS domain.
 DR Pfam; PF00027; cNMP_binding; 1.
 DR Pfam; PF00520; ion_trans; 1.
 DR Pfam; PF00785; PAC; 1.
 DR PRINTS; PR01470; ERGCHANNEL.
 DR SMART; SM00100; cNMP; 1.
 DR SMART; SM00086; PAC; 1.
 DR PROSITE; PS00888; cNMP_BINDING_1; FALSE_NEG.
 DR PROSITE; PS00889; cNMP_BINDING_2; FALSE_NEG.
 DR PROSITE; PS00042; cNMP_BINDING_3; 1.
 DR PROSITE; PS0112; PAS; 1.
 DR PROSITE; PS0113; PAC; 1.
 KW Transport; Ion transport; Ionic channel; Voltage-gated channel;
 KW Potassium channel; Potassium; Potassium transport; Transmembrane;
 KW Phosphorylation; Glycoprotein; Multigene family; Polymorphism;
 KW Alternative splicing.
 FT DOMAIN 1 405 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 406 426 SEGMENT S1 (POTENTIAL).
 FT TRANSMEM 453 473 SEGMENT S2 (POTENTIAL).
 FT DOMAIN 474 497 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 498 518 SEGMENT S3 (POTENTIAL).
 FT TRANSMEM 523 543 SEGMENT S4 (POTENTIAL).
 FT DOMAIN 544 549 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 550 570 SEGMENT S5 (POTENTIAL).
 FT DOMAIN 614 634 SEGMENT H5 (PORE-FORMING) (POTENTIAL).
 FT TRANSMEM 641 661 SEGMENT S6 (POTENTIAL).
 FT DOMAIN 662 1162 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 17 88 PAC.
 FT DOMAIN 92 144 POLY-PRO.
 FT DOMAIN 299 302 CNMP.
 FT NP_BIND 744 861 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 600 600 Missing (in isoform 2).
 FT VARSPLIC 1 59 /FtId=VSP_000969.
 FT VARSPLIC 1 378 MPVRGHVAFQNTFLDTIIRKFGQSRKFIANARVENCAY
 FT IYCNDFGCELCGVSAEVMQPCDFLHGFTORRAAQI
 FT AQALLGAERKEVIAFYKDGSCFLCLVDVVPVKNEDGAVI
 FT MFLNPFVVMKQMGVSPADHTNHRGPTSLWASGRKTR
 FT LKLPALLALTARESSVRTSGMHSAGAPVAVVDLTPAAP
 FT SSSSLADEVSMNDHVAGLGPAERFALYGRGSPVASI
 FT RGHPSRAQSLNEDPASGSSCLARTSRSCASVRRASSA
 FT DDTEAMRAGALPPPHRSTAGMHPRLSGLNLSDSLVR
 FT YRTISKIPQITLNFVDLKGDFFLASPTSDREIIAPTKERT
 FT HNVTEKVTQ -> MAIPTGKESRTGALQRAQKGRVRAVR
 FT ISSILVAQE (in isoform 3).
 FT /FtId=VSP_000970.
 FT H -> R (IN STRAIN BALB/C).
 FT A -> T (IN STRAIN BALB/C).
 FT C -> Y (IN STRAIN BALB/C).
 FT D -> N (IN STRAIN BALB/C).
 FT D -> G (IN REF. 3).
 FT I -> V (IN REF. 3).
 FT V -> A (IN REF. 3).
 FT E -> G (IN REF. 3).
 FT V -> A (IN REF. 3).
 FT S -> P (IN REF. 3).
 FT
 FT VARIANT 186 186
 FT VARIANT 455 455
 FT VARIANT 752 752
 FT VARIANT 1006 1006
 FT VARIANT 111 111
 FT CONFLICT 126 126
 FT CONFLICT 198 198
 FT CONFLICT 214 214
 FT CONFLICT 537 537
 FT CONFLICT 908 908

```

FT CONFLICT 929 929 G -> R (IN REF. 3).
SQ SEQUENCE 1162 AA; 126885 MW; A9455F7F10B61E46 CRC64;

Alignment Scores:
Pred. No.: 2,03e-61 Length: 1162
Score: 1547.00 Matches: 413
Percent Similarity: 44.21% Conservative: 144
Best Local Similarity: 32.78% Mismatches: 352
Query Match: 25.41% Indels: 351
DB: 1 Gaps: 31

US-09-965-830-1_COPY_6_3257 (1-3252) x KCH2_MOUSE (1-1162)

QY 1 ATGCCGGCCATCGGGGCTCTGCGCTCAGAACACCTCTGCTGACACCATCGCTACG 60
Db 1 MetProValArgArgGlyHisValAlaProGlnAsnThrPheLeuAspThrIleLeuArg 20
QY 61 CGCTTCGACGGCAGCAGACAGTAACTCGTGTGGGCAAGCCCGAGGTGGCGGCTCTTC 120
Db 21 LysPheGluGlyGlnSerArgLysPheIleAlaAsnAlaArgValGluAsnCys--- 39
QY 121 CCCGTGGTCTACTGCTCTGATGCTCTGTGACCTCAGGGCTTCTCCGGGCTGAGTTC 180
Db 40 AlaValIleTyrCysAsnAspGlyPheCysGluLeuCysGlyTyrSerArgAlaGluVal 59
QY 181 ATGCAGCGGGCTGTGCTCTCTCTCTCTTATGGCCAGACACAGCAGTGTGCTCCGC 240
Db 60 MetGlnArgProCysThrCysAspPheLeuHisGlyProArgThrGlnArgAlaAla 79
QY 241 CAACAGATCCGACAGCCCTGACGACGACACAGGAGTTCAGGCTGAGCTGATCCTGTAC 300
Db 80 AlaGlnIleAlaGlnAlaLeuGlyAlaGluGluArgLysValGluIleAlaPheTyr 99
QY 301 CGGAAGAGCGGCTCCCGTCTCTGCTCTCTGATGATACCCATAAAGATGAGAAA 360
Db 100 ArgLysAspGlySerCysPheLeuLeuValValProValLysAsnGluAsp 119
QY 361 GGGAGGTGGCTCTCTCTCTA-----GTCTCTCAAGGACATC----- 399
Db 120 GlyAlaValIleMetPheIleLeuAsnPheGluValValMetGluLysAspMetValGly 139
QY 400 -----ACGAAACACAGACAGCGGGGCCCGACAGATGGAAGACACAGT--- 447
Db 140 SerProAlaHisAspThrAsnHisArgGlyProSerThrSerTrpLeuAlaSerGlyArg 159
QY 447 ----- 447
Db 160 AlaLysThrPheArgLeuLysLeuProAlaLeuLeuAlaLeuThrAlaArgGluSerSer 179
QY 447 ----- 447
Db 180 ValArgThrGlySerMetHisSerAlaGlyAlaProGlyAlaValValValAspValAsp 199
QY 447 ----- 447
Db 200 LeuThrProAlaAlaProSerSerSerGluSerLeuAlaLeuAspGluValSerAlaMetAsp 219
QY 447 ----- 447
Db 220 AsnHisValAlaGlyLeuGlyProAlaGluGluArgAlaLeuValGlyProGlySer 239
QY 447 ----- 447
Db 240 AlaSerProValAlaSerIleArgGlyProHisProSerProArgAlaGlnSerLeuAsn 259
QY 448 -----GTTGGCCGGCCGATATGGCCGGCAGCATCCAAAGCTTCAATGCC 495
Db 260 ProAspAlaSerGlySerSerCysSerLeuAlaArgThrArgSerArgGluSerCysAla 279
QY 496 AACCGCGCGGAGCCGGCC-----GTGCTCTACACCTGTCCGGGCGACCTGCAG 546
Db 280 SerValArgArgAlaSerSerAlaAspAspIleGluAlaMetArgAlaGlyAlaLeuPro 299

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QY 547 AAGCAGCCCAAG-----GGCAGCACAAGCTCAATAAGGGGTGTTGGG 591
Db 300 ProProProArgHisAlaSerThrGlyAlaMetHisProLeuArgSerGlyLeuLeuAsn 319
QY 592 GAGAAACCAAC----- 603
Db 320 SerThrSerAspSerAspLeuValArgTyrArgThrIleSerLysIleProGlnIleThr 339
QY 603 ----- 603
Db 340 LeuAsnPheValAspLeuLysGlyAspProPheLeuAlaSerProThrSerAspArgGlu 359
QY 603 ----- 603
Db 360 IleIleAlaProLysIleLysGluArgThrHisAsnValThrGluLysValThrGlnVal 379
QY 604 -----TTGCTGAGTACAAAGTAGCCGCGCATCCGGGAAGTCGCC 642
Db 380 LeuSerLeuGlyAlaAspValLeuProGluTyrLysLeuGlnAlaProArgIleHisArg 399
QY 643 TTCATCTGTGCTGCTGGGCACTGAGAGCCACTGGGATGGCTTATCTCTGCTCGCC 702
Db 400 TrpThrIleLeuHisTyrSerProPheLysAlaValTrpAspTrpLeuIleLeuLeu 419
QY 703 ACATCTATGTGGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 744
Db 420 ValIleTyrThrAlaValPheThrProTyrSerAlaAlaPheLeuLeuLysGluThrGlu 439
QY 745 -----AGCAGCAGCAGCGGAGCCAGTCCCGCGCGCGCGCGCGCGCGCGCGCGCTG 798
Db 440 AspGlySerGlnAlaProAspCysGlyTyrAlaCysGlnProLeuAlaValAspLeu 459
QY 799 GCGGTGAGGTCTCTTCATCTTCATCTTCATCTTCATCTTCATCTTCATCTTCATCTTC 858
Db 460 IleValAspIleMetPheIleValAspIleLeuLeuAsnPheArgThrTyrValAsn 479
QY 859 AAGTCGGGCCAGGTGGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 918
Db 480 AlaAsnGluGluValValSerHisProGlyArgIleAlaValHisTyrPheLysGlyTrp 499
QY 919 TTCCTGTGTGATGTATCGCAGCGCTGCCCTTTCACCTGCTACATGCTTCAAGTCAAC 978
Db 500 PheLeuIleAspMetValAlaAlaIleProPheAspLeuLeu----- 513
QY 979 GTGTACTTCCGGGCC-----CATCTGTGAAGACGGTCCGCTGCTGTG 1020
Db 514 ---IlePheGlySerGlySerGluGluLeuIleGlyLeuLeuLysThrAlaArgLeuLeu 532
QY 1021 CGCTGTGTGCGGCTGCTCCGCGGCTGACCGGCTACTCGAGTACAGCGCGCTGGTGTG 1080
Db 533 ArgLeuValArgValAlaAlaArgLysLeuAspArgTyrSerGluTyrGlyAlaAlaValLeu 552
QY 1081 ACATGTCTATGCGGCTGCTGCGGCTGCTGCGGCTGCTGCGGCTGCTGCTGCTGCTGCT 1140
Db 553 PheLeuLeuMetCysThrPheAlaLeuLeuAlaHisTrpLeuAlaCysIleTrpTyrAla 572
QY 1141 ATTGGCCAGCGGAGATCGAGAGCAGCGAATCCGAGCTGCTGAGATGCTGCTGCTGCTG 1200
Db 573 IleGlyAsnMetGluGlnProHisMetAspSer-----HisIleGlyTrpLeuHis 589
QY 1201 GAGTGGCCCGCGACTGGAGACTCCCTACTACTGCTGGCGCGGAGCGCGCTGGAGGG 1260
Db 590 AsnLeuGlyAspGlnIleGlyLysProTyr----- 599
QY 1261 AACAGCTCCGGCCAGAGTGTACAACTGCGAGCAGCAGCGAGCGCAACGCGGCGGCTG 1320
Db 600 AsnSerSerGly----- 603
QY 1321 GAGCTGCTGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
Db 604 -----LeuGlyGlyProSerIleLysAspLysTyrValThrAlaLeuTyrPheThrPhe 621
QY 1381 AGCAGCTCACCAGCGTGGGCTTCGCGCAAGTGTCCGCCAACACGCGACCGGAGAAGATC 1440

```

[illegible]

Wymore R.S., Gintant G.A., Wymore R.T., Dixon J.E., McKinnon D., Cohen I.S.;
"Tissue and species distribution of mRNA for the IKr-like K+ channel, Circ. Res. 80:261-268(1997).
[3]
TISSUE SPECIFICITY.
MEDLINE=20183472; PubMed=10718922;
Wulfen I., Hauber H.P., Schiemann D., Bauer C.K., Schwarz J.R.;
"Expression of mRNA for voltage-dependent and inward-rectifying K channels in GH3/B6 cells and rat pituitary";
J. Neuroendocrinol. 12:263-272(2000).
[4]
INTERACTION WITH KCNH6 AND KCNH7, AND MUTAGENESIS OF GLY-630.
MEDLINE=21079731; PubMed=11212207;
Wimmers S., Wulfen I., Bauer C.K., Schwarz J.R.;
"Erg1, erg2, and erg3 K channel subunits are able to form heteromultimers";
Pfluegers Arch. 441:450-455(2001).
-!- FUNCTION: pore-forming (alpha) subunit of voltage-gated inwardly rectifying potassium channel. Channel properties are modulated by cAMP and subunit assembly. Mediates the rapidly activating component of the delayed rectifying potassium current in heart (IKr) (By similarity).
-!- SUBUNIT: The potassium channel is probably composed of a homo- or heterotetrameric complex of pore-forming alpha subunits that can associate with modulating beta subunits. Heteromultimer with KCNH6/ERG2 and KCNH7/ERG3. Heteromultimer with KCNE1 and KCNE2 (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: Highly expressed in brain and testis, slightly less so in heart, adrenal, retina and thymus. Detected at lower levels in lung, soleus, tibialis, and at very low levels in cornea and lens. A shorter transcript is detected in skeletal muscle. Found in pituitary.
-!- DOMAIN: The segment S4 is probably the voltage-sensor and is characterized by a series of positively charged amino acids at every third position.
-!- PM: Phosphorylated on serine and threonine residues (By similarity).
-!- SIMILARITY: Belongs to the potassium channel family. H (Eag) subfamily.
-!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
-!- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.
-!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
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EMBL; Z96106; CAB09536.1; --
DR EMBL; U75210; AAC53160.1; --
DR InterPro; IPR000595; cNMP binding.
DR InterPro; IPR003967; Erg_Channel.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000700; PAS-assoc_C.
DR InterPro; IPR000014; PAS_domain.
DR Pfam; PF00027; cNMP_binding; 1.
DR Pfam; PF00520; Ion_trans; 1.
DR Pfam; PF00785; PAC; 1.
DR PRINTS; PR01470; ERGCHANNEL.
DR SMART; SM001100; cNMP; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 1.
DR PROSITE; PS00888; cNMP_BINDING_1; FALSE_NEG.
DR PROSITE; PS00889; cNMP_BINDING_2; FALSE_NEG.


```
QY 2140 GACACAGCTCCCTGAGCGGCGCAATACCTTATGTCTCCAGCTGGAGGAGGAGACA 2199
Db      :::::
QY 880 GluSerGlyPheAsnArgGlnArgLysLeuSerPheArgArgGlnThrAspLys 899
Db      :::::
QY 2200 GATGGGAGGAGCGGCCCGCCAGCTGCTCCCGAGCCAGCTGATGAGCCCTCCAGCCCTG 2259
Db      ||| ||| |||
QY 900 AspThrGluGln----- 903
QY 2260 CTGCTCCCTGGCTGCACCTCCTCATCTCAGTGCACCAAGCTGCTATCCCACTGCAACA 2319
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 904 -----ProGlyGluValSerAlaLeuGlyGln-----GlyProAlaArgVal 917
QY 2320 GCACCCCGGCTGCTAGTGTCGACGAGGAGCCAGGAGCCAGGCGGCTTTGAAGCT 2379
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 918 GlyProGlyProSerCys-----ArgGlyGlnProGlyGlyProThrGlyGluSerPro 935
QY 2380 GAGGCTGGCCCTCTGCTCCCA-----CGGCGCCCTAGAG 2415
Db      ::::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 936 SerSerGlyProSerSerProGluSerSerGluAspGluGlyProGlyArgSerSer 955
QY 2416 GGGCTACGGCTGCCCCCATGCTCATGGAATGTGCCCCAGATCTGAGCCCGGCTAGTA 2475
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 956 ProLeuArgLeuValProPheSerSerProArgProGlyAspSerProGlyGlyGlu 975
QY 2476 GATGGCAITGAGACGGCTGTGCTCGACACGCC----- 2511
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 976 ProLeuThrGluAspGlyGlySerSerAspThrCysAsnProLeuSerGlyAlaPhe 995
QY 2512 -----AAGTCTCTTTC-----CGTGTGGCCAGTCT 2538
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 996 SerGlyValSerAsnIlePheSerPheThrPglyAspSerArgGlyArgGlnThrGlnGlu 1015
QY 2539 GCGCCGGAATGAGCAGCGCCCTCCCTGACAGAGCGGCTGCTACTGTCTCC 2598
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1016 LeuProArgCys-----ProAlaProAlaProSerLeuLeuAsnIlePro 1030
QY 2599 -----CATGGCCCGAGCGGCTGCTCGACACACACACACACACACACACACACAC 2634
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1031 LeuSerSerProGlyArgArgSerArgGlyAspValGluSerArg-----Leu 1046
QY 2635 GACAGCTTCGGCAGCGGTGACAGAGCTGTGACAGCAGGTG---CTGACAGTGGGAA 2691
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1047 AspAlaLeuGlnArgGlnLeuAsnArgLeuGluThrArgLeuSerAlaAspMetAlaThr 1066
QY 2692 GGAAGTCACTGCTGCGCAGCTGTGAGCTGTGCTGCTGCGGCCCGCCACAGGAGGCTCG 2751
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1067 ValLeuGlnLeuGln-ArgGlnMetThrLeu----- 1077
QY 2752 TGCCCTGGGATCGGGAGAGGGCGGTGCCAGCCAGCCTCGCGGCTTCTGAGCCT 2811
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1078 -----ValProAlaThrSerAla-- 1084
QY 2812 CTGTGTGTGACATGGGCGATCTCTTACTGCTGAGCCCGGCTGAGCCAGCTTCTGAGCC 2871
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1085 -----ValThrProGlyProGlyProThrSerThrSerProLeuLeuPro-- 1100
QY 2872 AGTGGGACTTGGCCCGCCCTGCTGCGGGGCTCTCTCCCTCATGGCAGCCCTGCGCCCTGG 2931
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1101 -ValGlyProValProThrLeuThrLeuAspSerLeuSerGln----- 1114
QY 2932 GTTCCCCAG-----CGTCTCAGAGCTGCCCTGGCTGAGCCAGCTTCTGAGCC 2985
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1115 -ValSerGlnPheValAlaPheGluGluLeuProAlaGlyAlaProGluLeuProGlnAs 1134
QY 2986 TCACCTCAGACTCAGAGCCCTGCTCTCAGGAGACCTCTGCTGAGCCCGCAGCCCT 3045
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1134 pGlyProThrArgArgLeuSerLeuProGlyGlnLeuGlyAlaLeuThrSerGlnProLe 1154
QY 3046 G 3046
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1154 u 1154
```

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RESULT 13
KCH2_RABIT
ID KCH2_RABIT STANDARD; PRT; 1161 AA.
AC Q8WNY2; O02731; O19119; O97586; Q9TV06;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Potassium voltage-gated channel subfamily H member 2 (Ether-a-go-go
DE related gene potassium channel 1) (ERGL) (RERG) (ra-erg) (Ether-a-go-
DE go related protein 1) (Eag related protein 1).
GN KCN2 OR ERG.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RA Witchel H.J., Hancox J.C., Levi A.J., Meech R.W.;
RT "ERG - rabbit ventricular ERG K+ channel subunit.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 411-571 FROM N.A. (ISOFORM 1/2).
RX MEDLINE=97164986; PubMed=9012748;
RA Wymore R.S., Gintant G.A., Wymore R.T., Dixon J.E., McKinnon D.,
RA Cohen I.S.;
RT "Tissue and species distribution of mRNA for the Ikr-like K+ channel,
RT erg.";
RL Circ. Res. 80:261-268 (1997).
CC -!- FUNCTION: Pore-forming (alpha) subunit of voltage-gated inwardly
CC rectifying potassium channel. Channel properties are modulated by
CC CAMP and subunit assembly. Mediates the rapidly activating
CC component of the delayed rectifying potassium current in heart
CC (Ikr) (By similarity).
CC -!- SUBUNIT: The potassium channel is probably composed of a homo- or
CC heterotetrameric complex of pore-forming alpha subunits that can
CC associate with modulating beta subunits. Heteromultimer with
CC KCNH6/ERG2, KCNH7/ERG3, KCNE1 and KCNE2 (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q8WNY2-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q8WNY2-2; Sequence=VSP_000971;
CC -!- TISSUE SPECIFICITY: Detected in heart, both in atrium and in left
CC ventricle.
CC -!- DOMAIN: The segment S4 is probably the voltage-sensor and is
CC characterized by a series of positively charged amino acids at
CC every third position.
CC -!- PTM: Phosphorylated on serine and threonine residues (By
CC similarity).
CC -!- SIMILARITY: Belongs to the potassium channel family. H (Eag)
CC subfamily.
CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
CC -!- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.
CC -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; U87513; AAB68612.1; -
CC EMBL; AF068736; AAC99425.1; -
CC EMBL; AF105061; AAC39357.1; -
CC EMBL; U75212; AAC48723.1; -
CC InterPro; IPR00595; cNMP binding.
CC InterPro; IPR003967; Erg_Channel.
CC InterPro; IPR005821; Ion_trans.
CC InterPro; IPR001622; K+channel_pore.
```

DR InterPro; IPR005820; M+channel_nlg.
 DR InterPro; IPR001610; PAC.
 DR InterPro; IPR007000; PAS-assoC.
 DR InterPro; IPR000014; PAS domain.
 DR Pfam; PF00027; CNMP binding; 1.
 DR Pfam; PF00520; ion trans; 1.
 DR Pfam; PF00785; PAC; 1.
 DR PRINTS; PR01470; ERGCHANNEL.
 DR SMART; SM00100; CNMP; 1.
 DR SMART; SM00086; PAC; 1.
 DR PROSITE; PS00888; CNMP BINDING 1; FALSE NEG.
 DR PROSITE; PS00889; CNMP BINDING 2; FALSE NEG.
 DR PROSITE; PS00442; CNMP BINDING 3; 1.
 DR PROSITE; PS01112; PAS; 1.
 DR PROSITE; PS01113; PAC; 1.
 DR PROSITE; PS01114; PAC; 1.
 KW Transport; Ion transport; Ionic channel; Voltage-gated channel;
 KW Potassium channel; Potassium; Potassium transport; Transmembrane;
 KW Phosphorylation; Glycoprotein; Multigene family; Alternative splicing.
 FT DOMAIN 1 405 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 406 426 SEGMENT S1 (POTENTIAL).
 FT TRANSMEM 453 473 SEGMENT S2 (POTENTIAL).
 FT DOMAIN 474 497 SEGMENT S3 (POTENTIAL).
 FT TRANSMEM 498 518 SEGMENT S4 (POTENTIAL).
 FT TRANSMEM 523 543 SEGMENT S5 (POTENTIAL).
 FT DOMAIN 544 549 SEGMENT S6 (POTENTIAL).
 FT TRANSMEM 550 570 SEGMENT S7 (POTENTIAL).
 FT DOMAIN 614 634 SEGMENT S8 (POTENTIAL).
 FT TRANSMEM 641 661 SEGMENT S9 (POTENTIAL).
 FT DOMAIN 662 1161 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 17 88 PAS.
 FT DOMAIN 92 144 POLY-PRO.
 FT DOMAIN 299 302 CNMP.
 FT NP BIND 744 861 Missing (in isoform 2).
 FT CARBOHYD 600 600 Missing (in isoform 2).
 FT VARSPLIC 69 85 FTID=VSP_000971.
 FT CONFLICT 411 411 V -> A (IN REF. 2).
 FT CONFLICT 445 446 PE -> TD (IN REF. 2).
 FT CONFLICT 553 553 L -> F (IN REF. 2).
 FT CONFLICT 561 561 L -> C (IN REF. 2).
 SQ SEQUENCE 1161 AA; 126961 MW; 79B532B2FFD9ABE CRC64;

Alignment Scores:
 Pred. No.: 6,19e-61 Length: 1161
 Score: 1536.00 Matches: 425
 Percent Similarity: 44.45% Conservative: 136
 Best Local Similarity: 33.68% Mismatches: 347
 Query Match: 25.23% Indels: 354
 DB: 1 Gaps: 38

US-09-965-830-1_COPY_6_3257 (1-3252) x KCH2_RABIT (1-1161)

Qy 1 ATGCCGGCCATGCGGGGCTCTGCGGCTCAGAACACCTCTCTGACACCATCCTACG 60
 Db 1 MetProValArgArgGlyHisValAlaProGlnAsnThrPheLeuAspThrIleLeuArg 20
 Qy 61 CGCTTCGACGACCCACAGTAACCTGCTGCTGGGCAAGCCGACGCTGCGGGGCTCTTC 120
 Db 21 LysPheGluGlyGlnSerArgLysPheIleIleAlaAsnAlaArgValGluAsnCys--- 39
 Qy 121 CCCGTGGTCTACTGCTGATGGCTCTGTGACCTCACGGGCTCTCCCGGCTGAGGTC 180
 Db 40 AlaValIleTyrCysAsnAspGlyPheCysGluLeuCysGlyTyrSerArgAlaGluVal 59
 Qy 181 ATGCAGCGGGGCTGCTGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
 Db 60 MetGlnArgProCysThrCysAspPheLeuHisGlyProArgThrGlnArgArgAlaAla 79
 Qy 241 CAACAGATCCGCAAGCCCTCGACGACGACCAAGAGCTTCAAGGCTGAGCTGATCTCTGTAC 300
 Db 80 AlaGlnIleAlaGlnAlaLeuLeuGlyAlaGluGluArgLysValGluIleAlaPheTyr 99
 Qy 301 CGGAAGAGCGGGGCTCCCGTCTCTGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 360

Db 100 ArgLysAspGlySerCysPheLeuValAspValValProValLysAsnGluAsp 119
 Qy 361 GGGGAGGTGGTCTCTCTCTCTA-----GTCTCTCAACAGGACATC----- 399
 Db 120 GlyAlaValIleMetPheIleLeuAsnPheGluValValMetGluLysAspMetValGly 139
 Qy 400 -----AGCAAAACCAAGAACCGAGGGGCGCCGACAGATGG----- 435
 Db 140 SerProAlaArgAspThrAsnHisArgGlyProProThrSerThrLeuAlaProGlyArg 159
 Qy 435 ----- 435
 Db 160 AlaLysThrPheArgLeuLysLeuProAlaLeuLeuAlaLeuThrAlaArgGluSerSer 179
 Qy 436 ---AAGGAGACAGGTGGTGGCGGCGCGATATGGCGGCGGACGATC----- 479
 Db 180 ValArgProGlyGlyAlaGlyGlyAlaGlyAlaProGlyAlaValValValAspVala 199
 Qy 480 -----CAAGGGCTTCAATGCCAACCGCGC----- 503
 Db 199 splLeuThrProAlaAlaProSerSerGluSerLeuAlaLeuAspGluValProAlaMet 219
 Qy 504 -----GCGGAGCGGGCGGCTGCTCTA----- 524
 Db 219 splAsnHisValAlaGlyLeuGlyProAlaGluGluArgArgAlaLeuValGlySerCys 239
 Qy 525 -----CCACCTGTCGGGCGACCTGCGAAGCAGCCCAAGGCGAAG-----CACAAGCTC 573
 Db 239 erProProProValSerAlaProGly-ProHisProSerLeuArgAlaHisSerLeu 258
 Qy 574 AATAAGGGGTGTTGGG----- 591
 Db 259 AsnProAspAlaSerGlySerSerCysSerLeuAlaArgThrArgSerArgGluSerCys 278
 Qy 591 ----- 591
 Db 279 AlaSerValArgArgAlaSerSerAlaAspAspIleGluAlaMetArgAlaGlyAlaLeu 298
 Qy 591 ----- 591
 Db 299 ProProProProArgHisAlaSerThrGlyAlaMetHisProLeuArgSerGlyLeuLeu 318
 Qy 591 ----- 591
 Db 319 AsnSerThrSerSerAspLeuValArgTyrArgThrIleSerLysIleProGlnIle 338
 Qy 591 ----- 591
 Db 339 ThrLeuAsnPheValAspLeuLysGlyAspProPheLeuAlaSerProThrSerAspArg 358
 Qy 592 -----GAGAAACCAAC----- 603
 Db 359 GluIleIleAlaProLysIleLysGluArgThrHisAsnValThrGluLysValThrGln 378
 Qy 604 -----TTGCTGAGTACAAAGTAGCGCCATCGGAGTCG 639
 Db 379 ValLeuSerLeuGlyAlaAspValLeuProGluTyrLysLeuGlnAlaProArgIleHis 398
 Qy 640 CCCTTCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 699
 Db 399 ArgTyrThrIleLeuHisTyrSerProPheLysAlaValTyrAspTyrLeuIleLeuLeu 418
 Qy 700 GCCACACTTATGTGGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 750
 Db 419 LeuValIleTyrThrAlaValPheThrProTyrSerAlaAlaPheLeuLeuLysGluThr 438
 Qy 751 GCACGGGAGCCAGTGGC-----GCCCGCGCGCGCGCGCGCGCGCTGTGTGAC 795
 Db 439 GluGluGlyProProAlaProGluCysGlyTyrAlaCysGlnProLeuAlaValValAsp 458
 Qy 796 CTGGCGGCTGGAGGTCT 855

Db	459	LeuIleValAspIleWecPheIleValAspIleLeuIleAsnPheArgThrThrTyrVal	478
QY	856	TCCAAAGTCGGGCAGCTGGTGTTCGCCAAAGTCATTTGCCCTCCACGTACGTCAACACC	915
Db	479	AsnAlaAsnGluValValSerHisProGlyArgIleAlaValHisTyrPheLysGly	498
QY	916	TGTTCTCTGCTGGATGTGCATCGCAGCGCTGCCCTTTGACCTGTCTACATGCCTTCAAGTCT	975
Db	499	TrpPheLeuIleAspMetValAlaIleProPheAspLeuLeu-----	513
QY	976	AACGTGTACTTCGGGGCC-----CATCTGCTGAAGCGTGGCGCTG	1017
Db	514	-----IlePheGlySerGlySerGluLeuLeuIleGlyLeuLeuLysThrAlaArgLeu	531
QY	1018	CTGCGCTCTGCTGGCTGCTCTCCGCGGTGACCGGTACTCGAGTACAGCGCGCTGGT	1077
Db	532	LeuArgLeuValArgValAlaArgLysLeuAspArgTyrSerGluTyrGlyAlaAlaVal	551
QY	1078	CTGACACTGCTCATGGCCGCTGTTTCGCCCTGCTTCGCGACTGGGTGCGCTGCTGTGTTT	1137
Db	552	LeuLeuLeuLeuMetCysThrPheAlaLeuIleAlaHisTrpLeuAlaCysIleTrpTyr	571
QY	1138	TACATTGGCCAGCGGGAGATCGAGGACGAGCGAATCCGAGCTGCTGAGATTGCTGGCTG	1197
Db	572	AlaIleGlyAsnMetGluInProHisMetAspSer-----ArgIleGlyTrpLeu	588
QY	1198	CAGGAGCTGGCCCGCACTCGAGACTCCCTACTACTCTGGTGGCGCGGACGCTGGA	1257
Db	589	HisAsnLeuGlyAspGlnMetGlyLysProTyr-----	599
QY	1258	GGGAACAGCTCCGGCCAGTAGTGAACAATGTCAGCAGCAGCAGCGACGACCGAGCGGG	1317
Db	600	---AsnSerSerGly-----	603
QY	1318	CTGAGAGCTGGTGGCGGCGCGTCTGCTGGCAGCGCCTACATCACTCCCTCTACTTCGCA	1377
Db	604	-----LeuGlyGlyProSerIleLeuAspLysTyrValThrGlyLeuTyrPheThr	620
QY	1378	CTCAGACCTCACACGCTGGGGCTTCGGCAACGTGTCGCCCAACACGACACCGAGAG	1437
Db	621	PheSerSerLeuThrSerValGlyPheGlyAsnValSerProAsnThrAsnSerGluLys	640
QY	1438	ATCTTCTCATCTGCACCATCTCATCGCGCCCTGATGCACGCGTGGTGTGTTGGGAAC	1497
Db	641	IlePheSerIleCysValMetLeuIleGlySerLeuMetTyrAlaSerIlePheGlyAsn	660
QY	1498	GTCAGCGCCATCATCCAGCCCATGTACGCCCGCGCTTCTGTACACAGCCGACGCGC	1557
Db	661	ValSerAlaIleIleGlnArgLeuTyrSerGlyThrAlaArgTyrHisThrGlnMetLeu	680
QY	1558	GACCTGCGCACTACATCCGATCCACCGTATCCCAAGCCCTCAAGCAGCGCATCTG	1617
Db	681	ArgValArgGluPheIleArgPheHisGlnIleProAsnProLeuargGlnArgLeuGlu	700
QY	1618	GAGTACTTCAGCGCCACCTGGCGGGTGAACAATGGCATCGACACACCGAGTGTCTGCAG	1677
Db	701	GluTyrPheGlnHisAlaTrpSerTyrThrAsnGlyIleAspMetAsnAlaValLeuLys	720
QY	1678	AGCCTCCCTGACAGCTGGCGCAGACATGCCATCGACTCGACAGAGAGTCTCTGAG	1737
Db	721	GlyPheProGluCysLeuGlnAlaAspIleCysLeuHisLeuAsnArgSerLeuGln	740
QY	1738	---CTGCCACTGTTTGAGCGCGCACCGCGGTGCTGCGGGCACTGCTCTGCGCCCTG	1794
Db	741	HisCysLysProPheArgGlyAlaThrLysAspCysLeuArgAlaLeuAlaMetLysPhe	760
QY	1795	CGCGCCGCTTCTGACGCGCGCGCGAGTACCTCATCCACCAAGGCGATGCCCTGCGAGCC	1854
Db	761	LysThrThrHisAlaProProGlyAspThrLeuValHisAlaGlyAspLeuLeuThrAla	780
QY	1855	CTCTACTTTGTCTGCTCTGGCTCCATGGAGGTGCTCAAGGTGGGCACCGTGTCTCCCATC	1914
Db	781	LeuTyrPheIleSerArgGlySerIleGluIleLeuArgGlyAspValValValAlaIle	800

QY	1915	CTAGGGAAGGCGACCTTGATCGGTGTCAGCTGCCCGCGGAGCAGCAGTGTGTAAGGCC	1974
Db	801	LeuGlyLysAsnAspIlePheGlyGluProLeuAsnLeuTyrAlaArgProGlyLysSer	820
QY	1975	AATGCCGACGCTGAAGGGGCTACGCTACTCGTCTCGTCAAGTGTCTGCAGCTGTGCGTGGCTG	2034
Db	821	AsnGlyAspValArgAlaLeuThrTyrCysAspLeuHisLysIleHisArgAspAspLeu	840
QY	2035	CACGACACGCTGGCGTGTACCCCGAGCTTTGGCCCGCTTCAGTCGTGCGCTCCGAGGG	2094
Db	841	LeuGluValLeuAspMetTyrProGluPheSerAspHisPheTrpSerSerLeu	858
QY	2095	GAGCTCAGCTACAACCTG-----GGTCTGGGGAGGCTCTGCAGAG	2136
Db	859	GluIleThrPheAsnLeuArgAspThrAsnMetIleProGlySerProGlySerThrGlu	878
QY	2137	GTGACACCAAGCTCCCTGAGGGGGCAATACCTTATGTCACGCTGGAGGAGAGGAG	2196
Db	879	TrpGluGlyGlyPheAsnArgInArgLysArgLysLeuSerPheArgArgThrAsp	898
QY	2197	ACAGATGGGAGAGGGCCCAACGGTCTCCCAAGCCCACTGATGAGCCCTCCAGCCC	2256
Db	899	LysAspThrGluGln-----	903
QY	2257	CTGCTGCCCTGGCTGCACCTCTCATCTCAGCTGCCAAGTGTATCCCCACATCGA	2316
Db	904	-----ProGlyGluValSerAla-----LeuGlyProGlyArg	914
QY	2317	ACAGACCCCGGCTCGTCTAGTGGCAGGAGGCGCAGGCGAGGGCGGGCTTTGAAG	2376
Db	915	AlaGlyAlaGlyPro-----SerSerArgIleArgProGlyProTrpGlyGluSer	932
QY	2377	GCTGAGCTGGCCCTCTGCTCCCCCA-----CGGGCCCTA	2412
Db	933	ProSerSerGlyProSerSerProGluSerSerGluAspGluGlyProGlyArgSerSer	952
QY	2413	GAGGGGCTACGGCTG-----CCCCCATGCCATGGAATGTGCCCCCAGATCTG	2460
Db	953	SerProLeuArgLeuValProPheSerSerProArgProProGlyGluProProGlyGly	972
QY	2461	AGCCCCAGGTATGATGTCATTGAAGCGGTGTGGCTCGGACGACGCCCAAG-----	2514
Db	973	GluPro-----LeuThrGluAspCysGluLysSerSerAspThrCysAsnProLeuSerGly	991
QY	2515	-----TTCTCTTTC-----CGCTGGGC	2532
Db	992	AlaPheSerGlyValSerAsnIlePheSerPheTrpGlyAspSerArgGlyArgGlnTyr	1011
QY	2533	CAGTCTGGCCCGGAATGTAGCAGCAGCCCCCTCCCTGGACACAGACGGCTGTCTACT	2592
Db	1012	GlnGluLeuProArgCys-----ProAlaProAlaProSerLeuLeuAsn	1026
QY	2593	GTTCCTCC-----CATGGGCCAGCAGCGCAGGAACACAGACACA-----CTGGACAAG	2640
Db	1027	IleProLeuSerSerProSerArgArgProArgGlyAspValGluSerArgLeuAspAla	1046
QY	2641	CTTCGCGACGGCTGACAGAGCTGTACAGCAGGTG-----CTGCAGATCGGGAGGACTG	2697
Db	1047	LeuGlnArgGlnLeuAsnArgLeuGluThrArgLeuSerAlaAspMetAlaThrValLeu	1066
QY	2698	CAGTCACTTCGCGAGGCTGTGAGCTGTGCTGGCGGCCCAAGCGGGGCTCGTGCCT	2757
Db	1067	GlnLeuLeuGln-ArgGlnMetThrLeu-----	1075
QY	2758	CGGGCATCGGAGAGGGCGGTGCCAGCCACCTCCGGGCTTCTGCAGCCTCTGTGT	2817
Db	1076	-----ValProProAlaTyrSerAla-----Va	1083
QY	2818	GTGGACTGTGGGCATCTCTTACTGCTGCTGAGCGCCCGAGCTGGCTGTGCTTGAAGTGG	2877
Db	1083	ThrProGlyProGlyProThrSerThrSerProLeuLeuProValSerProPhe--	1102

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QY 2878 ACTTGGCCACCCCTGCTCCGGGCTCCTCCCTCATGCGACCTGGCCCTGGGCTCC 2937
Db 1103 -----ProThrLeuThrLeuAspSerLeuSerGln-----Valse 1114
QY 2938 CCAGCGCTCTC-----AGAGTCCCTCCCTGCGCTCGAGCCACAGCTTTCGGACTCC 2988
Db 1114 rGlnPheMetAlaCysGluGluLeuProGly----AlaProGluLeuProGlnGluG 1133
QY 2989 ACTCAGACTCAGACCCCTGCTCCTCAGGAGACTCTGCTGAGCCACGACCCCTG 3046
Db 1133 yProThrArgArgLeuSerLeuProGlyGlnLeuGlyAlaLeuThrSerGlnProLeu 1152

RESULT 14
KCH6 HUMAN STANDARD; PRT; 994 AA.
ID KCH6 HUMAN Q9H252; Q9H252;
AC Q9H252; Q9H252; (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Potassium voltage-gated channel subfamily H member 6 (Ether-a-go-go
DE related gene potassium channel 2) (Ether-a-go-go related protein 2)
DE (bag related protein 2).
GN KCNH6 OR ERG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Titus S.A., Ganetky B.S.;
RT "Human Bag-related gene member 2 (Herg2) potassium channel.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Amalgama, and Kidney;
RA Nimomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,
RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Tanigami A.,
RA Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F., Wakebe H.,
RA Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,
RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RT "NEO human cDNA sequencing project.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RC TISSUE=Uterus;
RX MEDLINE=22389257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.R.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalius D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Pore-forming (alpha) subunit of voltage-gated potassium
channel. Elicits a slowly activating, rectifying current (By

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similarity). Channel properties may be modulated by cAMP and
subunit assembly.
-!- SUBUNIT: The potassium channel is probably composed of a homo- or
heterotetrameric complex of pore-forming alpha subunits that can
associate with modulating beta subunits. Heteromultimers with
KCNH2/ERG1 and KCNH7/ERG3 (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
Comment=Experimental confirmation may be lacking for some
isoforms;
Name=1;
IsoId=Q9H252-1; Sequence=Displayed;
Name=2;
IsoId=Q9H252-2; Sequence=VSP_000977, VSP_000978;
Name=3;
IsoId=Q9H252-3; Sequence=VSP_000979, VSP_000980;
-!- DOMAIN: The segment S4 is probably the voltage-sensor and is
characterized by a series of positively charged amino acids at
every third position.
-!- SIMILARITY: Belongs to the potassium channel family. H (Bag)
subfamily.
-!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
-!- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.
-!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
-----
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or send an email to license@isb-sib.ch).
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EMBL; AF311913; AAC40871.1; -
EMBL; AK090969; BAC03559.1; -
EMBL; AK091877; BAC03764.1; -
EMBL; BC006334; AAH06334.1; -
Genew; HGNC:18862; KCNH6.
InterPro; IPR000595; cNMP binding.
InterPro; IPR003967; Erg channel.
InterPro; IPR005821; Ion trans.
InterPro; IPR001622; K-channel pore.
InterPro; IPR005820; M-channel_nlg.
InterPro; IPR001610; PAC.
InterPro; IPR00700; PAS-associ. C.
InterPro; IPR000014; PAS domain.
Pfam; PF000027; cNMP binding; 1.
Pfam; PF00520; ion_trans; 1.
Pfam; PF00785; PAC; 1.
PRINTS; PR01470; ERGCHANNEL.
SMART; SM00100; cNMP; 1.
SMART; SM00086; PAC; 1.
PROSITE; PS00888; cNMP_BINDING_1; FALSE NEG.
PROSITE; PS00889; cNMP_BINDING_2; FALSE NEG.
PROSITE; PS00842; cNMP_BINDING_3; 1.
PROSITE; PS50042; cNMP_BINDING_3; 1.
PROSITE; PS50113; PAC; FALSE NEG.
PROSITE; PS50112; PAC; FALSE NEG.
KW Transport; Ion transport; Ionic channel; Voltage-gated channel;
KW Potassium channel; Potassium; Potassium transport; Transmembrane;
KW Multigene family; Alternative splicing.
DOMAIN 1 261 CYTOPLASMIC (POTENTIAL).
DOMAIN 262 282 SEGMENT S1 (POTENTIAL).
FT TRANSMEM 299 319 SEGMENT S2 (POTENTIAL).
FT DOMAIN 320 340 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 341 361 SEGMENT S3 (POTENTIAL).
FT TRANSMEM 371 391 SEGMENT S4 (POTENTIAL).
FT DOMAIN 392 398 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 399 419 SEGMENT S5 (POTENTIAL).
FT DOMAIN 464 484 SEGMENT H5 (PORE-FORMING) (POTENTIAL).
FT TRANSMEM 491 511 SEGMENT S6 (POTENTIAL).
FT DOMAIN 512 594 CYTOPLASMIC (POTENTIAL).
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 Best Local Similarity: 34.39% Mismatches: 336
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US-09-965-830-1_COPY_6_3257 (1-3252) x KCH6_HUMAN (1-994)

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 DB 195 LysHisArgSerSerThrThrGluIleIleAlaProHisLysValValGlu 214
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Search completed: September 1, 2004, 15:54:29
Job time : 195 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 1, 2004, 15:52:14 ; Search time 345 Seconds

(without alignments)
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Searched: 1297172 seqs, 314612898 residues

Total number of hits satisfying chosen parameters: 2594344

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	5659	92.9	1080	9	US-09-119-855-2	Sequence 2, Appli
5	5649.5	92.8	1082	14	US-10-121-746-20	Sequence 20, Appli
6	5629.5	91.5	1107	14	US-10-185-867-16	Sequence 16, Appli
7	2515	41.3	1102	14	US-10-185-867-36	Sequence 36, Appli
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9	1901	31.2	1284	9	US-09-119-855-11	Sequence 11, Appli
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42	1395.5	22.9	1195	14	US-10-192-440-10	Sequence 10, Appli
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44	1384.5	22.7	1196	14	US-10-255-532-2	Sequence 2, Appli
45	1384.5	22.7	1196	15	US-10-391-399-82	Sequence 82, Appli

ALIGNMENTS

RESULT 1
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; Sequence 2, Application US/09965830
; Patent No. US20020177201A1
; GENERAL INFORMATION:
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: A novel potassium channel protein
; FILE REFERENCE: Y9903-PCT
; CURRENT APPLICATION NUMBER: US/09/965,830
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 09/600,776
; PRIOR FILING DATE: 2001-07-21
; PRIOR APPLICATION NUMBER: JP P1998-346198
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1083
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-965-830-2

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US-10-160-224-1
; Sequence 1, Application US/10160224
; Publication No. US2003007731A1
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy J.
; APPLICANT: Wickenden, Alan
; APPLICANT: ICAGEN, Incorporated
; TITLE OF INVENTION: Human Elk, a Voltage-Gated Potassium Channel Subunit
; FILE REFERENCE: 018512-001320US
; CURRENT APPLICATION NUMBER: US/10/160,224
; CURRENT FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: US/09/343,494
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1083
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Elk (hElk; Eag (ether a go-go)-like K+ gene)
; OTHER INFORMATION: potassium channel monomer protein
US-10-160-224-1

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Best Local Similarity: 99.91% Mismatches: 1
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601 AACTTGCTGAGTACAAGAGTAGCCGCCATCCGGAAAGTGCCTTCACTCTGTGTGACTGT 660
201 AsnLeuProGluTyrLysValAlaAlaIleArgLysSerProPheIleLeuLeuHisCys 220
661 GGGGCACTGAGACCACTGGGATGCGTTCATCTGCTCGCCACACTCTATGTGGCTGTC 720
221 GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal 240
721 ACTGTGCCCTACAGCGTGTGTGAGCACAGCAGCGAGCCAGTGCCTGCCCGCGCCCG 780
241 ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro 260
781 CCCAGCTCTGACCTGCGCTGAGTGCCTTCATCTTCATCTTGACATTTGCTGTAATTC 840
261 ProSerValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPhe 280
841 CGTACCACTTCGTCCTCAAGTCGGGCGGAGGTGTTTGGCCCAAGTCCATTTGCCCTC 900
281 ArgThrThrPheValSerLysSerGlyGlnValPheAlaProLysSerIleCysLeu 300
901 CACTACGTCAACACCTGTTCTCGTGGATGTATGTCAGCGCTGCTCCCTTACCTGCTA 960
301 HisTyrValThrTrpPheLeuLeuAspValIleAlaAlaLeuProPheAspLeuLeu 320
961 CATGCTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 1020
321 HisAlaPheLysValAsnValTyrPheGlyAlaHisLeuLeuLysThrValArgLeuLeu 340
1021 CGCTGCTCGCTGCTCGCGGTGGACCGGTACTCGCAGTACAGCGCGGTGGTGGT 1080
341 ArgLeuLeuArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValValLeu 360
1081 ACATGCTCATGCGCGTGTGCTCGCTGCTCGCTGCTCGCTGCTCGCTGCTGCTGCT 1140
361 ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr 380
1141 ATTGGCCAGCGGAGATCGAGACGACGAAATCGAGCTGCCTCAGATTGGCTGGTGCAG 1200
381 IleGlyGlnArgGluLysSerSerGluSerGluLeuProGluIleGlyTrpLeuGln 400
1201 GAGCTGGCGCGCGACTGGAGACTCCCTACTACTGCTGGCGCGGAGCGCGAGTGGGG 1260
401 GluLeuAlaArgArgLeuGluThrProTyrTyrLeuValGlyArgArgProAlaGlyGly 420
1261 AACAGTCCGGCCAGAGTGACAACTGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1320
421 AsnSerSerGlyGlnSerAspAsnCysSerSerSerSerGluAlaAsnGlyThrGlyLeu 440
1321 GAGCTGCGGGCGCGCTGCTGCGCAGCGCTACATCCTCCCTACTCTACTCTGCACTC 1380
441 GluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeu 460
1381 AGCAGCTCACCAGCGTGGCTTCGGCAACGTGCTCCGCCAACACCGACACCGAGAGATC 1440
461 SerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGluLysIle 480
1441 TTCTCATCTGCAACATGCTCATCGGGCGCTGATGACCGCGTGTGTGTGGGAACGTG 1500
481 PheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValValPheGlyAsnVal 500
1501 ACGGCCATCATCAGCGCATGTACCGCGCTTCTGTACACACCGCGCAGCGCGAC 1560

501 ThrAlaIleIleGlnArgMetTyrAlaArgArgPheLeuTyrHisSerArgThrArgAsp 520
1561 CTGCGCGACTACATCCGCATCCACCGTATCCCAAGCCCTCAACAGCAGCGCATGTGGAG 1620
521 LeuArgAspTyrIleArgIleHisArgIleProLysProLeuLysGlnArgMetLeuGlu 540
1621 TACTTCCAGGCGACTGCGCGGTGACAAATGGCATCGACACACCGAGCTGCTGCAGAGC 1680
541 TyrPheGlnAlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeuLeuGlnSer 560
1681 CTCCCTGACGAGCTCGCGCGCAGACATCGCATGACCTGCACCAAGAGAGTCTCGCAGCTG 1740
561 LeuProAspGluLeuArgAlaAspIleAlaMetHisLeuHisLysGluValLeuGlnLeu 580
1741 CCATGTTTGGCGCGCGCGCTGCTCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800
581 ProLeuPheGluAlaAlaSerArgGlyCysLeuArgAlaLeuSerLeuAlaLeuArgPro 600
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601 AlaPheCysThrProGlyIleTyrLeuIleHisGlnGlyAspAlaLeuGlnAlaLeuTyr 620
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621 PheValCysSerGlySerMetGluValLeuLysGlyGlyThrValLeuAlaIleLeuGly 640
1921 AAGCGCGACCTGATCGCTGTGAGTGCCTCGCGCGGAGCAGGTGGTAAAGCCCAATGCC 1980
641 LysGlyAspLeuIleGlyCysGluLeuProArgGluGlnValValLysAlaAsnAla 660
1981 GACGTGAAGGGCTCAGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
661 AspValLysGlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGlyLeuHisAsp 680
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2101 AGCTACAACCTGGTCTGGGGAGGCTGTGAGAGGTGGACACACAGCTCCCTGAGCGGC 2160
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Db	561	GluLeuArgAlaAspIleAlaMetHisLeuHisLysGluValLeuGlnLeuProLeuPhe	580	921	GluGlyProCysProAlaSerThrSerGlyLeuLeuGlnProLeuCysValAspThrGly	940
QY	1750	GAGGGGCGAGCGGCTGCTGGCGGACATGTCCTGGCCCTCGCGCCGCTTCTGC	1809	2830	GCATCTCTACTGCTGACGCCCCAGCTGCTCTCTTGTAGTGGACTTGGCCCCAC	2889
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QY	1810	ACGCGGGCGAGTACTCTCATCACCAAGCGATGCCCTGCGAGGCCCTTACTTTGTCTGC	1869	2890	CCTCTCGCGGGCTCTCTCCCTCATGGCACCTGGCCCTGGGCTGCCAGCGTCTCAG	2949
Db	601	ThrProGlyGluTyrLeuIleHisGlnGlyAspAlaLeuGlnAlaLeuTyrPheValCys	620	961	ProArgProGlyProProProLeuMetAlaProTrpProTrpGlyProProAlaSerGln	980
QY	1870	TCTGGCTCATGAGTGTCTCAAGGTGGCACCGTCTCGCCATCTAGGGAGGCGGAC	1929	2950	AGCTCCCTGCTGCTGACGACACAGCTTCTTGGACCTCCACCTCAGACTCAGAGCCCT	3009
Db	621	SerGlySerMetGluValLeuLysGlyThrValLeuAlaIleLeuGlyLysGlyAsp	640	981	SerSerProTrpProArgAlaThrAlaPheTrpThrSerThrSerAspSerGluProPro	1000
QY	1930	CTGATCGGCTGTGAGTGTCCCGCGGAGGAGGTGTAAAGGCCAATGCCGACGTGAAG	1989	3010	GCCTCAGAGACCTCTGCTGAGCCGACACCCCTGCTCCCTCCCTCTCTTGTAGGAA	3069
Db	641	LeuIleGlyCysGluLeuProArgGluGlnValValLysAlaAsnAlaAspValLys	660	1001	AlaSerGlyAspLeuCysSerGluProSerThrProAlaSerProProSerGluGlu	1020
QY	1990	GGGCTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2049	3070	GGGGCTAGGACTGGGCCCGGACAGAGCTCTGAGCCAGGCTGAGGCTACACGACTGAGAG	3129
Db	661	GlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGlyLeuHisAspSerLeuAla	680	1021	GlyAlaArgThrGlyProProGluProValSerGlnAlaGluAlaThrSerThrGlyGlu	1040
QY	2050	CTGTACCCGAGTTTCCCGCGCTTTCAGTCTGTGCTCGAGGGAGTCTAGCTACAAC	2109	3130	CCCCCACCAGGCTCAGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3189
Db	681	LeuTyrProGluPheAlaProArgPheSerArgGlyLeuArgGlyGluLeuSerTyrAsn	700	1041	ProProProValSerGlyGlyLeuAlaLeuProTrpAspProHisSerLeuGluMetVal	1060
QY	2110	CTGGTGTCTGGGAGGCTCTGACAGAGGTGGACACAGCTCTGAGCGGCGACATACC	2169	3190	CTTATTGGCTGCATGGCTCTGCGACAGTCCAGTGGACCCGAGGAAGAGGACAGGGGTC	3249
Db	701	LeuGlyAlaGlyGlySerAlaGluValAspThrSerSerLeuSerGlyAspAsnThr	720	1061	LeuIleGlyCysHisGlySerGlyThrValGlnTrpThrGlnGluGlyThrGlyVal	1080
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QY	2230	GCCCGAGCTGATGAGCCCTCAGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2289	; Sequence 20, Application US/10121746		
Db	741	AlaProAlaAspGluProSerSerProLeuLeuSerProGlyCysThrSerSerSer	760	; Publication No. US20030036648A1		
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Db	761	AlaAlaLysLeuLeuSerProArgThrAlaProArgProArgLeuGlyArgGly	780	; APPLICANT: Miller, Andrew P.		
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Db	781	ArgProGlyArgAlaGlyAlaLeuLysAlaGluAlaGlyProSerAlaProArgAla	800	; APPLICANT: Hu, Ping		
QY	2410	CTAGAGGGCTACGGCTGCCCCCATGCCATGCCATGCTGCCCCCAGATCTGAGCCCCAGG	2469	; APPLICANT: Rutter, Marc		
Db	801	LeuGluGlyLeuArgLeuProProMetProTrpAsnValProProAspLeuSerProArg	820	; APPLICANT: Wang, Jian-Wang		
QY	2470	GTAGTAGATGTCATGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2529	; TITLE OF INVENTION: No. US20030036648A1 Human Potassium Channels		
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QY	2530	GCCGAGTCTGCGCGGATGTAGCAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2589	; CURRENT APPLICATION NUMBER: US/10/121,746		
Db	841	GlyGlnSerGlyProGluCysSerSerSerProSerProGlyProGluSerGlyLeuLeu	860	; PRIOR FILING DATE: 2002-04-11		
QY	2590	ACTGTTCCCATGGGCCGAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2649	; PRIOR APPLICATION NUMBER: US/09/336,643A		
Db	861	ThrValProHisGlyProSerGluAlaArgAsnThrAspThrLeuAspLysLeuArgGln	880	; PRIOR FILING DATE: 1999-06-18		
QY	2650	GCGGTGACAGAGTGTGACAGAGGTGTGACAGAGGTGTGACAGAGGTGTGACAGAGGT	2709	; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07		
Db	881	AlaValMetGluLeuSerGluGlnValLeuGlnMetArgGluGlyLeuGlnSerLeuArg	900	; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-01-19		
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				; SEQ ID NO 20		
				; LENGTH: 1082		
				; TYPE: PRT		
				; ORGANISM: H. sapiens		
				US-10-121-746-20		
				Alignment Scores:		
				Pred. No.: 6,78-283		
				Score: 5649.50		
				Length: 1082		
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				Mismatch: 6		
				Best Local Similarity: 99.35%		
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				Query Match: 92.78%		
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QY 61 CGCTTCGACGGCACGACAGTAACCTTCGTGCTGGGCAACGCCAGGTGGCGGCTCTTC 120
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QY 121 CCCGTGGTCTACTGCTGTGATGGCTTCTGTGACCTCACGGGCTTCTCCGGGCTGAGTC 180
Db 40 ProValValTyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal 59
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QY 241 CAACAGATCCGCAAGCCCTCGACGACACAGAGAGTTCAGGCTGAGTGCATCTGTAC 300
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QY 301 CGGAAGACGGGCTCCCT 360
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QY 361 GGGAGGTGGCT 420
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QY 421 GGCCCCGACAGATGGAAGACAGGACAGGTGGTGGCGCGGCGGCTCTCTCTCTCTCT 480
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QY 481 AAAGGCTTCATGCAACCGCGGCGGAGCGCGGCGGCTCTCTCTCTCTCTCTCTCTCT 540
Db 160 LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis 179
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; Sequence 16, Application US/10185867
; Publication No. US2003010429A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-055CP
; CURRENT APPLICATION NUMBER: US/10/185,867
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: US/09/358,383
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: USSN 09/119,855
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 1107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-185-867-16

Alignment Scores:
Pred. No.: 3,1e-122 Length: 1107
Score: 2529.50 Matches: 559
Percent Similarity: 60.24% Conservative: 150
Best Local Similarity: 47.49% Mismatches: 267
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Db	760	SerSerSerAlaAlaLysLeuLeuSerProArgThrAlaProArgProArgLeuGly	779
QY	2341	GGCAGAGGAGGCCAGGAGGCGGGCTTTGAAGCTTGAGCTGGCCCTCTGCTCC	2400
Db	780	GlyArgGlyArgProGlyArgAlaGlyAlaLeuLysAlaGluAlaGlyProSerAlaPro	799
QY	2401	CCACGGGCCCTAGAGGGGCTACGGCTGCCCCCATGCCATCGGAATGTGCCCCAGATCTG	2460
Db	800	ProArgAlaLeuGluGlyLeuArgLeuProProMetProTrpAsnValProProAspLeu	819
QY	2461	AGCCCCAGGTAGTAGATGCAATTGAAGCGGTGTGGCTCGGACAGCCCAAGTCTCT	2520
Db	820	SerProArgValValAspGlyIleGluAspGlyCysGlySerAspGlnProLysPheSer	839
QY	2521	TTCCGGCTGGCCAGTCTGGCCCGGAATGTAGCAGCAGCCCTCCCTGGACAGAGAGC	2580
Db	840	PheArgValGlyGlnSerGlyProGluCysSerSerSerProSerProGlyProGluSer	859
QY	2581	GGCTGTCTACTGTTCCTCCATGGGCCCGACGAGGCAAGGAACACAGACACACTGGACAAG	2640
Db	860	GlyLeuLeuThrValProHisGlyProSerGluAlaArgAsnThrAspThrLeuAspLys	879
QY	2641	CTTCGGCAGGCGGTGACAGAGCTGTACAGACAGGTCTGCAGATGGGGAGGACTGCAG	2700
Db	880	LeuArgGlnAlaValThrGluLeuSerGluGlnValLeuGlnMetArgGluGlyLeuGln	899
QY	2701	TCACCTCGCAGGCTGTCAGCTGTCTCTCGCGCCACAGGAGGCTCGTCCCTCCG	2760
Db	900	SerLeuArgGlnAlaValGlnLeuValLeuAlaProHisArgGluGlyProCysProArg	919
QY	2761	GCATCGGAGAGGGCGCGTCCCGCCAGCCAGCACCTCCGGGCTTCGACGCTCTGTGTG	2820
Db	920	AlaSerGlyGluGlyProCysProAlaSerThrSerGlyLeuLeuGlnProLeuCysVal	939
QY	2821	GACACTGGGGGATCCTCTACTGCTGCTGAGCCGCCACGCTGGCTCTGTCTGAGTGGACT	2880
Db	940	AspThrGlyAlaSerSerTyrCysLeuGlnProProAlaGlySerValLeuSerGlyThr	959
QY	2881	TGGCCCCACCTCGTCCGGGGCCCTCCCTCATGCGCACCTCGGCGCTGGGGTCCGCCA	2940
Db	960	TrpProHisProArgProGlyProProProLeuMetAlaProArgProTrpGlyProPro	979
QY	2941	CGCTCTCAGAGCTCCCCCTGGCCCTCGAGCCACAGCTTTCTGGACCTCCACTCAGACTCA	3000
Db	980	AlaSerGlnSerSerProTrpProArgAlaThrAlaPheTrpThrSerThrSerAspSer	999
QY	3001	GAGCCCCCTGCTCAGAGAGACTCTGTCTGAGGCCAGCACCCCTGGCTCCCTCTCTCT	3060
Db	1000	GluProProAlaSerGlyAspLeuCysSerGluProSerThrProAlaSerProProPro	1019
QY	3061	TCTGAGGAAGGGGCTAGACTGGGCGCCAGAGCTGTGAGCCAGGCTGAGGCTACGAGC	3120
Db	1020	SerGluGluGlyAlaArgThrGlyProAlaGluProValSerGlnAlaGluAlaThrSer	1039
QY	3121	ACTGAGAGACCCCCACACAGGCTCAGGGGCGCTGGCTTCCTGGGACCCCCCAGCGCTG	3180
Db	1040	ThrGlyGluProProProGlySerGlyGlyLeuAlaLeuProTrpAspProHisSerLeu	1059
QY	3181	GAGATGGTCTATTGGCTGCCATGGCTCTGGCAGCTCCAGTCCAGCCAGGAGAGGC	3240
Db	1060	GluMetValLeuIleGlyCysHisGlySerGlyThrValGlnTrpThrGlnGluGly	1079
QY	3241	ACAGGGGTC	3249
Db	1080	ThrGlyVal	1082

RESULT 6

US-10-185-867-16

Db	877	LeuThrGlnGluValSerGlnLeuGlyLysAspMetArgAsnValIleArgLeuLeuGlu	896
Qy	2722	CTTGCTGGCGCC-----CACAGGAGGGTCCGTC	2754
Db	897	AsnValLeuSerProGlnProSerArgPheCysSerLeuHisThrSerValCys	916
Qy	2755	CCTGGGCA-----TCGGAGAGGGCCGTGCCAGCC	2787
Db	917	ProSerArgGluSerLeuGlnThrArgThrSerTrpSerAlaHisGlnProCys	934
Qy	2788	AGCACCCTCGGGCTTCGACGCTCTGTGTGTGGACATGGGGCATCTCTACTGTC	2844
Db	935	-----LeuHisLeuGlnThrGlyAlaAlaIleThrGln	946
Qy	2845	CTGAGCCCCCAGCTGGCTCTGTCTGTGTGGATCTGGCCCCCCTCGTCCGGGGCT	2904
Db	947	AlaGlnLeuCysSerAsnIleThrSerAspIleTrpSer	960
Qy	2905	CCTCCCTCATGGCACCTGGCCCTGGGTCCCCAGGCTCTCAGAGCTCCCTCGGCT	2964
Db	961	-----ValAspProSerSerValGlySerSer---Pro	970
Qy	2965	CGAGCCACAGCTTCTGACCTCCACCTCAGACTCAGACCCCTCCCTCAGAGACCTC	3024
Db	971	GlnArgThrGly-----AlaHisGlnGlnAsnProAlaAspSerGluLeu	985
Qy	3025	TGCTGAGCCAGCACCCCTGCCCTCCCT-----	3054
Db	986	TyrHisSerProSerLeuAspTyrSerProSerHisTyrGlnValGlnGluGlyHis	1005
Qy	3055	-----CCTCCTCTGAGGAGGGGCTAGGACTGGGCGCCGACAG	3093
Db	1006	LeuGlnPheLeuArgCysIleSerProHisSerAspSerThrLeuThr---ProLeuGln	1024
Qy	3094	CCTGTGAGCCAGCTGAGCTACAGACTGAGAGCCCTCCACAGGGTACAGGGCCCTG	3153
Db	1025	SerIleSerAlaThrLeuSerSerValCysSerSerSerGlnThrSerLeuHisLeu	1044
Qy	3154	GCTTGCCTGGACCCACAGCTGGAGATGGTCTATTGGCTGCCATGCTGGC	3213
Db	1045	ValLeuPro-----SerArgSerGluGlu-----GlySerPheSerGlnGly	1058
Qy	3214	ACAGTC-----CAGTGGACCCAGGAA	3234
Db	1059	ThrValSerSerPheSerLeuGluAsnLeuProGlySerTrpAsnGlnGlu	1075
RESULT 7			
US-10-185-867-36			
; Sequence 36, Application US/10185867			
; Publication No. US20030104429A1			
; GENERAL INFORMATION:			
; APPLICANT: Curtiss, Rory A.J.			
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR			
; FILE REFERENCE: MNI-055CP			
; CURRENT APPLICATION NUMBER: US/10/185,867			
; CURRENT FILING DATE: 2002-06-27			
; PRIOR APPLICATION NUMBER: US/09/358,383			
; PRIOR FILING DATE: 1999-07-21			
; PRIOR APPLICATION NUMBER: USSN 09/119,855			
; PRIOR FILING DATE: 1998-07-21			
; NUMBER OF SEQ ID NOS: 36			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 36			
; LENGTH: 1102			
; TYPE: PRT			
; ORGANISM: Rattus norvegicus			
US-10-185-867-36			
Alignment Scores:			
Pred. No.:	1.73e-121	Length:	1102
Score:	2515.00	Matches:	551
Percent Similarity:	62.00%	Conservative:	149

Best Local Similarity: 48.80%		Mismatches: 295	
Query Match: 41.30%		Indels: 134	
DB: 14		Gaps: 24	
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QY	1	ATGCGCGCATCGGGGCTCTCGCGCTCAGAACACCTTCTCTGGACACCATCGCTACG	60
DB	1	MetProValMetLysGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr	20
QY	61	CGCTTCGACGCGCACAGTAACCTTCGTGTGGGCAACGCCCGAGGTGCGGGGCTCTTC	120
DB	21	ArgPheAspGlyThrHisSerAsnPheIleLeuAlaAsnAlaGlnValAlaLysGlyPhe	40
QY	121	CCCGTGTCTACTGCTCTGATGGCTTCGTGACCTCAGCGGCTTCTCCGGGCTGAGTC	180
DB	41	ProIleValTyrCysSerAspGlyPheCysGluLeuAlaGlyPheAlaArgThrGluVal	60
QY	181	ATGCGCGGGCTGTGCT	240
DB	61	MetGlnLysSerCysSerCysLysPheLeuPheGlyValGluThrAsnGluGlnLeuMet	80
QY	241	CAACAGATCCGCAAGGCCCTGGACGAGCAACAAGGAGTTCAAGGCTGAGCTGATCTGTAC	300
DB	81	LeuGlnIleGluLysSerLeuGluGluLysValGluPheLysGlyGluIleMetPheTyr	100
QY	301	CGGAGAGCGGGCTCCGCTTCTGCTGCTCTCTGATGTATACCCATAAAGATGAGAAA	360
DB	101	LysLysAsnGlyAlaProPheTrpCysLeuLeuAspIleValProIleLysAsnGluLys	120
QY	361	GGGAGGTGGCT	417
DB	121	GlyAspValValLeuPheLeuAlaSerPheLysAspIleThrAspThrLysValLysIle	140
QY	418	GGGCGGCCCGACAGATGGAAGGAGACAGGTGTGGCGCGCGGATATGGCGGGCACGA	477
DB	141	ThrSerGluAspLysLysGluAspArgAlaLysGlyArgSerArgAlaGly-----	157
QY	478	TCCAAGGCTTCAATGCCAACCGCGCGGAGCGCGCGCTCTTACCACCTGTCCGG	537
DB	158	---SerHisPheAspSerAlaArgArgSerArgAlaValLeuTyrHisIleSerGly	176
QY	538	CACCTGCAGAGCAGCCCAAGGCGACAGCAAGCTCAATAAGGGGTGTGGGGAGAAA	597
DB	177	HisLeuGlnArgArgGluLysAsnLysLeuLysIleAsnAsnValPheValAspLys	196
QY	598	CCAACTTCGCTCAGTACAAAGTAGCGCCATCCGGAAGTCGCCCTTCTATCTGTTCAC	657
DB	197	ProAlaPheProGluTyrLysValSerAspAlaLysSerLysPheIleLeuLeuHis	216
QY	658	TGTGGGCACTGAGAGCCACCTGGGATGGCTTCATCTCTGCTCGCCACACTCTATGTGGCT	717
DB	217	PheSerThrPheLysAlaGlyTrpAspTrpLeuIleLeuLeuAlaThrPheTyrValAla	236
QY	718	GTCACTGTCCCTACAGCGTGTGTGTGAGCACAGCGGAGCCAGTGGCGCCCGCGG	777
DB	237	ValThrValProTyrAsnValCysPheIleGlyAsnGluAspLeuSerThrThrArgSer	256
QY	778	CCGCCCCAGCGTCTGTGACCTCGCGCGTGGAGGTCTCTTCACTCTTACATGTGTGCAAT	837
DB	257	---ThrThrValSerAspIleAlaValGluIleLeuPheIleAspIleIleLeuAsn	275
QY	838	TTCGGTACCATTCGTGTCCAAGTCCGCGCGAGTGTGTTCCTCCCAAGTCCATTTCG	897
DB	276	PheArgThrThrTyrValSerLysSerGlyGlnValIlePheGluAlaArgSerIleCys	295
QY	898	CTCCACTACGTACACCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	957
DB	296	IleHisTyrValThrThrThrPheIleIleAspLeuIleAlaLeuProPheAspLeu	315
QY	958	CTACATGCTTCAAGGTCAAGTGTACTCTCGGGGCCCATCTGTGTGAGACGCTGGCGCTG	1017
DB	316	LeuTyrAlaPheAsnValThrValValSerLeuValHisLeuLeuLysThrValArgLeu	335


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Db      1013 ThrThrLeuThrProLeuGlnSerIleSerAlaThrLeuSerSerValCysSerSer 1032
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QY      3034 CCCAGCACCCCT-----GCCCTCCCTCTCTCTCTAGGAGGGGCTAGGACT--- 3081
      |||
Db      1033 SerGluThrSerLeuHisLeuValLeuProSerArgSerGluGluGlySerIleThrHis 1052
      |||
QY      3082 GGGCCCGCAGAGCCTGTGAGCCAGCTGAGGCTACGAGCTGGAGAGCCCCACAGGG 3141
      |||
Db      1053 GlyProValSerSerPheSerLeu-----GluAsnLeuProGly 1065
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QY      3142 TCAGGGGGCCTGGCCTTCCCTCGGGAC 3169
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Db      1066 Ser-----TrpAsp 1068
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RESULT 8

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US-09-965-830-6
; Sequence 6, Application US/09965830
; Patent No. US20020177201A1
; GENERAL INFORMATION:
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: A novel potassium channel protein
; FILE REFERENCE: Y9903-PCT
; CURRENT APPLICATION NUMBER: US/09/965,830
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 09/600,776
; PRIOR FILING DATE: 2001-07-21
; PRIOR APPLICATION NUMBER: JP P1998-346198
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1017
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-965-830-6

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Alignment Scores:

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Pred. No.: 9,77e-119 Length: 1017
Score: 2461.50 Matches: 538
Percent Similarity: 59.19% Conservatives: 119
Best Local Similarity: 48.47% Mismatches: 245
Query Match: 40.43% Indels: 208
DB: 9 Gaps: 23

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US-09-965-830-1_COPY_6_3257 (1-3252) x US-09-965-830-6 (1-1017)

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QY      1 ATGCCGGCCATCGGGGGCTCTGGGGCTCAGAACACCTTCTCTGACACCATCGCTAGC 60
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Db      1 MetProValMetLysGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20
      |||
QY      61 CGCTTCAGCGCAGCAGCAGTAACTTCGTGGGCAACGCCCGAGGTGGCGGGCTCTTC 120
      |||
Db      21 ArgPheAspGlyThrHisSerAsnPheLeuLeuAlaAsnAlaGlnGlyThrArgGlyPhe 40
      |||
QY      121 CCGGTGGTCTACTGCTCTGATGCTTCTGTGACCTCAGCGGCTTCTCCGGGCTAGGTC 180
      |||
Db      41 ProIleValTyrcysSerAspGlyPheCysGluLeuThrGlyTyrglyArgThrGluVal 60
      |||
QY      181 ATGCAGCGGGCTGTCCTCTCTCTCTTATGGGCCAGACACAGTGTGCTGCCG 240
      |||
Db      61 MetGlnLysThrCysSerCysArgPheLeuTyrglyProGluThrSerGluProAlaLeu 80
      |||
QY      241 CAACAGATCCGCAAGCCCTGGAGCAGCAAGAGTTCAAAGCTGAGCTGATCCCTGTAC 300
      |||
Db      81 GlnArgLeuHisLysAlaLeuGluGlyHisGlnGluHisArgAlaGluLeuCysPheTy 100
      |||
QY      301 CGGAAGAGGGGGCTCCCGTCTCTGGTGTCTCTGGATGTGATACCCATAAGATGAGAAA 360
      |||
Db      101 ArgLysAspGlySerAlaPheTrpCysLeuLeuAspMetMetProIleLysAsnGluMet 120
      |||
QY      361 GGGGAGGTGGCTCTCTCTCTAGTCTCTCAAGGACATCAGCGCAACCAAGACCGAGGG 420
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Db      121 GlyGluValValLeuPheLeuPheSerPheLysAspIleThrGlnSerGlySerProGly 140
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QY      421 ---GGCCCGCAGACAGATGAAGAGACAGGTGTGTGGCCGCGCCGATATGGCCGGCAGCA 477
      |||
Db      141 LeuGlyProGln-----GlyGlyArgGlyAspSerAsnHisGluAsn 154
      |||
QY      478 TCCAAGGC-----TTCAATGCCAACCGCGCGCGGAGCGGGCC 516
      |||
Db      155 SerLeuGlyArgArgGlyAlaThrTrpLysPheArgSerAlaArgArgSerArgThr 174
      |||
QY      517 GTGCTCTACCACTGTCGGGCACCTGCAGAGCAGCCCAAGGGCAAGCACAAGCTCAAT 576
      |||
Db      175 ValLeuHisArgLeuThrGlyHisPheGlyArgArgGlyGlnGlyValMetLysAlaAsn 194
      |||
QY      577 AAGGGGTGTTTGGGGAGAAACCAACTTGCCTGAGTACAAAGTAGCCCGCATCCGGAG 636
      |||
Db      195 AsnAsnValPheGluProLysProSerValProGluTyrlsValAlaSerValGlyGly 214
      |||
QY      637 TCGCCCTTCATCTCTTGTGACCTGTGGGCACCTGAGAGCACCCTGGATGGCTTCCTCTG 696
      |||
Db      215 SerArgCysLeuLeuLeuHisTyrSerValSerLysAlaIleTrpAspGlyLeuLeu 234
      |||
QY      697 CTCGCCACACTCTATGTGCTGCTCACTGTGCCCTACAGCGTGTGTGTGAGCAGCAGC 756
      |||
Db      235 LeuAlaThrPheTyrlsValAlaValThrValProTyrAsnValCysPheSerGlyAsp 254
      |||
QY      757 GAGCCAGTGGCGCGCGCGCGCGCGCTGTGACCTGTGTGCTGGAGTCTCTCTTC 816
      |||
Db      255 AspThrProIleThrSerArgHisThrLeuValSerAspIleAlaValGluMetLeuPhe 274
      |||
QY      817 ATCCTTGACATGTGCTGAATTCGTTACCATTCCTGTGTCCAAAGTCGGCCGAGGTGGTG 876
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Db      275 IleLeuAspIleLeuAsnPheArgThrThrTyrlsValSerGlnSerGlyGlnValIle 294
      |||
QY      877 TTTGGCCCAAGCTCCATTGCTCCACTACGTCCACCTGTGTCTCTGTGGATGTCATC 936
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Db      295 SerAlaProArgSerIleGlyLeuHisTyrLeuAlaThrTrpPheIleAspLeuIle 314
      |||
QY      937 GCAGCGCTGCCCTTTGACCTGTACATGCTTCAAGGTCAACGTGTACTTCGGGGCCCAT 996
      |||
Db      315 AlaAlaLeuProPheAspLeuLeuTyrlsPheAsnIleThrValThrSerLeuValHis 334
      |||
QY      997 CTGCTGAGACCGGTGGCGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGT 1056
      |||
Db      335 LeuLeuLysThrValArgLeuLeuArgLeuLeuArgLeuGlnLysLeuGluArgTyr 354
      |||
QY      1057 TCGCAGTACAGCGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1116
      |||
Db      355 SerGlnCysSerAlaValValLeuThrLeuLeuMetSerValPheAlaLeuAlaHis 374
      |||
QY      1117 TGGGTGCGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1176
      |||
Db      375 TrpMetAlaCysIleTrpTyrlsValIleGlyArgGluMetGluAlaAsnAspProLeu 394
      |||
QY      1177 CTGCTGAGATTTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1236
      |||
Db      395 LeuTrpAspIleGlyTrpLeuHisGluLeuGlyLysArgLeuGluValProTyr 412
      |||
QY      1237 GTGGGCGGAGCGCAGCTGGAGGAACAGCTCCGGCCAGAGTGCACAACTGCAGCAGCAG 1296
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Db      412 ----- 412
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QY      1297 AGCGAGGCCAACGGGAGCGGGCTGTGGAGTGTGTGGCGCGCGCTGTGTGTGTGTGTGT 1356
      |||
Db      413 -----ValAsnGlySer-----ValGlyGlyProSerArgSerAlaTyr 426
      |||
QY      1357 ATCACCTCTCTTCTTCCACTCAGCAGCTCAGCAGCTCAGCAGCTCAGCAGCTCAGCAG 1416
      |||
Db      427 IleAlaAlaLeuTyrlsPheThrLeuSerSerLeuThrSerValGlyPheGlyAsnValCys 446
      |||
QY      1417 GCCAACACGACGACCCAGAGAGATCTTCTCATCTGTCCACCATGTCTCATCGCGCGCTGATG 1476
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Db      447 AlaAsnThrAspAlaGluLysIlePheSerIleCysThrMetLeuIleGlyAlaLeuMet 466
      |||

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QY 1477 CACGGGTGGTGTGGAACTGACGGCCATCATCCAGCGCATGTACGCCGCGCTTT 1536
Db 467 HisAlaValAlpGlyAsnValThrAlaIleIleGlnArgMetTyrSerArgArgSer 486
QY 1537 CTGTACACAGCGGACAGCGGACCTGGCGGACTACATCCGATCCACCGTATCCCAAG 1596
Db 487 LeuTyrHisSerArgMetTyrAspLeuLysAspPheIleArgValHisArgLeuProArg 506
QY 1597 CCCCTCAAGCAGCGCATCTGGAGTACTTCAGGCGCATCTGGCGGTGAACATGGCATC 1656
Db 507 ProLeuLysGlnArgMetLeuGluTyrPheGlnThrThrAlaValAsnSerGlyIle 526
QY 1657 GACACACCGAGCTGCTGCAGCGCTCCCTGACGAGCTGCGCGCAGACATGCCATGCAC 1716
Db 527 AspAlaAsnGluLeuLeuArgAspPheProAspGluLeuArgAlaAspIleAlaMetHis 546
QY 1717 CTGCACAGGAGGCTCTGCAGTGCATCTGTAGGCGGCGGCGGCTGCTCGG 1776
Db 547 LeuAsnArgGluIleLeuGlnLeuProLeuPheGlyAlaAlaSerArgGlyCysLeuArg 566
QY 1777 GCATGCTCTGGGCGCTCGGCGCGCTCTCTGCAGCGCGGCGGAGTACTCATCCACCA 1836
Db 567 AlaLeuSerLeuHisIleLysThrSerPheCysAlaProGlyGluTyrLeuLeuArgArg 586
QY 1837 GCGCATGCTCTGCAGGCGCTCTACTTGTCTGCTCTGCTGCATGGAGGTGCTCAAGGCT 1896
Db 587 GlyAspAlaLeuGlnAlaHisTyrTyrValCysSerGlySerLeuGluValLeuArgAsp 606
QY 1897 GGCACCGTGTGCGCATCTAGGAGGCGGCGGAGTGTGCTGAGTGTGCTGCGGCGG 1956
Db 607 AsnMetValLeuAlaIleLeuGlyLysGlyAspLeuIleGlyAlaAspIleProGluPro 626
QY 1957 GAGCAG-----GTGTAAGGCCAATGCCGAGCTG 1986
Db 627 GlyGlnGluProGlyLeuGlyAlaAspProAsnPheValLeuLysThrSerAlaAspVal 646
QY 1987 AAGGGGTGACGTACTGCTGCTCAGTGTGTGAGTGTGCTGCGCTGCAGCAGCGCTT 2046
Db 647 LysAlaLeuThrTyrCysGlyLeuGlnLeuSerSerArgGlyLeuAlaGluValLeu 666
QY 2047 GCGGTGTACCCGAGTTTGGCCCGCTTTCAGTGTGCTGCTGCGCTGCGGAGGAGTCA 2106
Db 667 ArgLeuTyrProGluTyrGlyAlaAlaPheArgAlaGlyLeuProArgAspLeuThrPhe 686
QY 2107 AACCTGGGTGTGGGGAGGCTCTGCAGAGTGTGACACCGACTCCCTG----- 2154
Db 687 AsnLeuArgGlnGlySer-----AspThrSerGlyLeuSerArgPheSer 701
QY 2155 -----AGCGGCGCAATACC 2169
Db 702 ArgSerProArgLeuSerGlnProArgSerGluSerLeuGlySerSerSerAspLysThr 721
QY 2170 CTATGTCTCAGCTGGAGGAGGAGACAGATGGGAGGAGGCGCCCGCTCTCCCA 2229
Db 722 LeuProSerIle-----ThrGluAlaGluSerGly-----AlaGluPro 734
QY 2230 GCCCCAGCTGATGAGCCCTCCAGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2289
Db 735 GlyGlyGlyProArgProArgProArgProLeuLeuLeuProAsnLeuSerProAlaArgPro 754
QY 2290 GCTGCCAAGCTG----- 2301
Db 755 ArgGlySerLeuValSerLeuLeuGlyGluLeuProProPheSerAlaLeuValSer 774
QY 2302 -----CTATCCCACTGCAACAGCACCGCGCTCTCTAGTGTGCGAGGAGG 2352
Db 775 SerProSerLeuSerProSerLeuSer-----ProAlaLeuAlaGlyGlnGlyHis 791
QY 2353 CCAGGAGGCGGGGCTTTGAAGCTGTGAGGCTGGCGCTGCTGCTGCTGCTGCTGCTGCT 2412
Db 792 -----SerAlaSerProHisGlyProProArgCysSer 802

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QY 2413 GAGGGG-----CTACGGCTGCCCCCATGCCATGGAATGTGTCCCCAGAT 2457
Db 803 AlaAlaThrLysProProGlnLeuLeuIleProProLeuGlyThrPheGlyProProAsp 822
QY 2458 CTGAGCCCCAGGTAGATGGCATTTGAAGAC-----GGCTGTGGCTCGGACCCAGCCCAAG 2514
Db 823 LeuSerProArgIleValAspGlyIleGluAspSerGlySerThrAlaGluAlaProSer 842
QY 2515 TTCTCTTTCCGGTGGGCGAGTGTGGCCCGGAATGTAGCAGAGCCCTCCCTCGACCA 2574
Db 843 PheArgPhe-----SerArgArgProGluLeuProArgProArgSerGlnAlaPro 859
QY 2575 GAGAGCGCGCTGCTCACTGTTCCCATGGCGCCAGGAGGCAAGAAACACA---GACACA 2631
Db 860 ProThrGlyThrArgProSerProGluLeuAlaSerGluAlaGluValLysGluLys 879
QY 2632 CTGACCAAGCTTCGGCGGTGCAGAGGTGTGCAGAGGTGTCTGCAGATGGGAA 2691
Db 880 ValCysArgLeuAsnGlnLuiLeSerArgLeuAsnGlnLuiValSerGlnLeu---SerAr 899
QY 2692 GCATGCAAGTCACTTCGCCAGGCTGTGCAGCTGTGCTGTGGCGCCCAACAGGAGGCTCG 2751
Db 899 gGluLeuArgHisIleMetGlyLeuLeu----- 908
QY 2752 TGCCCTCGGGCATCGGAGAGGGCGCTGCCAGCCAGCACCTCGGGCTTCTGCAGCCT 2811
Db 909 -----GlnAlaArgLeuGlyProPro----- 915
QY 2812 CTGTGTGTGACACTGGGCGATCTCTCTACTCTGCTGCGAGCCCGCCAGCTGCTGTCTTG 2871
Db 916 -----GlyHisProAlaGlySer----- 921
QY 2872 AGTGGAGTGTGGCCCACTTCGCTGCGGGCGCTCTCTCCCTCATGCGACCCCTGCGCTGG 2931
Db 922 -----AlaThrThrProAspProPr 928
QY 2932 GGTCCCGCAGCGTCTCAGAGCTCCCGCTGGCGCTCGAGCCACAGCTTCTGACCTCCACC 2991
Db 928 oCysProGln---LeuArg-----ProProCysLeuSerProCysAlaSerArgProProPr 946
QY 2992 TCAGACTCAGAGC----- 3004
Db 946 oSerLeuGlnAspThrThrLeuAlaGluValHisCysProAlaSerValGlyThrMetGl 966
QY 3005 -----CCCTGTGCTCAGGAGAC 3021
Db 966 uThrGlyThrAlaLeuLeuAspLeuArgProSerIleLeuProProTyrProSerGluPr 986
QY 3022 CTCTGTCTCAGCCAGCACCCCTGCT 3049
Db 986 oAspProLeuGlyProSerProValPro 995

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RESULT 9

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US-09-119-855-11
; Sequence 11, Application US/09119855
; Patent No. US20020099197A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: mni-055
; CURRENT APPLICATION NUMBER: US/09/119,855
; CURRENT FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 11
; LENGTH: 1284
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-119-855-11

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Alignment Scores: 7.28e-90 Length: 1284
Pred. No.: 1901.00 Matches: 455
Score:

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Percent Similarity:	53.85%	Conservative:	146
Best Local Similarity:	40.77%	Mismatches:	273
Query Match:	31.22%	Indels:	242
DB:	9	Gaps:	31
US-09-965-830-1_COPY_6_3257 (1-3252) x US-09-119-855-11 (1-1284)			
QY	1	ATGCGCGGCTCGGGCTCTGGCGCTCAGAACACCTTCTGACACCATCGCTAGC	60
DB	1	MetProAlaArgLysGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr	20
QY	61	CGCTTCGACGCGCACAGTAACTTCGTGCGGCAACGCCAGGTGGCGGGCTCTTC	120
DB	21	ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnAlaAsnGly---Asn	39
QY	121	CCGTGGTCTACTGCTCTGATGGCTCTGTGACCTCACGGGCTTCTCCGGGCTGAGTC	180
DB	40	ProfileValTyxCysSerAspGlyPheValAspLeuThrGlyTySerArgAlaGlnIle	59
QY	181	ATGCGCGGGCTGTGCTGCTCTCTCTTATGGCCACAGACACAGTGTGCTGCTCGC	240
DB	60	MetGlnLysGlyCysSerCysHisPheLeuTyGlyProAspThrLysGluGluHisLys	79
QY	241	CAACAGATCCGACGAGCCCTGACGAGCACAGAGATTCAAGCTGAGTGTCTGTATC	300
DB	80	GlnGlnIleGluLysSerLeuSerAsnLysMetGluLeuLysLeuGluValIlePheTy	99
QY	301	CGGAGAGCGGGCTCCGCTCTGCTCTCTCTGATGTGATACCCATAAGATGAGAAA	360
DB	100	LysLysGluGlyAlaProPheTrpCysLeuPheAspIleValProIleLysAsnGluLys	119
QY	361	GGGAGGTGGCT	411
DB	120	ArgAspValValLeuPheLeuAlaSerHisLysAspIleThrHisThrLysMetLeuGlu	139
QY	411	-----	411
DB	140	MetAsnValAsnGluGlyCysAspSerValPheAlaLeuThrAlaAlaLeuGlyAla	159
QY	412	-----	412
DB	160	ArgPheArgAlaGlySerAsnAlaGlyMetLeuGlyLeuGlyGlyLeuProGlyLeuGly	179
QY	421	GGCCCC-----GACAGATGGAAGGACACAGGTGGTGGCGGCGCGCGATATGCGCG	471
DB	180	GlyProAlaAlaSerAspGlyAspThrGluAlaGlyGluGlyAsnAsnLeuAspValPro	199
QY	472	GCACGATCCAAAGCTTCAATGCCAACCGCGCGGAGCGCGCGGTCTCTACACCTG	531
DB	200	Ala-----GlyCysAsnMetGlyArgArgSerArgAlaValLeuTyGlnLeu	216
QY	532	TCCGGGCACTGTCAGAGAGCCCAAGGGC---AAGCACAGCTCAATAAGGGG-----	582
DB	217	SerGlyHisTyLysProGluLysGlyGlyValLysThrLysLeuLysLeuGlyAsnAsn	236
QY	583	---GTGTTTGGGAGAAACCAACTTCTCTGAGTACAAAGTAGCGCCATCCGGAAGTCG	639
DB	237	PheMetHisSerThrGluAlaProPheProGluTyLysThrGlnSerIleLysLysSer	256
QY	640	CCCTTCATCTGTTGCACTGTGGGGCACTGAGAGCCACCTGGAGTGGCTTCATCTCTC	699
DB	257	ArgLeuIleLeuProHisTyGlyValPheLysGlyIleTrpAspTrpValIleLeuVal	276
QY	700	GCACACTCTATGTGGCTGTCACTGTCCCTTACAGCGTGTGTGACACAGACGGGAG	759
DB	277	AlaThrPheTyValAlaLeuMetValProTyTrAsnAlaAlaPheAlaLysAlaAspArg	296
QY	760	CCAGTCCCGCGCGCGCGCGCGCTGTGTGACCTGTGACCTGGCGGTGGAGTCTCTTCATC	819
DB	297	GlnThr-----LysValSerAspValIleValGluAlaLeuPheIle	310
QY	820	CTTGACATGTGCTGAATTTCCGTACACATTTCTGTGTCCTGTCCTGTCCTGTCCTG	879

DB	311	ValAspIleLeuLeuAsnPheArgThrThrPheValSerArgLysGlyGluValValSer	330
QY	880	GCCCCAAAGTCCATTGGCTCCACATACCTACACCTGCTGCTGCTGCTGCTGCTGCTG	939
DB	331	AsnSerLysGlnIleAlaIleAsnTyLeuArgGlyTrpPheAlaLeuAspLeuLeuAla	350
QY	940	GGCTGCTCTTTCAGCTCTACCTCTCAAGGTCAAGTCTACTTCGGG-----	990
DB	351	AlaLeuProPheAsp-----HisLeuTyAlaSerAspLeuTyAspGlyGluAspSer	368
QY	991	---GCCCATCTCTCAAGACGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1047
DB	369	HisIleHisLeuValLysLeuThrArgLeuLeuArgLeuAlaArgLeuGlnLysIle	388
QY	1048	GACCGTACTTCAGCTACAGCCCGTGTGTGTGACACTGCTCATGGCCGTGTTCGCCCTG	1107
DB	389	AspArgTySerGlnHisThrAlaMetIleLeuThrLeuLeuMetPheSerPheThrLeu	408
QY	1108	CTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1167
DB	409	AlaAlaHisTrpLeuAlaCysIleTrpTyValIleAlaValLysGluTyGlu-----	426
QY	1168	GAATCCGAGCTCCCTGAG-----ATTGGCTGGCTGACGAGCTGGCCCGCCAGTGGAG	1221
DB	427	-----TrpPheProGluSerAsnIleGlyTrpLeuGlnLeuLeuAlaGluArg-----	442
QY	1222	ACTCCCTACTACTGCTGGTGGCGGAGCCAGCTGGAGGAAACAGCTCCGCGCCAGATGAC	1281
DB	442	-----	442
QY	1282	AACTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	1341
DB	443	-----LysAsnAlaSerValAlaIleLeuThrThrAlaGlu-----	454
QY	1342	CTGCGCAGCGCTTACATCACCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1401
DB	455	-----ThrTySerThrAlaLeuTyPheThrPheThrSerLeuThrSerValGly	471
QY	1402	TTGCGCAACGTCTCCCAACACGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	1461
DB	472	PheGlyAsnValSerAlaAsnThrThrAlaGluLysValPheThrIleIleMetLeu	491
QY	1462	ATCGCGCCCTGTATGACCGGT	1521
DB	492	IleGlyAlaLeuMetHisAlaValPheGlyAsnValThrAlaIleIleGlnArgMet	511
QY	1522	TAGCCCGCGCTTCTGTACACACGCGCACCGCGCACCTGCGCGACTACATCCGCGATC	1581
DB	512	TyrSerArgSerLeuTyGluSerLysTrpArgAspLeuLysAspPheValAlaLeu	531
QY	1582	CACCGTATCCCCAAGCCCTCAAGCGGCGATGCTGGAGTACTTCCAGGCCACTGGCGG	1641
DB	532	HisAsnMetProLysGluLeuLysGlnArgIleGluAspTyPheGlnThrSerTrpSer	551
QY	1642	GTCAACAATGGCATCCAGCACCCAGCGAGCTCTCAGAGCCTCTCCAGAGCTGCGCGCA	1701
DB	552	LeuSerHisGlyIleAspIleTyGluThrLeuArgGluPheProGluGluLeuArgGly	571
QY	1702	GACATGCCCATCCCTGACAAAGAGGTCTCTGACAGCTGCGACTGTTTGTAGGCGGCGCAGC	1761
DB	572	AspValSerMetHisLeuHisArgGluIleLeuGlnLeuProIlePheGluAlaAlaSer	591
QY	1762	CGCGCTGCTGCGGGGACTGTCTGTGGCCCTCGGGCCCGCTTCTGCACGCGCGGCGAG	1821
DB	592	GlnGlyCysLeuLysLeuLeuSerLeuHisIleLysThrAsnPheCysAlaProGlyGlu	611
QY	1822	TACTCATCCCAAGCGGATGCCCTGACGCGCTCTACTTGTCTCTCTGCTGCTGCTGCTGCTG	1881
DB	612	TyrLeuIleHisLysGlyAspAlaLeuAsnTyIleTyTrpLeuCysAsnGlySerMet	631
QY	1882	GAGTGTCTCAAGGTGGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1941
DB	632	GluValIleLysAspMetValValAlaIleLeuGlyLysGlyAspLeuValGlySer	651

Qy	1942	GAGCTG	-----	1947
Db	652	Asp:::G		
Qy	1948	CCCGCGGGAGCAGGTGGTAAAGGCCAATCCGACGTGAAGGGCGCTGACGTACTCGGTC	2007	
Db	672	AlaGlyGlnAspValValArgSerSerAspIleIysAlaLeuThrTyrCysAsp	691	
Qy	2008	CTGAGTCTCTGCAGCTGGCTGCACACAGCTTCGCGCTGATACCCGAGTTTGC	2067	
Db	692	LeuIysCysIleHisMetGlyIleuValGluValLeuArgLeuIleProGluTyrGln	711	
Qy	2068	CCGCGTTCTAGTCTGGCTCCGAGGGAGCTCAGCTACAACCTGGGTGGTGGGGAGGC	2127	
Db	712	GlnGlnPheAlaAsnAspIleGlnHisAspLeuThrCysAsnLeuArgGluGlyTyrGlu	731	
Qy	2128	TCTGCAGGTGGACACGAGC-----	2169	
Db	732	AsnGlnAspSerAspIleGlyProSerPheProLeuProSerIleSerGluAspAspGlu	751	
Qy	2170	CTTATGTCCACGCTGGAG-----	2214	
Db	752	AsnArgGluGluAlaGluGluGlyGlyIysGlyGluIysGluAsnGlyGly-----	769	
Qy	2215	CCC-----	2250	
Db	770	ProProSerGlyAlaSerProLeuHisAsnIleSerAsnSerProLeuHisAlaThrArg	789	
Qy	2251	AGCCCCCTGTCTCCCTGGCTGCACCTCTCATCTCTCAGTCCAGCTGCTATCCCCA	2310	
Db	790	SerProLeuLeuGlyMetGly-----	798	
Qy	2311	CGTCGAACAGCACCCCGCTCTGCTTAGTGGCAGAGGGAGCGGCAGGCAGGGCAGGGGCT	2370	
Db	799	Arg-----	807	
Qy	2371	TTGAAGCTGAGGCTGGCCCTCTGCTCCCCACGGGCCCTAGAGGGCTACGGCTGCC	2430	
Db	808	-----	814	
Qy	2431	CCCATGCCATGGATGTGCCCCGAGATCTGAGCCCCAGGTAGTAGATGATGAGAC	2490	
Db	815	-----	825	
Qy	2491	GGCTGTGGCTCGGACCAAGCTCTCTTCGCGTGGCCAGTCTGCCCGGATGT	2550	
Db	826	AlaCysSerLeuAspArgGlySerPhe-----	834	
Qy	2551	AGCAGAGCCCTCCCTCGACACAGAGCGGCTGCTCACTGTCCCCATGGGCCAGC	2610	
Db	835	---GluGluProGluProLeuGluGlu-----	845	
Qy	2611	GAGCGAAGNACACACACACTGGACAGCTTCGGCAGCGGTGACAGAGTGTACAG	2670	
Db	846	SerGlyGlyIysArgProSerLeuGluArgLeuAspSerGlnValSerThrLeuHisGln	865	
Qy	2671	CAGTGTCTGAGTACGGGAAGGACTTCGAGTCACTTCGCCAGGCTGTGCAGTGTCTCTG	2730	
Db	866	AspValAlaGlnLeuSerAlaGluValArgAsnAlaIleSerAlaLeuGluMet---	884	
Qy	2731	GGCCCCACAGGAGGGTCCGTGCCCTCGGGCATCGGAGAGGGGCGGTGCCAGCCAGC	2790	
Db	885	-----	886	
Qy	2791	ACCTCGGGCTTCGACGCTCTGTGTGGACACTGGGGGCATCTCTCTACTGCTGCAG	2850	
Db	887	ThrSerAsnAlaMet-----	899	
Qy	2851	CCCCAGCTGGCTCTCTC-----	2904	
Db	900	ProProAlaArgSerIleProAsnIleSerGly--ValAlaGlyThrArgSerGlyVala	919	

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QY 2905 CTCCCTCATGGCACCGTGCCTGGGTCCTCCACAGCGTCTCAGAGCTCCCTCCGTGCCCT 2964
Db   :      |||||  ::      |||  ::      |||  ::      |||||  ::
919 lavalGluHisGlyLeuMetGly----GlyValLeuAlaAlaGluLeu--AlaAlaMe 937
QY 2965 CGAGCCACAGCTTTCTGGACTCCACCT-----CAGACTCAGAGCCCCCTGCC 3012
Db   :      ::::  |||  |||||  |||  |||  |||  |||  |||  |||  |||
937 tGlnArgSerSerHisProGluValTrpGlyArgAspValGlnLeuProThrSe 957
QY 3013 TCAGGACACTCTGCTGTGAGCCCGACGACCCTGCGCTCCC 3052
Db   :      ||:::  ::||:::  ||:::  |||  |||  |||  |||  |||
957 rAsnThrAlaSerSerLysAlaProSerProValGluPro 970

RESULT 10
US-10-160-224-9
; Sequence 9, Application US/10160224
; Publication No. US2003007731A1
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy J.
; APPLICANT: Wickenden, Alan
; APPLICANT: ICAGEN, Incorporated
; TITLE OF INVENTION: Human Elk, a Voltage-Gated Potassium Channel Subunit
; FILE REFERENCE: 018512-001320US
; CURRENT APPLICATION NUMBER: US/10/160,224
; CURRENT FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: US/09/343,494
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 1284
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Drosophila Elk (dElk), Bag (ether a go-go)-like K+
; OTHER INFORMATION: gene protein
US-10-160-224-9

Alignment Scores:
Pred. No.:          7,28e-90           Length:       1284
Score:             1901.00            Matches:        455
Percent Similarity: 53.85%            Conservative:    146
Best Local Similarity: 40.77%         Mismatches:     273
Query Match:       31.22%              Indels:         242
DB:                14                 Gaps:           31

US-09-965-830-1_COPY_6_3257 (1-3252) x US-10-160-224-9 (1-1284)
QY 1 ATCCGGCATGGCGGGGCTCTGGCGCTCAGAACACCTTCTCTGGACACCATCGCTACG 60
Db   :      ::      ::      ::      ::      ::      ::      ::      ::
1 MetProAlaArgLysGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20
QY 61 CGCTTCAGCGGACGACGACAGTAGTAATTCGTGCTGGGCAAGCCCGAGTGCGGGCTCTTC 120
Db   :      ::      ::      ::      ::      ::      ::      ::      ::
21 ArgPheaspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnAlaAsnGly--Asn 39
QY 121 CCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCAGGGCTTCTCCGGGCTCGAGTC 180
Db   :      ::      ::      ::      ::      ::      ::      ::      ::
40 ProIleValTy-CysSerAspGlyPheValAspLeuThrGlyTySerArgAlaGlnIle 59
QY 181 ATGCACGGGGCTGTGCTGCTCTTCCTTTATGGGCGACAGCACCGAGTGAGTCTCGCGC 240
Db   :      ::      ::      ::      ::      ::      ::      ::      ::
60 MetGlnLysGlyCysSerCysHisPheLeuTyGlyProAspThrLysGluGluHisLys 79
QY 241 CAACAGATCCGAAGCGCTCGACGACGACAGGAGTTCAAGGCTGAGCTGATCTGTAC 300
Db   :      ::      ::      ::      ::      ::      ::      ::      ::
80 GlnGlnIleGluLysSerLysSerAsnLysMetGluLeuLysLeuGluValIlePheTy 99
QY 301 CGGAAGAGCGGGCTCCCGTCTCTGGTGCTCTCTGGATGTGATACCATAAAGAATGAGAAA 360
Db   :      ::      ::      ::      ::      ::      ::      ::      ::
100 LysLysGluGlyAlaProPheTrpCysLeuPheAspIleValProIleLysAsnGluLys 119
QY 361 GGGGAGTGGCTCTCTTCTAGTCTCTCACAGGACATCAGCAAACAAG----- 411
Db   :      ::      ::      ::      ::      ::      ::      ::      ::

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120 ArgAspValValLeuPheLeuAlaSerHisLysAspIleThrHisThrLysMetLeuGlu 139
411 ----- 411
140 MetAsnValAsnGluGluCysAspSerValPheAlaLeuThrAlaAlaLeuLeuGlyAla 159
412 -----AACCAGGG 420
160 ArgPheArgAlaGlySerAsnAlaGlyMetLeuGlyLeuGlyGlyLeuProGlyLeuGly 179
421 GGCCCC-----GACAGATGGAAGGACACAGAGTGGTGGCGGCGCGATATGCGCGG 471
180 GlyProAlaAlaSerAspGlyAspThrGluAlaGlyGluGlyAsnAsnLeuAspValPro 199
472 GCAGATCCAAAGCTTCAATGCCAACCGCGCGGAGCGCGCGCTGCTTACCACCTG 531
200 Ala-----GlyCysAsnMetGlyArgArgSerArgAlaValLeuTyrGlnLeu 216
532 TCCGGGCACCTGCAGAAAGCAGCCCAAGGCG--AAGCACAAGCTCAATAAGGG----- 582
217 SerGlyHisTyrLysProGluLysGlyValLysThrLysLeuLysLeuGlyAsnAsn 236
583 ---GTGTTTGGGAGAAACAACTTCCTGAGTACAAAGTAGCCGCCATCCGGAAAGTCG 639
237 PheMetHisSerThrGluAlaProPheProGluTyrLysThrGlnSerIleLysLysSer 256
640 CCTTTCATCTGTTGCACTGTGGGCACTGAGAGCCACCTGGGATGCTTCATCTGCTC 699
257 ArgLeuIleLeuProHisTyrGlyValPheLysGlyIleTrpAspTrpValIleLeuVal 276
700 GCCACACTCTATGTGGGTGTCACTGTGCCCTCAGCGTGTGTGAGCAGCAGCAGGGAG 759
277 AlaThrPheTyrValAlaLeuMetValProTyrAsnAlaAlaPheAlaLysAlaAspArg 296
760 CCCAGTGGCCCGGGCCGCCACCGTGTGTGACCTGCGCGTGGAGGTCTCTTCATC 819
297 GlnThr-----LysValSerAspValIleValGluAlaLeuPheIle 310
820 CTTGACATTGTGCTGAATTTCCGTACCACACTCTGTGCCAAGTCGGCGAGGTGGTGT 879
311 ValAspIleLeuLeuAsnPheArgThrThrPheValSerArgLysGlyGluValSer 330
880 GCCCAAAGTCCATTGCTCCACTAGCTACCACTGCTGGTCTCTGTGTGATCATCGCA 939
331 AsnSerLysGlnIleAlaIleAsnTyrLeuArgGlyTyrPheAlaLeuAspLeuLeuAla 350
940 GCGCTGCGCTTGTACCTGCTACATGCTCCATCAAGCTCAAGTCAAGTACTTCGG-- 990
351 AlaLeuProPheAsp-----HisLeuTyrLysAlaSerAspLeuTyrAspGlyGluAspSer 368
991 ---GCCCATCTGCTGAAGACCGTGCCTGTGCGCTGTGCGCTGTGCGCTGTTCGCGCGCTG 1047
369 HisIleHisLeuValLysLeuThrArgLeuLeuArgLeuAlaArgLeuLeuGlnLysIle 388
1048 GACCGTACTCGACTAGCGCGCTGTGTGCTGACCTGTCTGCTGCGCGCTGTTCGCGCTG 1107
389 AspArgTyrSerGlnHisThrAlaMetIleLeuThrLeuLeuMetPheSerPheThrLeu 408
1108 CTCGGCACTGGTGCCTGCGCTGTGTTTACATTGGCCAGCGGAGATCGAGAGCAGC 1167
409 AlaAlaHisTrpLeuAlaCysIleTrpTyrValIleAlaValLysGluTyrGlu----- 426
1168 GAATCCGAGTCCCTAG-----ATTGGCTGGCTGCGAGAGCTGCGCGCGCTGAG 1221
427 -----TrpPheProGluSerAsnIleGlyTrpLeuGlnLeuLeuAlaGluArg----- 442
1222 ACTCCCTACTACTGTGTGGCGGAGGCCAGCTGTGGAGGAACAGCTCCGCGCCAGAGTGAC 1281
442 ----- 442
1282 AACTGACGACGACGACGAGGCCAACGGAGCGGGCTGTGAGCTGTGCGGCGCGCTGCG 1341
443 -----LysAsnAlaSerValAlaIleLeuThrThrAlaGlu----- 454

QY	1342	CTGGCAGCGCCTACATCACTCCCTCTACTTCGCACCTCAGCAGCCTCACCACGCGTGGGC	1401
DB	455	-----ThrTyrSerThrAlaLeuTyrPheThrPheThrSerLeuThrSerValGly	471
QY	1402	TTGGCAACCGTGTCCGCCAACACGACGACCGAGAGATCTTCTCCATCTGACCATGTCTC	1461
DB	472	PheGlyAsnValSerAlaAsnThrThrAlaGluLysValPheThrIleIleMetMetLeu	491
QY	1462	ATCGCGCCCTGATGACGCGCGTGTGTGGAAACGTGACCGCCCATCATCCAGCGCATG	1521
DB	492	IleGlyAlaLeuMetHisAlaValPheGlyAsnValThrAlaIleIleGlnArgMet	511
QY	1522	TACGCCCGCGCTTCTGTACCAACGACGCGACGCGACCTGCGCACTACATCCGCATC	1581
DB	512	TyrSerArgArgSerLeuTyrGluSerLysTrpArgAspLeuLysAspPheValAlaLeu	531
QY	1582	CACCGTATCCCCAAGCCCTCAAGACGCGCATCTCGGAGTACTTCCAGGCCCATCTGGCG	1641
DB	532	HisAsnMetProLysGluLeuLysGlnArgIleGluAspTyrPheGlnThrSerTrpSer	551
QY	1642	GTGAACAATGGCATCGACACCAACGCGACTCTCCAGACGCTCCCTCAGCAGCTGCGCGCA	1701
DB	552	LeuSerHisGlyIleAspIleTyrGluThrLeuArgGluPheProGluGluLeuArgGly	571
QY	1702	GACATCGCCATGACCTGCACAGGAGGTCTCTGACGTGCACTGTGTGAGCGCGGCAGC	1761
DB	572	AspValSerMetHisLeuHisArgGluIleLeuGlnLeuProIlePheGluAlaAspSer	591
QY	1762	CGCGCTGCTCGCGGCACCTGTCTCTGCGCCCTGCGGCCCGCTCTGACGCGCGGCGAG	1821
DB	592	GlnGlyCysLeuLysLeuLeuSerLeuHisIleLysThrAsnPheCysAlaProGlyGlu	611
QY	1822	TACCTCATGCACAAAGCGATGCCCTCGACGCCCTCTACTTGTCTGCTCTGCTCCATG	1881
DB	612	TyrLeuIleHisLysGlyAspAlaLeuAsnTyrIleTyrTyrLeuCysAsnGlySerMet	631
QY	1882	GAGTGTCTCAAGGTGGCACCGTCTCGCCATCTTAGGGAAGGCGACCTGATCGGCTGT	1941
DB	632	GluValIleLysAspAspMetValValAlaIleLeuGlyLysGlyAspLeuValGlySer	651
QY	1942	GAGCTG-----	1947
DB	652	AspIleAsnValHisLeuValAlaThrSerAsnGlyGlnMetThrAlaThrThrAsnSer	671
QY	1948	CCCCGGCGGACGAGTGTGTAAAGCCCAATGCCACGTGAAGGGCTGACGTACTGCGTC	2007
DB	672	AlaGlyGlnAspValValValArgSerSerAspIleLysAlaLeuThrTyrCysAsp	691
QY	2008	CTGCAGTCTCTGCAGCTGGCTGGCTGCACACACGCTTGGCTGTGATCCCGAGTTTGCC	2067
DB	692	LeuLysCysIleHisMetGlyGlyLeuValGluValLeuArgLeuTyrProGluTyrGln	711
QY	2068	CGCGCTTCTCAGTCTGGCTCCGAGGGAGCTCAGCTACACCTGGGTGCTGGGGAGGC	2127
DB	712	GlnGlnPheAlaAsnAspIleGlnHisAspLeuThrCysAsnLeuArgGluGlyTyrGlu	731
QY	2128	TCTGCAGAGGTGGACACACG-----	2169
DB	732	AsnGlnAspSerAspIleGlyProSerPheProLeuProSerIleSerGluAspAspGlu	751
QY	2170	CTTATGTCACGCTGGAG-----	2214
DB	752	AsnArgGluGluAlaGluGluGlyClyLysGlyGluLysGluAsnGlyGly-----Gly	769
QY	2215	CCC-----	2250
DB	770	ProProSerGlyAlaSerProLeuHisAsnIleSerAsnSerProLeuHisAlaThrArg	789
QY	2251	AGCCCTCTGCTGCTCCCTGGCTGACCTCTCTCATCTCTCAGCTGCCAAGCTGCTATCCCCA	2310
DB	790	SerProLeuGluGlyMetGly-----	798


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QY 2851 CCCCAGCTGGCTCTGTC-----TTGAGGGAGCTTGGCCCAACCTCTGTCGGGGCCT 2904
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900 ProProAlaArgSerIleProAsnIleSerGly--ValAlaGlyThrArgSerGlyVala 919
QY 2905 CTTCCTCCTCATGGCACCTGGCCCTGGGTCCTCCAGCGTCTCAGAGTCCCTCGCCT 2964
Db :: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
919 lavalGluHisGlyLeuMetGly--GlyValLeuAlaAlaGluLeu--AlaAlaMe 937
QY 2965 CGAGCCACAGCTTTCGACCTCCACCT-----CAGACTCAGAGCCCTCGCC 3012
Db ::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
937 tclnArgSerSerHisProGluValTrpGlyArgAspValGlnLeuProThrSe 957
QY 3013 TCAGGAGACCTTGCTCTGAGCCAGCACCTCGCTGCC 3052
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
957 rAsnThrAlaSerSerLysAlaProSerProValGluPro 970

RESULT 12
US-09-119-855-5
; Sequence 5, Application US/09119855
; Patent No. US20020099197A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: mnl-055
; CURRENT APPLICATION NUMBER: US/09/119,855
; CURRENT FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 542
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-119-855-5

Alignment Scores:
Pred. No.: 1,59e-86 Length: 542
Score: 1835.50 Matches: 352
Percent Similarity: 77.64% Conservatives: 82
Best Local Similarity: 62.97% Mismatches: 92
Query Match: 30.14% Indels: 33
DB: 9 Gaps: 5

US-09-965-830-1_COPY_6_3257 (1-3252) x US-09-119-855-5 (1-542)

QY 1 ATGCGCGCATGGGGGCTCTGCGCCCTCAGAACCTTCTCTGGACACCATCGCTACG 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 MetProValMetLysGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20

QY 61 CGTTTCAGCGCACGACAGTAACCTTCTGCTGGGCAACGCCAGGTGGCGGGCTCTTC 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
21 ArgPheAspGlyThrHisSerAsnPheIleLeuAlaAsnAlaGlnValAlaLysGlyPhe 40

QY 121 CCGTGTCTACTGCTCTGATGCTTCTGAGCTCAGCGGCTTCTCCCGGGCTGAGTTC 180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
41 ProIleValTyrCysSerAspGlyPheCysGluLeuAlaGlyPheAlaArgThrGluVal 60

QY 181 ATGACGCGGGCTGCTGCTCTCTTATGGGCGACACCAAGTAGCTGCTCGCGC 240
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY 241 CAACAGATCCGAGCGCTGAGCAGACACAGGATTCAGGCTCAGCTGATTCCTGTAC 300
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81 LeuGlnIleGluLysSerLeuGluLysThrGluPheLysGlyIleMetPheTyr 100

QY 301 CGAAGAGCGGGCTCCGCTTCTGCTCTCTGATGTGATACCAAGTACCAAGATGAGAAA 360
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101 LysLysAsnGlySerProPheTrpCysLeuLeuAspIleValProIleLysAsnGluLys 120

QY 361 GGGAGGTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
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121 GlyAspValValLeuPheLeuAlaSerPheLysAspIleThrAspThrLysValIle 140

QY 421 GSCCCCGACAGATGAGAGACAGGTGGTGGCGCGCGGATATGGCGCGGACGATCC 480
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Db 141 ThrProGluAspLysLysGluAsp-----LysValLysGlyArgSerArgAla 156
QY 481 ---AAAGGCTTCAATCCCAACCGCGCGGAGCGCGCGCTGCTCTACACCTGTCCGG 537
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157 GlyThrHisPheAspSerAlaArgArgSerArgAlaValLeuTyrHisIleSerGly 176
QY 538 CACCTGCGAAGACGAGCCCAAGGCAAGCAAGCTCAATAAGGGGCTGTTGGGGAGAA 597
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177 HisLeuGlnArgArgGluLysAsnLysLysIleAsnAsnValPheValAspLys 196
QY 598 CCAAACTTGCCCTGAGTACAAAGTAGCCGCATCCGGAAGTCGCCCTTCATCCTGTCAC 657
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197 ProAlaPheProGluTyrLysValSerAspAlaLysLysSerLysPheIleLeuLeuHis 216
QY 658 TGTGGGCACTGAGAGCCACCTGGGATGCTTCATCTGCTGCCACACTCTATGCGGT 717
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QY 718 GTCACTGTGCCCTACAGCGTGTGTGAGCACAGCACGGAGCCAGTCCGCCCGCGGC 777
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257 ---ThrThrValSerAspIleAlaValGluIleLeuPheIleAspIleIleLeuAsn 275
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276 PheArgThrThrTyrValSerLysGlyGlnValIlePheGluAlaArgSerIleCys 295
QY 898 CTCACATAGTCACACCTGCTCTGCTGATGTCATCGCAGCGCTGCCCTTTGACCTG 957
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296 IleHisTyrValThrThrTrpPheIleIleAspLeuIleAlaLeuProPheAspLeu 315
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376 ValIleGlyLysMetGluArgGluAsnSerLeuLeuLysTrpGluValGlyTyrLeu 395
QY 1198 CAGGAGCTGCCCGCGCTGAGACTCCCTACTACTGCTGGCGCGGAGCGGAGCTGGA 1257
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QY 1258 GGGAAACAGCTCCGCGCAGTAGTACAATCGACGAGCAGCAGGAGCGCAACGGGAG 1317
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1084 CTGCTCATGGCCGTGTTCGCCCTGCTCGCGCACTGGCTGCCTCGCTGTGTTTCAATT 1143

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589 LeuGlyAspGlnIleGlyLysProTyr-----Asn 598

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Qy	2143	ACCAGCTCCCTGAGCGGCGACAATACCCCTTATGTCACGCTGAGAGAGAGACAGAT	2202
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Qy	2203	GGGAGACAGGGCCCAAGTCTCCACGCCCGAGCTGATGAGCCCTCCAGCCCGCTG	2262
Db	899	ThrGluGln-----	901
Qy	2263	TCCCTGGCTGCACCTCTCACTCTCAGCTGCTGCAAGCTGATATCCCAAGTCCGAC	2322
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Qy	2323	CCCCGGCTCTAGTGGCAGAGGAGCGCAGGAGGGCGGCTTTGAAGGCTGAG	2382
Db	915	AlaGlyPro-----SerSerArgGlyArgProGlyGlyProThrProGlyGluSerProSer	932
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Qy	2419	CTACGGCTG-----CCGCCCATGCCATGATGTGCCCGCCAGATCTGAGCCCC	2466
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Qy	2515	-----TTCTCTTTC-----CGCTGGCGCAGTCT	2538
Db	992	SerGlyValSerAsnIlePheSerPheTrpGlyAspSerArgGlyArgGlnTrpGlnGlu	1011
Qy	2539	GGCCCGAATGTAGCAGACGCCCTCCCTCGACACGAGCGCGCTGCTCACTGTT---	2595
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Db	1111	-ValSerGlnPheMetAlaCysGluGluLeuProGly---AlaProGluLeuProGln	1129
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QY 3043 CCTG 3046
Db 1149 oLeu 1150

RESULT 15
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; Sequence 4, Application US/09735995
; Patent No. US2001003402A1
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: MUTATIONS IN AND GENOMIC STRUCTURE OF HERG - A LONG QT
; TITLE OF INVENTION: SYNDROME GENE
; FILE REFERENCE: 2323-136
; CURRENT APPLICATION NUMBER: US/09/735,995
; CURRENT FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 09/226,012
; PRIOR FILING DATE: 1999-01-06
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1159
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-735-995-4

Alignment Scores:
Pred. No.: 7,61e-72 Length: 1159
Score: 1551.00 Matches: 424
Percent Similarity: 44.86% Conservative: 143
Best Local Similarity: 33.54% Mismatches: 337
Query Match: 25.47% Indels: 360
DB: 9 Gaps: 38

US-09-965-830-1_COPY_6_3257 (1-3252) x US-09-735-995-4 (1-1159)

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Db 21 LysPheGluGlyGlnSerArgLysPheIleAlaAsnAlaArgValGluAsnCys--- 39
QY 121 CCCGTGCTACTGCTCTGTGCTTCTGTGACCTCAGGCTTCTCCGGCTGAGGTC 180
Db 40 AlaValIleTyrCysAsnAspGlyPheCysGluLeuCysGlyIleAlaPheTyr 59
QY 181 ATCCAGCGGGCTGTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
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QY 241 CAACAGATCCGACGCGCTGAGCAGCACAAGAGTTCAGGCTGAGCTGATCCTGAC 300
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QY 301 CGGAAGAGCGGGCTCCCGTCTCTGCTGCTCTCTGATGATACCCATAAAGATGAAA 360
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QY 361 GGGGAGTGTGCTCTCTCTCTA-----GTCTCTCACAGGACATC----- 399
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QY 400 -----AGCGAAACCAAGACCGAGGGGGCCCGACAGATGG----- 435
Db 140 SerProAlaHisAspThrAsnHisArgGlyProProThrSerTrpLeuAlaProGlyArg 159
QY 435 ----- 435
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572	GlyAsnMetGluGlnProHisMetAspSer-----ArgIleGlyTrpLeuHisAsn	588
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589	LeuGlyAspGlnIleGlyLysProTyr-----Asn	598
1264	AGTCCCGCCAGAGTGTCAACTGCAGCAGCAGCAGCAGGAGCCAAACCGGAGCGGGCTGGAG	1323
599	SerSergly-----	601
1324	CTGCTGGCGCGCGCTGCTGCGCAGCGCTACATCATCCCTCTACTCTTCGCACATCAGC	1383
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741	LysProPheArgGlyAlaThrLysGlyCysLeuArgAlaLeuAlaMetLysPheLysThr	760
1801	GCCTTCTGCACGCCCGCGGAGTACCTCATCCACCAAGCGCATGCCCTGCAGGCCCTCTAC	1860
761	ThrHisAlaProProGlyAspThrLeuValHisAlaGlyAspLeuLeuThrAlaLeuTyr	780
1861	TTTGTCTGCTCGGCTCATGAGGTGTCTCAAGGTGCACCGCTGCTCGCCATCTCTAGG	1920
781	PheIleSerArgGlySerIleGluIleLeuArgGlyAspValValAlaIleLeuGly	800
1921	AAGGGCGACCTCATCGGCTGTGAGCTGCGCGCGGAGCAGGTGTAAAGCCCAATGCC	1980
801	LysAsnAspIlePheGlyGluProLeuAsnLeuTyrAlaArgProGlyLysSerAsnGly	820
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841	ValLeuAspMetTyrProGluPheSerAspHisPheTrpSerSerLeu-----GluIle	858
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Thu Sep 2 12:18:20 2004

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Page 27

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GenCore version 5.1.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 1, 2004, 15:37:55 ; Search time 61 Seconds

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Searched: 389414 seqs, 51625971 residues

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-DB=Issued Patents AA -QMT=fastan -SUFFIX=ra1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents AA:*
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6: /cgn2_6/ptodata/2/iaa/backfiles.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5704	93.7	1083	4	US-09-600-776-2
2	5698	93.6	1083	4	US-09-343-494-1
3	5675	93.2	1083	4	US-09-358-383C-2
4	5649.5	92.8	1082	4	US-09-336-643A-20
5	5229.5	41.5	1107	4	US-09-358-383C-16
6	2515	41.3	1102	4	US-09-358-383C-36
7	2461.5	40.4	1017	4	US-09-600-776-6
8	1901	31.2	1284	4	US-09-343-494-9
9	1901	31.2	1284	4	US-09-358-383C-11
10	1835.5	30.1	542	4	US-09-358-383C-5
11	1551	25.5	1159	2	US-08-956-242-13
12	1551	25.5	1159	3	US-09-351-215-13

13	1551	25.5	1159	3	US-09-226-012-2	Sequence 2, Appli
14	1551	25.5	1159	3	US-09-226-012-4	Sequence 4, Appli
15	1551	25.5	1159	4	US-09-358-383C-10	Sequence 10, Appl
16	1551	25.5	1159	4	US-09-275-252A-12	Sequence 12, Appl
17	1487	24.4	290	4	US-09-358-383C-8	Sequence 8, Appli
18	1378.5	22.6	962	4	US-09-694-777A-24	Sequence 24, Appl
19	1378	22.6	960	4	US-09-694-777A-21	Sequence 21, Appl
20	1370.5	22.5	989	4	US-09-694-777A-23	Sequence 23, Appl
21	1370	22.5	962	4	US-09-614-480-9	Sequence 9, Appli
22	1369	22.5	962	4	US-09-694-777A-3	Sequence 3, Appli
23	1367.5	22.5	987	4	US-09-694-777A-22	Sequence 22, Appl
24	1358.5	22.3	989	4	US-09-694-777A-4	Sequence 4, Appli
25	1339.5	22.0	988	4	US-10-162-012-12	Sequence 12, Appl
26	1332.5	21.9	988	4	US-09-614-480-2	Sequence 2, Appli
27	1332.5	21.9	988	4	US-10-162-012-5	Sequence 5, Appli
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33	693.5	11.4	181	4	US-09-358-383C-26	Sequence 26, Appl
34	594.5	9.8	180	4	US-09-358-383C-24	Sequence 24, Appl
35	495	8.1	910	4	US-08-997-685A-2	Sequence 2, Appli
36	454.5	7.5	749	4	US-08-997-685A-10	Sequence 10, Appl
37	422	6.9	319	4	US-09-358-383C-22	Sequence 22, Appl
38	421	6.9	528	4	US-08-997-685A-4	Sequence 4, Appli
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40	411.5	6.8	597	4	US-08-997-685A-12	Sequence 12, Appl
C 41	410	6.8	960	3	US-09-219-849-5	Sequence 5, Appli
C 42	409	6.8	1065	1	US-08-642-255-72	Sequence 72, Appl
43	407	6.7	690	4	US-08-275-252A-19	Sequence 19, Appl
44	405	6.7	506	4	US-08-997-685A-6	Sequence 6, Appli
C 45	403.5	6.7	1065	1	US-08-642-255-80	Sequence 80, Appl

ALIGNMENTS

RESULT 1

US-09-600-776-2
; Sequence 2, Application US/09600776
; Patent No. 6326168
; GENERAL INFORMATION:
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: A novel potassium channel protein
; FILE REFERENCE: Y9903-PCT
; CURRENT APPLICATION NUMBER: US/09/600,776
; CURRENT FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: JP P1998-011434
; PRIOR FILING DATE: 1998-01-23
; PRIOR APPLICATION NUMBER: JP P1998-346198
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1083
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-600-776-2

Alignment Scores:

Pred. No.: 0
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Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 93.68%
DB: 4
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Matches: 1083
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

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QY	121	CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCGGGCTGAGTTC	180	Db	401	GluLeuAlaAargArgLeuGluThrProTyrTyrLeuValGlyArgArgProAlaGlyGly	420
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QY	901	CACCTACCTCACCTGCTCTGCTGATGTCTATCGCAGCGCTGCGCTTTGACTGCTA	960	Db	661	AspValLysGlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGlyLeuHisAsp	680
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QY	961	CATGCCCTTCAAGGTCAACGTGATCTCGGGGCCCATCTGCTGGAAGAGCGTGGCTGCTG	1020	Db	681	SerLeuAlaLeuTyrProGluPheAlaProArgPheSerArgGlyLeuArgGlyGluLeu	700
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Db	361	ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr	380	QY	2221	GTCTCCCGCAGCCCGAGCTGATGACCTCTCCAGCCCTCTGTCTCCCTGGCTGACCTCC	2280
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QY	601	AACTTCCTGAGTACAAAGTAGCCGCCATCCGGAAGTGCCTTCCTCATCTCTGTCAGACTGT	660
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QY	661	GGGGCACTGAGACCCACTGGGATGGCTTCATCCCTGCTCGGCACACTCTATGTGGCTGTC	720
DB	221	GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal	240
QY	721	ACTGTGCCCTTACAGCGTGTGTGTGACACAGCACGGAGCCAGTGCCTCCGCGCGCCG	780
DB	241	ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro	260
QY	781	CCCAAGCTCTGTGACCTGGCGGTGGAGGTCTCTTCATCTCTTGACATGTGCTGAATTC	840
DB	261	ProSerValCysAspLeuAlaValGluValPheIleAspIleValLeuAsnPhe	280
QY	841	CGTACCACATTCGTGTCCAAGTCGGGCCAGGTGGTGTTCGCCAAAGTCCATTTGGCTC	900
DB	281	ArgThrThrPheValSerLysSerGlyGlnValPheAlaProLysSerIleCysLeu	300
QY	901	CACCTACGTCACACCTGGTTCCTGCTGGATGTTCATCGCAGCGTGCCTTTGACCTGCTA	960
DB	301	HisTyrValThrThrTrpPheLeuLeuAspValIleAlaAlaLeuProPheAspLeuLeu	320
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QY	1021	CGCTGTGCGCCTGCTTCGCGACTCGACCGGTACTCGCAGTACAGCCGGTGGTGTG	1080
DB	341	ArgLeuLeuArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValValLeu	360
QY	1081	ACACTGTCTATGGCGGTTCCTCGCCTGCTCGCGACTGGCTCGCTCGCTCGCTGGTTTAC	1140
DB	361	ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr	380
QY	1141	ATTGGCCACGCGAGATCGACAGACGGAATTCGAGCTGCTGAGATTGGCTGGCTGCAG	1200
DB	381	IleGlyGlnArgGluIleGluSerSerGluSerGluLeuProGluIleGlyTrpLeuGln	400
QY	1201	GAGCTGGCGCGCGACTGGAGACTCCCTACTACTGCTGGCGCGCGGAGCCAGCTGAGGG	1260
DB	401	GluLeuAlaArgArgLeuGluThrProTyrTyrLeuValGlyArgArgProAlaGlyGly	420
QY	1261	AACAGCTCCGCCACAGATGACAACCTGCAGCAGCAGCAGCGAGGCCAACCGGACGGGCTG	1320
DB	421	AsnSerSerGlyGlnSerAspAsnCysSerSerSerSerGluAlaAsnGlyThrGlyLeu	440
QY	1321	GAGCTGCTGGCGGCGCGCTGCTGCTGCGAGCGCTTACATCATCTCCCTCTACTTCGCNCTC	1380
DB	441	GluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeu	460
QY	1381	AGCAGCCTCACAGCGTGGGCTTCGGCAACGTGTCCGCCACACCGACACCGAGAGATC	1440
DB	461	SerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGluLysIle	480
QY	1441	TTCTCCATCTGCACCATGCTCATCCGGCGCCTGTATGCACGGGTGGTGTGGGAACGTG	1500
DB	481	PheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValPheGlyAsnVal	500
QY	1501	ACGGCCATCATCCAGCGCATGTACCGCCCGCGCTTCTGTACCAACAGCCGACCGCGGAC	1560
DB	501	ThrAlaIleIleGlnArgMetTyrAlaArgArgPheLeuTyrHisSerArgThrArgAsp	520
QY	1561	CTGGCGACTACATCCGATCCACGGTATCCCAAGCCCTCAGACGCGCATCTCGAG	1620
DB	521	LeuArgAspTyrIleArgIleHisArgIleProLysProLeuLysGlnArgMetLeuGlu	540
QY	1621	TACTTCCAGCGCACTTGGCGGTGAACATATGCATCGACCCACCGAGCTGCTCGAGGC	1680
DB	541	TyrPheGlnAlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeuLeuGlnSer	560

1681	QY	CTCCCTGCAGAGCTGCGCGCAGACATATCGCCATGCACTCTCCACAGAGAGTCTCTGCAGCTG	1740
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1741	QY	CCACTGTTTGGCGGCGCAGCGCGGCTCCCTGCGGCACTGCTCTGGCGCTTGGCGGCC	1800
581	Db	ProLeuPheGluAlaAlaSerArgGlyCysLeuA-galALeuSerLeuAlaLeuAArgPro	600
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601	Db	AlaPheCysThrProGlyGluTyrlleuIleHisGlnGlyAspAlaLeuGlnAlaLeuTyr	620
1861	QY	TTTGTCTGCTTGGCTCCATGAGGTGCTCAAGGGTGCCACCGTGTGCGCATCTTACGG	1920
621	Db	PheValCysSerGlySerMetGluValLeuLysGlyThrValLeuAlaIleLeuGly	640
1921	QY	AAGGCGACCTGATCGGCTGTGAGCTGCCCGCGGAGCAGGTGGTAAAGGCCAATGCC	1980
641	Db	LysGlyAspLeuIleGlyCysGluLeuProArgGluGlnValValLysAlaAsnAla	660
1981	QY	GACGTGAAGGGCTGACGTACTCGCTCTGCAGTGTCTGCAGCTGGCTGGCTGCACGAC	2040
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2041	QY	AGCCTTGCCTGTACCCCGAGTTTCCCGCGCTTCAGTCTGGCTCCGAGGGAGCTC	2100
681	Db	SerLeuAlaLeuTyrProGluPheAlaProArgPheSerArgGlyLeuArgGlyGluLeu	700
2101	QY	AGCTCAACCTGGTCTCGGGGAGGCTCTGCAGAGGTGCACACAGCTCCCTCAGGGGC	2160
701	Db	SerTyrAsnLeuGlyAlaGlyGlyGlySerAlaGluValAspThrSerSerLeuSerGly	720
2161	QY	GACAAATACCTTATGTCCACCTGGAGGAGAAGGAGACAGATGGGAGCGGCCACG	2220
721	Db	AspAsnThrLeuMetSerThrLeuGluGlyGluThrAspGlyGluGlnGlyProThr	740
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2281	QY	TCATCTCAGCTGCCAAGCTGCTATCCCAAGTTCGAACAGCACCCGCGCTCTGTAGT	2340
761	Db	SerSerSerAlaAlaLysLeuLeuSerProArgArgThrAlaProArgProArgLeuGly	780
2341	QY	GGCAGAGGAGGCGCAGCGAGGAGGGCTTTGAAGGCTGAGGCTGGCGCTCTCTCTCC	2400
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821	Db	SerProArgValValAspGlyIleGluAspGlyCysGlySerAspGlnProLysPheSer	840
2521	QY	TTCCGCTGGCGCCAGTCTGGCCCGAATGTAGCAGCAGCGCTCCCTCCCTGGACAGAGAGC	2580
841	Db	PheArgValGlyGlnSerGlyProGluCysSerSerProSerProGlyProGluSer	860
2581	QY	GGCTGTCTCACTGTTCCCATGGGCGCCAGCGAGGCAAGAAACACACACTGGACAAAG	2640
861	Db	GlyLeuLeuThrValProHisGlyProSerGluAlaA-gAsnThrAspThrLeuAspLys	880
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881	Db	LeuArgGlnAlaValThrGluLeuSerGluGlnValLeuGlnMetArgGluGlyLeuGln	900
2701	QY	TCATCTCGCAGGCTGTGACGCTGTACAGCAGGTGTCTGCAGATCGGGAAGGACTCGG	2760
901	Db	SerLeuArgGlnAlaValGlnLeuValLeuAlaProHisArgGluGlyProCysProArg	920
2761	QY	GCATCGGAGAGGGGCGCTGTCGCCACGACCACTCGGCGCTTCTGACGCGCTGTGTG	2820

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QY 2821 GACACTGGGGATCTCTACTGCTGAGCCAGCCAGCTGCTGCTTGGTGGGACT 2880
Db 941 AspThrGlyAlaSerSerTyrCysLeuGlnProProAlaGlySerValLeuSerGlyThr 960
QY 2881 TGGCCCCACCCCTGCTCCGGGGCTCTCTCCCTCATGGCACCTGCGCCCTGGGGTCCCCCA 2940
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Db 1041 ThrGlyGluProProProGlySerGlyGlyLeuAlaLeuProTrpAspProHisSerLeu 1060
QY 3181 GAGATGCTGCTTATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3240
Db 1061 GluMetValLeuLeuLeuGlyCysHisGlySerGlyThrValGlnTrpThrGlnGluGly 1080
QY 3241 ACAGGGGTC 3249
Db 1081 ThrGlyVal 1083

RESULT 3

US-09-358-383C-2
; Sequence 2, Application US/09358383C
; Patent No. 6518398
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A. J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-055CP
; CURRENT APPLICATION NUMBER: US/09/358,383C
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: USSN 09/119,855
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1083
; TYPE: PRT
; ORGANISM: Macaca sp.
US-09-358-383C-2

Alignment Scores:

Pred. No.: 0 Length: 1083
Score: 5675.00 Matches: 1078
Percent Similarity: 99.63% Conservative: 1
Best Local Similarity: 99.54% Mismatches: 4
Query Match: 93.20% Indels: 0
DB: 4 Gaps: 0

US-09-965-830-1_COPY_6_3257 (1-3252) x US-09-358-383C-2 (1-1083)

QY 1 ATCCGGCCCATCGGGGCTCTCTGCGGCTCTCAGAACACCTTCTCTGGACACCATCGCTACG 60
Db 1 MetProAlaMetArgGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20
QY 61 CGCTTCAGCGGACGACAGTACTTCTGCTGGGCAAGCCAGGTCGGGGCTCTTC 120
Db 21 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnValAlaGlyLeuPhe 40

QY 121 CCCGTGCTACTGCTCTGTATGGCTTCTGTACCTCAGCGGCTTCTCCCGGCTCAGGTC 180
Db 41 ProValValTyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal 60
QY 181 ATGACAGGGGGCTGCTGCTCTCTTATGGCCAGACACCCAGTGAGCTGCTCGC 240
Db 61 MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArg 80
QY 241 CAACAGATCCCAAGGCCCTGGACGAGCAACAGAGTTCAAGGCTGAGCTGATCTGTAC 300
Db 81 GlnGlnIleArgIysAlaLeuAspGluHisIysGluPheIysAlaGluLeuIleLeuTyr 100
QY 301 CGGAAGAGCGGCTCCCGTTCTGCTGCTCTGATGTATACCATTAAGAAAGTGAAGAA 360
Db 101 ArgIysSerGlyLeuProPheTrpCysLeuLeuAspValIleProIleLysAsnGluIys 120
QY 361 GGGGAGGTGGCTCTCTCTAGTCTCTCAAGAGACATCAGCGAAACCAACCAACCGAGG 420
Db 121 GlyGluValAlaLeuPheLeuValSerHisIysAspIleSerGluThrLysAsnArgGly 140
QY 421 GCGCCCGACAGATGAAGAGACAGAGTGGTGGCGCGCCGATATGCGCGGACGATCC 480
Db 141 GlyProAspArgTrpLysGluThrGlySerGlyArgArgArgTyrGlyArgAlaArgSer 160
QY 481 AAAGGCTTCAATGCCAACCGCGCGGCGGCGGCGCTGTCTACCACTGTCCGGGAC 540
Db 161 LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis 180
QY 541 CTGCAGAAAGCAGCCCAAGGGCAAGCAAGCTCAATAAGGGGGTGTGGGAGAAACCA 600
Db 181 LeuGlnIysGlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyGluLysPro 200
QY 601 AACTGCTGAGTACAAAGTAGCGCCATCCGGAAGTCGCCCTTCATCTCTGTTCACCTGT 660
Db 201 AsnLeuProGluTyrLysValAlaAlaIleArgLysSerProPheIleLeuLeuHisCys 220
QY 661 GGGGCACTGAGACCCACCTGGATGCTTCATCTGCTCGGCACACTCTATGCGGCTGC 720
Db 221 GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal 240
QY 721 ACTGTGCCCTTACAGCGTGTGTGAGCACAGCAGCGGAGCCAGTGCCTGCGCGGCGCG 780
Db 241 ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro 260
QY 781 CCCAGGCTCTGTCAGCTGCGCGCTGGAGGTCTCTTCATCTTGCATGTGCTGAATTC 840
Db 261 ProSerValCysAspLeuAlaValGluValPheIleLeuAspIleValLeuAsnPhe 280
QY 841 CGTACCACATTGCTGCTCCAGTCGGGCGGAGTGGTGTTCGCCCAAGTCCATTGGCTC 900
Db 281 ArgThrThrPheValSerLysSerGlyGlnValValPheAlaProLysSerIleCysLeu 300
QY 901 CACTAGCTCACCACTGCTTCTGCTGCTGATGTTCATCGCAGCGCTGCGCTTGTACCTGCTA 960
Db 301 HisTyrValThrThrTrpPheLeuLeuAspValIleAlaAlaLeuProPheAspLeuLeu 320
QY 961 CATGCTTCAAGTCAACGTGTACTTTCGGGGCCCATCTGCTGAAGACGCTGCGCTGCTG 1020
Db 321 HisAlaPheLysValAsnValTyrPheGlyAlaHisLeuLeuLysThrValArgLeuLeu 340
QY 1021 CGCTCTCGGCTGCTTCCGGGCTGGACCGGTACTCGCAGTACAGCGCGCTGGTCTG 1080
Db 341 ArgLeuLeuArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValValLeu 360
QY 1081 ACACCTGCTCATGGCGCTGTTGCGCCCTGCTCGGCACCTGGGTGCGCTGCTGCTGTTTAC 1140
Db 361 ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr 380
QY 1141 ATTGGCCAGCGGAGATCGAGAGCAGCGAATCCGAGCTGCTGAGATTGCTGGCTGCAG 1200
Db 381 IleGlyGlnArgGluIleGluSerSerGluLeuProGluIleGlyTrpLeuGln 400
QY 1201 GAGCTGGCGCGGCTGAGGACTCCCTACTACTGCTGGCGGAGCGGCGGCTGGAGG 1260

Db 401 GluLeuAlaArgArgLeuGluThrProTyrTyrLeuValGlyArgArgProAlaGlyGly 420
 QY 1261 AACAGCTCCGCGCAGAGTGACAACATGCGAGCAGCAGCGGCGCAACGGAGCGGGCTG 1320
 Db 421 AsnSerSerGlyGlnSerAspAsnCysSerSerSerGluAlaAsnGlyThrGlyLeu 440
 QY 1321 GAGCTGCTGGGGCGGCGCTGCTGCGCGAGCGCTACATCACCCTCCCTCTACTTCCCACTC 1380
 Db 441 GluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeu 460
 QY 1381 AGCAGCCTCACAGCGTGGCTTCGGCAACGTTCCGCAACACCGACACCGAGAAGATC 1440
 Db 461 SerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGluLysIle 480
 QY 1441 TTCTCATCTGACCATGCTCATCGCGCGCTGATGCGCGCTGGTGTGGGACGCTG 1500
 Db 481 PheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValPheGlyAsnVal 500
 QY 1501 ACGGCATCATCAGCGATGTACGCGCGCGCTTCTGTACACAGCGCGCACGCGCGAC 1560
 Db 501 ThrAlaIleIleGlnArgMetTyrAlaArgPheLeuTyrHisSerArgThrArgAsp 520
 QY 1561 CTGCGGACTACATCCGATCCACCGTATCCCAAGCCCTCAAGAGCGCATGCTGGAG 1620
 Db 521 LeuArgAspTyrIleArgIleHisArgIleProLysProLeuLysGlnArgMetLeuGlu 540
 QY 1621 TACTTCCAGGCCATCGCGCGTGACATGTCATCGACACCGAGCTGCTGCAGAGC 1680
 Db 541 TyrPheGlnAlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeuGlnSer 560
 QY 1681 CTCCCTGACGAGTGGCGGCGACATCGCCATCGACCTGCACAAAGGAGTCTCTGAGCTG 1740
 Db 561 LeuProAspGluLeuArgAlaAspIleAlaMetHisLeuHisLysGluValLeuGlnLeu 580
 QY 1741 CAACCTGTTAGCGGCCAGCGCGCTGCTGCGGGGACTGCTCTGCGCCCTGCGGCC 1800
 Db 581 ProLeuPheGluAlaAlaSerArgGlyCysLeuArgAlaLeuSerLeuAlaLeuArgPro 600
 QY 1801 GCCTTCTGACCGCGCGGCTGACCTCATCCACAGGCGATGCTGCGAGCGCTCTAC 1860
 Db 601 AlaPheCysThrProGlyGluTyrLeuIleHisGlnGlyAspAlaLeuGlnAlaLeuTyr 620
 QY 1861 TTTGTCTGCTGCTGCTCCATGAGGTGCTCAAGGGTGGACCGTGTCTGCCATCTTAGGG 1920
 Db 621 PheValCysSerGlySerMetGluValLeuLysGlyGlyThrValLeuAlaIleLeuGly 640
 QY 1921 AAGGCGACCTGATCGCTGTGAGCTGCGCGCGGAGCAGTGTGTAAAGGCCAATGCC 1980
 Db 641 LysGlyAspLeuIleGlyCysGluLeuProArgGluGlnValValLysAlaAsnAla 660
 QY 1981 GAGCTGAAGGGCTGACGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
 Db 661 AspValLysGlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGlyLeuHisAsp 680
 QY 2041 AGCTTTGCGGTGTACCCCGAGTTGCGCGCTTCAAGTGTGCGCTTCCAGGGGAGCTC 2100
 Db 681 SerLeuAlaLeuTyrProGluPheAlaProArgPheSerArgGlyLeuArgGlyGluLeu 700
 QY 2101 AGCTTACAACTGGGTGTGGGAGGCTGTGAGAGTGTGACACCGCTCTCTGAGCGGC 2160
 Db 701 SerTyrAsnLeuGlyAlaGlyGlySerAlaGluValAspThrSerLeuSerGly 720
 QY 2161 GACAATACCTTATGTCACGCTGGAGGAGAGAGACAGATGGGAGCAGGCGGCCACG 2220
 Db 721 AspAsnThrLeuMetSerThrLeuGluGluLysGluThrAspGlyGluGlnGlyProThr 740
 QY 2221 GTCTCCCGACCGCAGCTGATGACCGCTCCAGCGCCCTGTGCTGCTGCTGCTGCTGCTG 2280
 Db 741 ValSerProAlaProAlaAspGluProSerSerProLeuLeuSerProGlyCysThrSer 760
 QY 2281 TCATCTCAGCTGCGAGCTGCTATCCCGAGCTGACACAGACCGCGCTGCTGCTGCTGCT 2340

Db 761 SerSerSerAlaAlaLysLeuLeuSerProArgArgThrAlaProArgProArgLeuGly 780
 QY 2341 GGCAGAGGAGGAGCCAGGCGAGGCTTTGAAGGTGAGGTGAGGCTGCGCCCTCTCTCTCC 2400
 Db 781 GlyArgGlyArgProGlyArgAlaGlyAlaLeuLysAlaGluAlaGlyProSerAlaPro 800
 QY 2401 CCAGGGCCCTAGAGGGCTAGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2460
 Db 801 ProArgAlaLeuGluGlyLeuArgLeuProMetProTyrAsnValProProAspLeu 820
 QY 2461 AGCCCGAGGAGTGTAGATGGCATTCAGACGCGCTGCTGCGCGCGCGCGCGCGCGCGCG 2520
 Db 821 SerProArgValValAspGlyIleGluAspGlyCysGlySerAspGlnProLysPheSer 840
 QY 2521 TTCCCGCTGGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2580
 Db 841 PheArgMetGlyGlnSerGlyProGluCysSerSerSerProSerProGlyProGluSer 860
 QY 2581 GGCCTGCTCACTGTTCCTCCATGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2640
 Db 861 GlyLeuLeuThrValProHisGlyProSerGluAlaArgAsnThrAspThrLeuAspLys 880
 QY 2641 CTTCCGCGAGGCGCTCACAGAGCTGTACAGACAGGTGTGCGAGTGGGAGGAGTGTGCG 2700
 Db 881 LeuArgGlnAlaValMetGluLeuSerGluGlnValLeuGlnMetArgGluGlyLeuGln 900
 QY 2701 TCATCTCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2760
 Db 901 SerLeuArgGlnAlaValGlnLeuValLeuAlaProHisArgGluGlyProCysProArg 920
 QY 2761 GCATCGGAGGAGGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2820
 Db 921 AlaSerGlyGluGlyProCysProAlaSerThrSerGlyLeuLeuGlnProLeuCysVal 940
 QY 2821 GACACTGGGCGCT 2880
 Db 941 AspThrGlyAlaSerSerTyrCysLeuGlnProProAlaGlySerValLeuSerGlyThr 960
 QY 2881 TGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2940
 Db 961 TrpProHisProArgProGlyProProLeuMetAlaProTrpProTrpGlyProPro 980
 QY 2941 GCGTCTCAGAGCTCCCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3000
 Db 981 AlaSerGlnSerSerProTrpProArgAlaThrAlaPheTrpThrSerThrSerAspSer 1000
 QY 3001 GAGCGCGCTGCTCAGGAGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3060
 Db 1001 GluProProAlaSerGlyAspLeuCysSerGluProSerThrProAlaSerProProPro 1020
 QY 3061 TCTGAGGAGGCGCTAGGACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3120
 Db 1021 SerGluGluGlyAlaArgThrGlyProProGluProValSerGlnAlaGluAlaThrSer 1040
 QY 3121 ACTGGAGCG 3180
 Db 1041 ThrGlyGluProProProValSerGlyLeuAlaLeuProTrpAspProHisSerLeu 1060
 QY 3181 GAGATCGTGTATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3240
 Db 1061 GluMetValLeuIleGlyCysHisGlySerGlyThrValGlnTrpThrGlnGluGly 1080
 QY 3241 ACAGGGGCTC 3249
 Db 1081 ThrGlyVal 1083

RESULT 4
 US-09-336-643A-20
 ; Sequence 20, Application US/09336643A
 ; Patent No. 6399761
 ; GENERAL INFORMATION:
 ; APPLICANT: Miller, Andrew P.
 ; APPLICANT: Curran, Mark Edward

Db 1045 ValLeuPro-----SerArgSerGluGlu-----GlySerPheSerGlnGly 1058

Qy 3214 ACAGTC-----CAGTGCACCCAGGAA 3234

Db 1059 ThrValSerSerPheSerLeuGluAsnLeuProGlySerTrpAsnGlnGlu 1075

RESULT 6

US-09-358-383C-36

; Sequence 36, Application US/09358383C

; Patent No. 6518398

; GENERAL INFORMATION:

; APPLICANT: CURTIS, ROY A. J.

; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR

; FILE REFERENCE: MNI-055CP

; CURRENT APPLICATION NUMBER: US/09/358,383C

; CURRENT FILING DATE: 1999-07-21

; PRIOR APPLICATION NUMBER: US98 09/119,855

; PRIOR FILING DATE: 1998-07-21

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 36

; LENGTH: 1102

; TYPE: PRT

; ORGANISM: Rattus norvegicus

US-09-358-383C-36

Alignment Scores: Length: 1102

Pred. No.: 2,59e-156 Matches: 551

Score: 2515.00

Percent Similarity: 62.00% Conservative: 149

Best Local Similarity: 48.80% Mismatches: 295

Query Match: 41.30% Indels: 134

DB: 4 Gaps: 24

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Qy 1 ATGCCCGCCATCGGGCGCTCTCTGCGCTTCAGAACACCTTCTCTGGACACCATCGCTACG 60

Db 1 MetProValMetLysGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20

Qy 61 CGCTTCGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 120

Db 21 ArgPheAspGlyThrHisSerAsnPheIleLeuAlaAsnAlaGlnValAlaLysGlyPhe 40

Qy 121 CCCTGGTCTACTGCTCTGATGCTTCTGATGCTTCTGATGCTTCTGATGCTTCTGATGCTT 180

Db 41 ProfileValTyrCysSerAspGlyPheCysGluLeuAlaGlyPheAlaArgThrGluVal 60

Qy 181 ATCCAGCGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240

Db 61 MetGlnLysSerCysSerCysLysPheLeuPheGlyValGluThrAsnGlnLeuMet 80

Qy 241 CAACAGATCCGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 300

Db 81 LeuGlnIleGluLysSerLeuGluLysValGluPheLysGlyGlyIleMetPheTyr 100

Qy 301 CGGAAGAGCGGGCTCCCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360

Db 101 LysLysAsnGlyAlaProPheTrpCysLeuLeuAspIleValProIleLysAsnGluLys 120

Qy 361 GGGGAGGTGGCT 417

Db 121 GlyAspValValLeuPheLeuAlaSerPheLysAspIleThrAspThrLysValLysIle 140

Qy 418 GGGGGCCCCGACAGATGGAAGAGACAGAGGTGGTGGCGCGCGCGCGCGCGCGCGCGCG 477

Db 141 ThrSerGluAspLysLysGluAspArgAlaLysGlyArgSerArgAlaGly----- 157

Qy 478 TCCAAAGCCTTCAATGCCAACCGCGGGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 537

Db 158 ---SerHisPheAspSerAlaArgArgSerArgAlaValLeuTyrHisIleSerGly 176

Qy 538 CACCTGACAGACGACCCCAAGGCGGACGACCAAGCTCAATAAGGGGGTGTGTTGGGAGAA 597

Db 738 ||||| Arg 738

Qy 2353 CCAGGACGAGGAGGCGCTTTGAAGCTGAGCTGGCCCTCTGCT- 2397

Db 739 AsnLysLysValGlySerAsnLysAlaTyrLeuGlyLeuSerLeuLysGlnLeuAlaSer 758

Qy 2397 ----- 2397

Db 759 GlyThrValProPheHisSerProIleArgValSerArgSerAsnSerProLysThrLys 778

Qy 2398 -----CGGGCCCTAGAGGGCTACGGCTGCGCCCGC 2433

Db 779 GlnGluIleAspProAsnHisAsnLysArgLysGluLysAsnLeuLysLeuGlnLeu 798

Qy 2434 ATGCCATGAAT-----GTGCCCCAGATCTGAGCCCCAGGTAGTAGTGCATTGAA 2487

Db 799 SerThrLeuAsnAlaGlyProAspLeuSerProArgIleValAspGlyIleGlu 818

Qy 2488 GACGCTGTGGCTCGGACGACCCCAAG---TTCTCTTCCGCTGGGCGCAGTCTGGCCCG 2544

Db 819 AspGlyAsnSerSerGlnGluSerGlnThrPheAspPheGlySerGluArgIleArgSer 838

Qy 2545 GAATGTAGCAGCAGCCCTCCCTCGA---CCAGAGAGCGGCTGCTCACTGTTCCCAT 2601

Db 839 GluProArgIleSerProLeuGlyAspProGluIleGlyAlaAlaValLeuPheIle 858

Qy 2602 GGGCCCCAGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 2661

Db 859 LysAlaGluGluThrLys-----GlnGlnIleAsnLysLeuAsnSerGluValThr 876

Qy 2662 CTGTACAGCAGGTGCTGAGATGCGGAGGAGTGCAGTCACTTCCGACGAGTGTGACG 2721

Db 877 LeuThrGlnGluValSerGlnLeuGlyLysAspMetArgAsnValIleArgLeuGlu 896

Qy 2722 CTGTCTCTGGCGCC-----CACAGGAGGCTCGCTGC 2754

Db 897 AsnValLeuSerProGlnGlnProSerArgPheCysSerLeuHisSerThrSerValCys 916

Qy 2755 CCTCGGCA-----TCGGAGAGGCGCTGCCCGC 2787

Db 917 ProSerArgGluSerLeuGlnThrArgThrSerTrpSerAlaHisGlnProCys----- 934

Qy 2788 AGCACTCCGGGCTTCTGACGCTCTGTGTGTGACACTGGGACACTGCTCTACTGCT- 2844

Db 935 -----LeuHisLeuGlnThrGlyAlaAlaTyrThrGln 946

Qy 2845 CTGACGCCCCAGTGTCTGTCTTCAAGTGGGACTTGGCCCCCACCCTCTGTCGGGGCCT 2904

Db 947 AlaGlnLeuCysSerSerAsnIleThrSerAspIleTrpSer----- 960

Qy 2905 CTTCCCTCATGGACCCCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 2964

Db 961 -----ValAspProSerSerValGlySerSer---Pro 970

Qy 2965 CGACCCACAGTTTCTGACCTCCACCTCAGACTCAGAGCCCCCTGCTCTCAGAGACCTC 3024

Db 971 GlnArgThrGly-----AlaHisGluGlnAsnProAlaAspSerGluLeu 985

Qy 3025 TGCTCTGAGCCACGACCCCTGCTCCCT----- 3054

Db 986 TyrHisSerProSerLeuAspTyrSerProSerHisTyrGlnValValGlnGluGlyHis 1005

Qy 3055 -----CCTCTCTCAGGAGGGGCTAGGACTGGCGCGCGCGCGCGCGCGCGCGCG 3093

Db 1006 LeuGlnPheLeuArgCysIleSerProHisSerAspSerThrLeuThr---ProLeuGln 1024

Qy 3094 CTTGTGACGAGGCTGAGCTACAGACACTGAGAGCCCCCACCAGGCTCAGGCGCGCTG 3153

Db 1025 SerIleSerAlaThrLeuSerSerSerValCysSerSerSerGluThrSerLeuHisLeu 1044

Qy 3154 GCCTTGCCCTGGGACCCCAACGACGCTGAGATGTGTATTGCTGTCATGGCTCTGCTGC 3213

US-09-965-830-1_copy_6_3257 (1-3252) x US-09-600-776-6 (1-1017)		Gaps: 23	
QY	1	ATGCGCGGCATGCGGGGCTCTCTGCGGCTCAGAACACCTTCTCTGGACACCATCCTCTAGC	60
Db	1	MetProValMetLeuGlyLeuLeuAlaProGlnAenThrPheLeuAspThrileAlaThr	20
QY	61	CGCTTCGACGCGCACAGTAACCTTCGTGGGCAACGCCAGTGGCGGGCTCTTC	120
Db	21	ArgPheAspGlyThrHisSerAsnPheLeuLeuAlaAenAlaGlnGlyThrArgGlyPhe	40
QY	121	CCGTGGTCTACTGCTGTGATGGCTTCTGACCTCAGGGCTTCTCCGGGCTCAGGTC	180
Db	41	ProileValTyCysSerAspGlyPheCysGluLeuThrGlyTyGlyArgThrGluVal	60
QY	181	ATGACAGCGGGCTGCTGCTCTCTCTTATGGCCAGACACAGTAGAGTCTGCTCCG	240
Db	61	MetGlnLysThrCysSerArgPheLeuTyGlyProGluThrSerGluProAlaLeu	80
QY	241	CAACAGATCCGCAAGCGCTGACAGCAAGAGATTCAAGGCTGAGCTGATCTCTGTAC	300
Db	81	GlnArgLeuHisLysAlaLeuGluGlyHisGlnGluHisArgAlaGluLeuLeuCysPheTy	100
QY	301	CGAAGAGCGGGCTCCGCTTCTGCTCTCTCTGATGTATACCCATTAAGAATGAGAAA	360
Db	101	ArgLysAspGlySerAlaPheTrpCysLeuLeuAspMetMetProileLysAsnGluMet	120
QY	361	GGGAGGCTGCT	420
Db	121	GlyGluValValLeuPheLeuPheSerPheLysAspPheLysAspPheLysAspPheLys	140
QY	421	---GGCCCGACAGATGGAG	477
Db	141	LeuGlyProGln-----GlyGlyArgGlyAspSerLysHisGluAsn	154
QY	478	TCCAAGGC-----TTCAATGCCAACCGCGCGCGAGAGCGCGGCC	516
Db	155	SerLeuGlyArgArgGlyAlaThrTrpLysPheArgSerAlaArgArgSerArgThr	174
QY	517	GTCTCTTACACCTGTCTGCGGCGACCTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAG	576
Db	175	ValLeuHisArgLeuThrGlyHisPheGlyArgGlyGlnGlyMetLysAlaAsn	194
QY	577	AAGGGGTGTTGGGAGAAACCAACTTCCCTGAGTACAAAGTAGCGCGCATCCGGAAG	636
Db	195	AsnAsnValPheGluProLysProSerValProGluTyLysValAlaSerValGlyGly	214
QY	637	TCGCCCTTCTCTCTGTTGCTGTGGGCGACTGAGAGCGACCTGGGATGGCTTCTCTG	696
Db	215	SerArgCysLeuLeuLeuHisTySerValSerLysAlaLeuTrpAspGlyLeuLeuLeu	234
QY	697	CTCGCCACACTTATGTGGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	756
Db	235	LeuAlaThrPheTyValAlaValThrValProTyLysValCysPheSerGlyAsp	254
QY	757	GAGCCGAGTGGCG	816
Db	255	AspThrProLysThrSerArgHisThrLeuValSerAspPheAlaValGluMetLeuPhe	274
QY	817	ATCCTTGACATTTGCTGATTTCCGTACCACTTCTGTGTCTCTCTCTCTCTCTCTCT	876
Db	275	IleLeuAspPheLeuLeuPheArgThrThrValSerGlnSerGlyGlnValIle	294
QY	877	TTTGGCCCAAGTCCATTGCTCTCACTACGTACACCTGCTCTCTCTCTCTCTCTCT	936
Db	295	SerAlaProArgSerLysLeuHisTyLysLeuAlaThrTrpPhePheLeuAspLeuLeu	314
QY	937	GCAGCGCTGCTCTTGTACCTGCTATGCTCTCAAGTCAAGTCAAGTCAAGTCAAGT	996
Db	315	AlaAlaLeuProPheAspLeuLeuTyLysPheAsnLeuThrValThrSerLeuValHis	334
QY	997	CTGCTGAAGACGGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1056

QY	2671	CAGTGTGACAGATGCGGGAAGAGACTGACGTACTTCCGACGCTGTGCACCTGTCTCTG	2730
Db	880	GluValSerGlnLeuGlyLysAspMetArgSerLeuLeuLeuGluLeuLeuLeuLeu	899
QY	2731	CGGCCCCACAGGAGGGTCCGTGCGCTCGGCATCGGAGAGAGGGCGCGCGCGCGCG	2790
Db	900	SerProGlnGlnProSerGlnPheCysSerLeuHisProThrSerLysCysProSerArg	919
QY	2791	ACCTCCGGGCTTCTGACGCTCTGTGTGTGACACTGGGGCATCTCTCTCTCTCTCTCT	2850
Db	920	GluSerPheGlnThrArg-----ValSerTrpSerAlaHisGlnProCysLeuHis	936
QY	2851	CCCCCAGCT-----GCTCTGCTTCTGAGTGGGACTGGCGCCAC	2889
Db	937	LeuGlnAlaAsnGlyAlaHisLeuTyHisGlyAsnValThrSerAspPheTrp	954
QY	2890	CCTGCTCGGGGCT	2949
Db	955	-----SerValAspProSerLeuValGlySerAsnProGlnArgThrGluAlaHisGlu	972
QY	2950	AGCTCCCC-----	2958
Db	973	GlnSerProValAspSerGluLeuHisHisSerProAsnLeuAlaTySerProSerHis	992
QY	2959	-----TGGCTCTGAGCCACA	2973
Db	993	CysGlnValIleGlnGluGlyHisLeuGlnPheLeuArgCysLysSerProHisSerAsp	1012
QY	2974	GCTTCTGACCTCCACCTCAGACTCAGAGCCCGCTCTCTCTCTCTCTCTCTCTCTCT	3033
Db	1013	ThrThrLeuThrProLeuGlnSerLysLeuAlaThrLeuSerSerValCysSerSer	1032
QY	3034	CCGACGACCCCT-----GCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	3081
Db	1033	SerGluThrSerLeuHisLeuValLeuProSerArgSerGluGluGlySerLysThrHis	1052
QY	3082	GGGCGCGCAGAGCTGTGAGCCAGCTGAGGCTACCGACCTGAGAGAGAGAGAGAGAG	3141
Db	1053	GlyProValSerSerPheSerLeu-----GluAsnLeuProGly	1065
QY	3142	TCAGGGGCGCTGGCTTGGCTGGGAC	3168
Db	1066	Ser-----TrpAsp	1068

RESULT 7
US-09-600-776-6
; Sequence 6, Application US/09600776
; Patent No. 6326168
; GENERAL INFORMATION:
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: A novel potassium channel protein
; FILE REFERENCE: Y9903-PCT
; CURRENT APPLICATION NUMBER: US/09/600,776
; CURRENT FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: JP P1998-011434
; PRIOR FILING DATE: 1998-01-23
; PRIOR APPLICATION NUMBER: JP P1998-346198
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1017
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-600-776-6

Alignment Scores:	7,86e-153	Length:	1017
Pred. No.:	2461.50	Matches:	538
Score:	59.19%	Conservative:	119
Best Local Similarity:	48.47%	Mismatches:	245
Query Match:	40.43%	Indels:	208

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Db	355	SerGlnCysSerAlaValValLeuThrLeuLeuMetSerValPheAlaLeuLeuAlaHis	374	
QY	1117	TGGTCTGGCTGGTCTGGTCTGTTTTCATTTGGCAGCGGGAGATCGAGAGCAGCAATCCGAG	1176	
Db	375	TrpMetAlaCysIleTrpTyrValIleGlyArgGluMetGluAlaAsnAspProLeu	394	
QY	1177	CTGCCTGAGATGGCTGCACGAGACTGCGCCCGCAGCTGGAGACTCCCTACTACTCTG	1236	
Db	395	LeuTrpAspIleGlyTrpLeuHisGluLeuGlyLysArgLeuGluValProTyr	412	
QY	1237	GTGGCCGAGGCCAGCTGGAGGGAAAGACCTCGCGCCAGAGTGACACTGCAGCAGCAGC	1296	
Db	412	-----	412	
QY	1297	AGCAGGCCAACGGGACGGGCTGGAGCTGTGTGGCGCGCCGTGTGTGCGCAGCGCTAC	1356	
Db	413	-----ValAsnGlySer-----	426	
QY	1357	ATCACCTCCCTCTACTTTCGCACTCAGCAGCCTCACACGCTGGGCTTCGGCAAGTGTCC	1416	
Db	427	IleAlaAlaLeuTyrPheThrLeuSerSerLeuThrSerValGlyPheGlyAsnValCys	446	
QY	1417	GCCAACACGGACACCGGAGAAGATCTTCTCATCTGCACCACTGTCTATCGCGCCCTGATG	1476	
Db	447	AlaAsnThrAspAlaGluLysIlePheSerIleCysThrMetLeuIleGlyAlaLeuMet	466	
QY	1477	CACCGGTGGTGTGGAAACGTGACGGCCATCATCCAGCGCATGTACGCCCGCCGCTTT	1536	
Db	467	HisAlaValValPheGlyAsnValThrAlaIleIleGlnArgMetTyrSerArgArgSer	486	
QY	1537	CTGTACACACGCGCAGCGCGACCTCGCGGACTACATCCGCAATCCACGTAATCCCAAG	1596	
Db	487	LeuTyrHisSerArgMetLysAspLeuLysAspPheIleArgValHisArgLeuProArg	506	
QY	1597	CCCCTCAAGCAGCGCATCTCGAGTAGTACTCCAGCCACCTGGCGCTGAGCAATGCATC	1656	
Db	507	ProLeuLysGlnArgMetLeuGluTyrPheGlnThrThrAlaValAsnSerGlyIle	526	
QY	1657	GACACACCGAGCTGTGACAGCCTCCCTGACGAGCTGGCGGACACATCCGCATGCAC	1716	
Db	527	AspAlaAsnGluLeuLeuArgAspPheProAspGluLeuArgAlaAspIleAlaMetHis	546	
QY	1717	CTGCACAAGCAGTCTCGACGTCGCCACTGTTTGAGCGCGCCAGCGCGGCTGCTGGCG	1776	
Db	547	LeuAsnArgLulleLeuGlnLeuProLeuPheGlyAlaAlaSerArgGlyCysLeuArg	566	
QY	1777	GCATCTGTCTGCGCCCTCGCGCCGCTCTGTGCACGCGCGGCGAGTACCTCATCCACCA	1836	
Db	567	AlaLeuSerLeuHisIleLysThrSerPheCysAlaProGlyGluTyrLeuLeuArgArg	586	
QY	1837	GGCGATGCCCTCAGGCGCTCTACTTTGTCTGTCTGTGCTCCATGAGGTGTCAAGGT	1896	
Db	587	GlyAspAlaLeuGlnAlaHisTyrTyrValCysSerGlySerLeuGluValLeuArgAsp	606	
QY	1897	GGCACCGTGTCCCATCTCAGGAGGGGACCTGATCGGCTGTGAGCTGCCCGCGCGG	1956	
Db	607	AsnMetValLeuAlaIleLeuGlyLysGlyAspLeuIleGlyAlaAspIleProGluPro	626	
QY	1957	GAGCAG-----GTGGTAAAGGCCCAATGCCGACCTG	1986	
Db	627	GlyGlnGluProGlyLeuGlyAlaAspProAsnPheValLeuLysThrSerAlaAspVal	646	
QY	1987	AAGGGGCTGAGTACTGCTGCTGCACTGTCTGCAGCTGTGCTGGCCTGCACGACAGCCTT	2046	
Db	647	LysAlaLeuThrTyrCysGlyLeuGlnLeuSerSerArgGlyLeuAlaGluValLeu	666	
QY	2047	GGCTGTACCCGAGTTCCCGCGCTTCAGTCTGTGGCTCCGAGGGAGCTCAGCTAC	2106	

667 ArgLeuTyrProGluTyrGlyAlaAlaPheArgAlaGlyLeuProArgAspLeuThrPhe 686
QY AACTCTGGTCTGGGGAGGCTCTGCAGAGTGGACACACAGCTCCCTG----- 2154
Db AsnLeuArgGlnGlySer-----AspThrSerGlyLeuSerArgPheSer 701
QY 2155 -----AGCGCGCACAAATACC 2169
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QY 2170 CTTATGTCCACGCTGGAGGAGAAGAGACACATGGGAGCAGGGCCCAAGTCTCCCA 2229
Db LeuProSerIle-----ThrGluAlaGluSerGly-----AlaGluPro 734
QY 2230 GCCCAGCTGATGAGCCCTCCAGCCCTGTGTCTCCCTGGCTGCACCTCTCATCTCA 2289
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QY 2290 GCTGCCAAGCTG----- 2301
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QY 2302 -----CTATCCCACTCGAACACGCCCGGCTCTCTAGTGGGACAGGAGG 2352
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QY 2353 CCAGGCAGGCAGGGGCTTTGAAGCTGAGGCTGGCCCTCTGTCTCCCCACGGGCCCTA 2412
Db 792 -----SerAlaSerProHisGlyProProArgCysSer 802
QY 2413 GAGGG-----CTAGGCTGCCCCCATGCCAATGTCGCCCCAGAT 2457
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QY 2692 GGACTGCATCTACTTCGCCAGGCTGTGCAGCTGTCTCTGGCGCCCAACAGGAGGGTCCG 2751
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Db 909 -----GluAlaArgLeuGlyProPro----- 915
QY 2812 CTGTGTGGACACTGGGGCATCTCTCTACTGCCTGCAGCCCCCAGCTGCTGTCTTG 2871
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QY 2932 GGTCCCCAGGCTCTCAGAGCTCCCTGGCTCGAGCCACAGCTTCTGGACCTCCACC 2991
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411 QY ----- 411
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 412 QY -----AACCAGGG 420
 160 Db ArgPheArgAlaGlySerAsnAlaGlyMetLeuGlyLeuGlyGlyLeuProGlyLeuGly 179
 421 QY -----GACAGATGGAAGAGAGACAGGTGGTGGCGCGCGGATATGGCCGG 471
 180 Db GlyProAlaAlaSerAspGlyAspThrGluAlaGlyGluGlyAsnAsnLeuAspValPro 199
 472 QY -----GCACGATCCAAAGGCTTCAATCCCAACCGCGCGAGCGCGCGCTGCTTACCACTCG 531
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 532 QY -----AAGACCAAGCTCAATTAAGGG----- 582
 217 Db SerGlyHisTyrLysProGluLysGlyGlyValLysThrLysLeuLysLeuGlyAsnAsn 236
 583 QY -----GTGTTTGGGAGAAACCAACTTGCCTGAGTACAAAGTAGCCGCCAGTCCGGAAGTCG 639
 237 Db PheMetHisSerThrGluAlaProPheProGluTyrLysThrGlnSerLysLysSer 256
 640 QY -----CCCTTCATCTGTTGACCTGTGGGCGACCTGGGATGGCTTCATCTCTGCTC 699
 257 Db ArgLeuLeuLeuProHisTyrGlyValPheLysGlyLysLysLysLysLysLysLysLys 276
 700 QY -----GCCACACTCTATGTGGCTGTCACTGTGCGCTACAGCGTGTGTGTGACAGCAGCGGAG 759
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 760 QY -----CCAGTGGCG 819
 297 Db GlnThr-----LysValSerAspValLeuValLeuValLeuPheLeu 310
 820 QY -----CTTGACATTTGCTGAATTTCCGTACACATTCGTGTCACAGTCCGCGCGAGTGGTGT 879
 311 Db ValAspLeuLeuLeuAsnPheArgThrThrPheValSerArgLysGlyValValSer 330
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 940 QY -----GCGTGGCTTTGACCTGCTACATGCTTCAAGTCAACGTGCTACTTTCGGG----- 990
 351 Db AlaLeuProPheAsp-----HisLeuTyrAlaSerAspLeuTyrAspGlyGluAspSer 368
 991 QY -----GCCCATCTGTGAAGACGGTGGCGCTGCTGCGCTGCTGCGCTGCTGCGCTGCTG 1047
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 1048 QY -----GACCGTACTCGCAGTACAGCGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1107
 389 Db AspArgTyrSerGlnHisThrAlaMetIleLeuThrLeuLeuMetPheSerPheThrLeu 408
 1108 QY -----CTCCGCACTGGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 1167
 409 Db AlaAlaHisTrpLeuAlaCysIleTrpTyrValIleAlaValLysGluTyrGlu----- 426
 1168 QY -----GAATCCGAGTGGCTGGAG-----ATTGGCTGGCTGGAGGAGTGGCGCGCGCTGGAG 1221
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 442 Db ----- 442
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3005 QY -----CCCTGCTCAGGAGAC 3021
 966 Db uThrGlyThrAlaLeuLeuAspLeuArgProSerIleLeuProTyrProSerGluPr 986
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 986 Db cAspProLeuGlyProSerProValPro 995
 RESULT 8
 US-09-343-494-9
 ; Sequence 9, Application US/09343494
 ; Patent No. 6413741
 ; GENERAL INFORMATION:
 ; APPLICANT: Jeggla, Timothy J.
 ; APPLICANT: Wickenden, Alan
 ; APPLICANT: ICAGEN, Incorporated
 ; TITLE OF INVENTION: Human Elk, a Voltage-Gated Potassium Channel Subunit
 ; FILE REFERENCE: 018512-001320US
 ; CURRENT APPLICATION NUMBER: US/09/343,494
 ; CURRENT FILING DATE: 1999-06-30
 ; EARLIER APPLICATION NUMBER: US 60/091,469
 ; EARLIER FILING DATE: 1998-07-01
 ; EARLIER APPLICATION NUMBER: US 60/116,621
 ; EARLIER FILING DATE: 1999-01-21
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 9
 ; LENGTH: 1284
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 ; FEATURES:
 ; OTHER INFORMATION: Drosophila Elk (dElk; Bag (ether a go-go)-like K+
 ; OTHER INFORMATION: gene) protein
 ; US-09-343-494-9
 Alignment Scores:
 Pred. No.: 3,44e-116 Length: 1284
 Score: 1901.00 Matches: 455
 Percent Similarity: 53.85% Conservative: 146
 Best Local Similarity: 40.77% Mismatches: 273
 Query Match: 31.22% Indels: 242
 DB: 4 Gaps: 31
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 QY 61 CGCTTCGACGCGCAGCAGTAACCTTCTGCTGGCGCAACGCCACAGTGGCGGGCTCTTC 120
 Db 21 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnAlaAsnGly--Asn 39
 QY 121 CCCGTGGTCTACTCTCTGATGGTCTTGTGACCTCAGCGGCTTCTCCGGGCTGAGTTC 180
 Db 40 ProIleValTyrCysSerAspGlyPheValAspLeuThrGlyTyrSerArgAlaGlnIle 59
 QY 181 ATGACGCGGGCTGCTGCTGCTCTCTCTTATGGCGCAGACACAGTGGCTGCTGCTGCT 240
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 Db 80 GlnGlnIleGluLysSerLeuSerAsnLysMetGluLeuLysLeuGluValIlePheTyr 99
 QY 301 CGGAAGACGGGCTCCGCTTCTGCTGCTCTCTGATGATGATACCCATTAAGAAATCAGAAA 360
 Db 100 LysLysGluGlyAlaProPheTyrCysLeuPheAspIleValProIleLysAsnGlnLys 119
 QY 361 GGGGAGGTGGCT 411
 Db 120 ArgAspValValPheLeuAlaSerHisLysAspIleThrHisThrLysMetLeuGlu 139

Score:	1901.00	Matches:	455
Percent Similarity:	53.85%	Conservative:	146
Best Local Similarity:	40.77%	Mismatches:	273
Query Match:	31.22%	Indels:	242
DB:	4	Gaps:	31
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DB	1	MetProAlaArgGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr	20
QY	61	CCCTTCGACGGCAGCAGCAGTAACTTCGTGCGCAACGCCAGCGCGGGGCTCTTC	120
DB	21	ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnAlaAsnGly---Asn	39
QY	121	CCCGTGTCTACTGCTGATGCTCTGTGACCTCAGCGGCTTCTCCGGGCTGAGTNC	180
DB	40	ProIleValTyrCysSerAspGlyPheValAspLeuThrGlyTyrSerArgAlaGlnIle	59
QY	181	ATGCAGCGGGCTGTGCTGCTCTCTTCTTATGGCCAGACACAGTGTGCTGCGC	240
DB	60	MetGlnLysGlyCysSerCysHisPheLeuTyrGlyProAspThrLysGluGlnHisLys	79
QY	241	CAACAGATCCGCAAGCCCTGACGAGCACAAGAGATTCAAGCTGAGTGTGCTGTAC	300
DB	80	GlnGlnIleGluLysSerLeuSerAsnLysMetGluLeuLysLeuGluValIlePheTyr	99
QY	301	CGAAGAGCGGGCTCCGCTTCTGCTCTCTGATGATACCCATTAAGATGAGAAA	360
DB	100	LysLysGluGlyAlaProPheTyrCysLeuPheAspIleValProIleLysAsnGluLys	119
QY	361	GGGAGGTGGCTCTCTCTCTAGTCTCTCACAAGCATCAGCGAAACCAAG	411
DB	120	ArgAspValValLeuPheLeuAlaSerHisLysAspIleThrHisThrLysMetLeuGlu	139
QY	411	-----	411
DB	140	MetAsnValAsnGluGluCysAspSerValPheAlaLeuThrAlaAlaLeuLeuGlyAla	559
QY	412	-----AACCGAGGG	420
DB	160	ArgPheArgAlaGlySerAsnAlaGlyMetLeuGlyLeuGlyLeuProGlyLeuGly	179
QY	421	GGCCCC-----CACAGATCGAAGAGACACAGGTGGTGGCGCGCGCCGATATGCGCGG	471
DB	180	GlyProAlaAlaSerAspGlyAspThrGluAlaGlyGluGlyAsnAsnLeuAspValPro	199
QY	472	GCACGATCCAAAGCTTCAATGCCAACCGCGCGGAGCGCGCGCTGTCTTACCACTG	531
DB	200	Ala-----GlyCysAsnMetGlyArgArgSerArgAlaValLeuTyrGlnLeu	216
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DB	237	PheMetHisSerThrGluAlaProPheProGluTyrLysThrGlnSerIleLysSer	256
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DB	257	ArgLeuIleLeuProHisTyrGlyValPheLysGlyIleTyrAspThrValIleLeuVal	276
QY	700	GCCACACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	759
DB	277	AlaThrPheTyrValAlaLeuMetValProTyrAsnAlaAlaPheAlaLysAlaAspArg	296
QY	760	CCCAGTGGCG	819
DB	297	GlnThr-----LysValSerAspValIleValGluAlaLeuPheIle	310
QY	820	CTTGACATGTGTGAATTTCCGTACCATCTCTGTGTCACATCTCTGTGTCACATCTCT	879

Db 632 GluValIleLysAspMetValValAlaIleLeuGlyLysGlyAspLeuValGlySer 651
QY 1942 GAGCTG----- 1947
Db 652 AspileAsnValHisLeuValAlaThrSerAsnGlyGlnMetThrAlaThrThrAsnSer 671
QY 1948 CCCCGGGGAGCAGTGGTAAAGCCCAATGCCGACGTGAAGGGCTGACGTACTGCGTC 2007
Db 672 AlaGlyGlnAspValValArgSerSerAspIleLysAlaLeuThrTyrCysAsp 691
QY 2008 CTGAGTCTCTGCAGCTGGCTGACGACGACCTTGCCTGACCCGAGTTGCC 2067
Db 692 LeuLysCysIleHisMetGlyLeuValGluValLeuArgLeuTyrProGluTyrGln 711
QY 2068 CCGGCTTCAGTCTGGCTCCGAGGGAGCTACAGCTGAGCTGCTGGGGAGGC 2127
Db 712 GlnGlnPheAlaAsnAspileGlnHisAspLeuThrCysAsnLeuArgGluGlyTyrGlu 731
QY 2128 TCTGAGAGGTGGACACAGC-----TCCCTGAGCGGGGACAAATACC 2169
Db 732 AsnGlnAspSerAspileGlyProSerPheProLeuProSerIleSerGluAspAspGlu 751
QY 2170 CTTATGTCACCTGGAG-----GAGAAGGAGACAGATGGGAGCAGGGC 2214
Db 752 AsnArgGluGluAlaGluGluGlyGlyLysGlyGluLysGluAsnGlyGly-----Gly 769
QY 2215 CCC-----ACGTCTCCCGAGCCCGAGCTGATGAGCCCTCC 2250
Db 770 ProProSerGlyAlaSerProLeuHisAsnIleSerAsnSerProLeuHisAlaThrArg 789
QY 2251 AGCCCCCTGTGTCCTCCCTGGCTGCACCTCTCATCTCAGCTGCCAAGCTGCTATCCCA 2310
Db 790 SerProLeuLeuGlyMetGly-----SerPro 798
QY 2311 CGTCGAACAGACCCCGCCCTCTCTAGTGGAGAGGGAGCCAGGAGGGCGGCT 2370
Db 799 Arg-----AsnGlnArgLeuHisGlnArgGly----- 807
QY 2371 TTGAAGCTGAGGTGGCCCTCTGCTCCCGAGCGCCCTAGAGGGCTAGCGGTGCC 2430
Db 808 -----ArgSerLeuIleThrLeuArg----- 814
QY 2431 CCCATGCATGAATGTGCCCCAGATCTGAGCCCGAGGGTAGTGGCATTTGAAGAC 2490
Db 815 -----GluThrAsnLysArgHisArgThrLeuAsnAla----- 825
QY 2491 GGCTGTGGCTCGGACACAGCCCAAGTTCTTTCGCGTGGGCCAGTCTGGCCCGAATGT 2550
Db 826 AlaCysSerLeuAspArgGlySerPhe----- 834
QY 2551 AGCAGCAGCCCTCCCTCGACACAGAGCGGCTGCTACTGTCTCCCATGGCCCGC 2610
Db 835 ---GluGluProGluProLeuGluGlu-----GlnSer 845
QY 2611 GAGCAAGAACACAGACACTGGACAAGCTTCGGCAGCGGTGACAGAGCTGTACAG 2670
Db 846 SerGlyGlyLysArgProSerLeuGluArgLeuAspSerGlnValSerThrLeuHisGln 865
QY 2671 CAGTGTCTGAGATCGGGAGGAGCTCGAGTCACTTCGCCAGGCTGTCAGCTGTGCTGT 2730
Db 866 AspValAlaGlnLeuSerAlaGluValArgAsnAlaIleSerAlaLeuGlnGluMet--- 884
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QY 2905 CTCTCCCTCATGGCACCCTGGCTGGCTCCCGAGCGCTCTCAGAGCTCCCTCGGCT 2964
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QY 2965 CGAGCCACAGCTTTCTGGACCTCCACCT-----CAGACTCAGAGCCCTGCTCC 3012
Db 937 tGlnArgSerSerHisProGluValTyrPheGlyArgAspValGlnLeuProThrSe 957
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Db 957 tAsnThrAlaSerSerLysAlaProSerProValGluPro 970
RESULT 10
US-09-358-383C-5
; Sequence 5, Application US/09358383C
; Patent No. 6518398
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rofy A. J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-055CP
; CURRENT APPLICATION NUMBER: US/09/358,383C
; CURRENT FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: USSN 09/119,855
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 542
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-358-383C-5
Alignment Scores:
Pred. No.: 4,95e-112 Length: 542
Score: 1835.50 Matches: 352
Percent Similarity: 77.64% Conservative: 82
Best Local Similarity: 62.97% Mismatches: 92
Query Match: 30.14% Indels: 33
DB: 4 Gaps: 5
US-09-965-830-1_copy_6_3257 (1-3252) x US-09-358-383C-5 (1-542)
QY 1 ATCGCGCCATCGGGGCTCTGCGGCTCAGAACCTTCTGGACACCATCGCTACG 60
Db 1 MetProValMetLysGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20
QY 61 CGCTTCAGCGCAGCAGACAGTAACTTCGCTGGCAACGCCAGGTGGGGGCTCTTC 120
Db 21 ArgPheAspGlyThrHisSerAsnPheIleLeuAlaAsnAlaGlnValAlaLysGlyPhe 40
QY 121 CCGTGTCTACTGCTCTGTGATGGCTTCTGACCTCAGCGGCTTCTCCGGGCTGAGGTC 180
Db 41 ProIleValTyrCysSerAspGlyPheCysGluLeuAlaGlyPheAlaAthrGluVal 60
QY 181 ATCAGCGGGGCTGTGCTGCTCTCTTCTTTATGGGCCACACACAGTGTGCTCGGC 240
Db 61 MetGlnLysSerCysSerCysLysPheLeuPheGlyValGluThrAsnGluLeuMet 80
QY 241 CAACAGATCGCAAGCCCTGAGCAGCACAAGAGTTCAGAGCTGAGCTGATCTCTGCTAC 300
Db 81 LeuGlnIleGluLysSerLeuGluGluLysThrGluPheLysGlyGluIleMetPheTyr 100
QY 301 CGGAAGAGCGGGCTCCCGTTCTGCTCTCTGATGTATACCCATTAAGAATGAGAA 360
Db 101 LysLysAsnGlySerProPheTyrCysLeuLeuAspIleValProIleLysAsnGluLys 120
QY 361 GGGGAGGTGCTCTCTCTCTAGTCTCTCAAGAGCATCAGCGAAACCAAGAACCGGAGG 420
Db 121 GlyAspValValLeuPheLeuAlaSerPheLysAspIleThrAspThrLysValLysIle 140
QY 421 GGGCCGACAGATGGAGGAGCAGAGTGTGGCCGCGGATATGCGCGGCGACATCC 480
Db 421 GGGCCGACAGATGGAGGAGCAGAGTGTGGCCGCGGATATGCGCGGCGACATCC 480

Db 141 ThrProGluAspLysLysGluAsp-----LysValLysGlyArgSerArgAla 156
Qy 481 ---AAAGCTTCAATGCCAACCGGCGGAGCGCGCTCTACACACCTGTCGCGG 537
Db 157 GlyThrHisPheAspSerAlaArgArgSerArgAlaValLeuTyHisIleSerGly 176
Qy 538 CACCTGCGAGAACGAGCCCAAGGCGGACGACAGCTCAATAGAGGGGTGTGGGAGAAA 597
Db 177 HisLeuGlnArgGluLysAsnLysLysLysLysLysLysLysLysLysLysLys 196
Qy 598 COAACTTTCCTGAGTACAAAGTACCGGCGATCCGGAAGTCCCTTCATCTGTTGCAC 657
Db 197 ProAlaPheProGluTyHisValSerAspAlaLysLysSerLysPheIleLeuLeuHis 216
Qy 658 TGTGGGCACTGAGACCACTGGATGCTTCATCTCGCCACACTCTATGTCGT 717
Db 217 PheSerThrPheLysAlaGlyTrpAspTrpLeuIleLeuLeuAlaThrPheTyValAla 236
Qy 718 GTCACTGTGCTTACAGCGTGTGTGAGCACAGCGGAGCCAGTCCCGCCCGCGC 777
Db 237 ValThrValProTyHisValCysPheIleGlyAsnAspAspLeuSerThrArgSer 256
Qy 778 CGGCCGAGCTGTGACCTGGCGGCTGCTCTTCATCTTCATCTGACATTGCTGAAT 837
Db 257 ---ThrThrValSerAspIleAlaValGluLeuPheIleIleAspIleIleLeuAsn 275
Qy 838 TTCGTACCACTTCGTGTCAGTCCGAGTCCGCGCGTGTGTTCGCCCAAGTCCATTGC 897
Db 276 PheArgThrThrTyHisValSerLysSerGlnValIlePheGluAlaArgSerIleCys 295
Qy 898 CTCACATAGTCACCACTGTTCTCTGCTGATGTATCGACGCGTGCCTTTGACCTG 957
Db 296 IleHisTyValThrThrPheIleAspLeuIleAlaLeuProPheAspLeu 315
Qy 958 CTACATGCTTCAAGTCAAGTGTACTTCGGGCGCATCTCTGAGAGCGTGCCTG 1017
Db 316 LeuTyAlaPheAsnValThrValSerLeuValHisLeuLeuLysThrValArgLeu 335
Qy 1018 CTGCGCTGCTGCGCTGCTTCGCGCTGAGCGGTACTCGCAGTACAGCGCGTGTG 1077
Db 336 LeuArgLeuLeuArgLeuGlnLysLeuAspArgTyHisSerThrIleVal 355
Qy 1078 CTGACACTGCTATGCGCTGCTGCTGCGCACTGCGTGGTGGCTGCTGCTGTTT 1137
Db 356 LeuThrLeuLeuMetSerPheAlaLeuAlaHisTrpMetAlaCysIleTrpTy 375
Qy 1138 TACATTGGCAGCGGAGATCGAGACGAGCAATCCAGTGTGCTGAGATTGCTGCTG 1197
Db 376 ValIleGlyLysMetGluArgGluAspAsnSerLeuLeuLysTrpGluValGlyTrpLeu 395
Qy 1198 CAGAGCTGCGCCGCGCTGAGACTCCCTACTACTGCTGGTGGCGCGGAGCCAGTGA 1257
Db 396 HisGluLeuGlyLysArgGluGluSerProTyHis----- 407
Qy 1258 GGGAAACAGCTCCGCGCGAGTGCACACTGCAGCAGCAGCAGCGAGCGGCGGAG 1317
Db 408 GlyAsnAsnThr----- 411
Qy 1318 CTGAGCTGCTGGCGCGCTGCTGCGGAGCGCTCATCATCCTCCCTCTACTTCGCA 1377
Db 412 -----LeuGlyGlyProSerIleArgSerIleAlaAlaLeuTyHisPheThr 428
Qy 1378 CTCAGCAGCTCAGCAGCTGCTGGCAAGCTGTCGCGCAACAGCAGCAGCAGCAGAG 1437
Db 429 LeuSerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspAlaGluLys 448
Qy 1438 ATCTTCTCATCTGACCATGCTCATCGCGCGCTGATGACGCGGTGTGTTGGGAAC 1497
Db 449 IlePheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaLeuValPheGlyAsn 468
Qy 1498 GTGAGCGGCATCATCCAGCATGTACCGCGCGCTTCTGTACCATCCAGCGCGCGC 557
Db 469 ValThrAlaIleIleGlnArgMetTyHisArgTrpSerArgTrpSerLeuTyHisArgThrLys 488

Qy 1558 GACCTGCGCGACTACATCCGATCCACCGTATCCCAAGCCCTCAAGCAGCGCTGCTG 1617
Db 489 AspLeuLysAspPheIleArgValHisIleLeuProGlnGlnLeuLysGlnArgMetLeu 508
Qy 1618 GAGTACTTCCAGCCACCTGGCGGTGAACATGTCATCGACACCCAGCGCTGCTG 1674
Db 509 GluTyPheGlnThrThrTrpSerValAsnAsnGlyIleAspSerAsnGluValMet 527
RESULT 11
US-08-956-242-13
; Sequence 13, Application US/08956242C
; Patent No. 5986081
; GENERAL INFORMATION:
; APPLICANT: Ganetzky, Barry S.
; APPLICANT: Titus, Steven A.
; TITLE OF INVENTION: Polynucleotides Encoding Herg-3
; FILE REFERENCE: 960296.94550
; CURRENT APPLICATION NUMBER: US/08/956,242C
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; TYPE: PRT
; ORGANISM: Homo sapien
; US-08-956-242-13
Alignment Scores:
Pred. No.: 2,41e-93 Length: 1159
Score: 1551.00 Matches: 424
Percent Similarity: 44.86% Conservative: 143
Best Local Similarity: 33.54% Mismatches: 337
Query Match: 25.47% Indels: 360
DB: 2 Gaps: 38
US-09-965-830-1_COPY_6_3257 (1-3252) x US-08-956-242-13 (1-1159)
Qy 1 ATCCCGCGCATGCGGGCGCTCTGCGCGCTCAGAACACCTCTCTGACACCATCGCTACG 60
Db 1 MetProValArgArgGlyHisValAlaProGlnAsnThrPheLeuAspThrIleArg 20
Qy 61 CGCTTCGACGGCAGCAGTAACTTCGTCTGCGCAACGCCAGCGGTGGCGGCTCTTC 120
Db 21 LysPheGluGlyGlnSerArgLysPheIleAlaAsnAlaArgValGluAsnCys--- 39
Qy 121 CCGCTGCTCTACTGCTCTGATGCTCTGCTGACTCTCAGCGGCTTCTCCCGGCTGAGGTC 180
Db 40 AlaValIleTyCysAsnAspGlyPheCysGluLeuCysGlyTySerArgAlaGluVal 59
Qy 181 ATCAGCGGGCTGTGCTGCTCTCTTCTTATGGGCGACACACCATGAGTCTGCTCGC 240
Db 60 MetGlnArgProCysThrCysAspPheLeuHisGlyProArgThrGlnArgAlaAla 79
Qy 241 CAACAGATCCGAGCGCTGCGAGCAGCAGCAGGTTCAAGGCTGAGCTGATCCTCTAC 300
Db 80 AlaGlnIleAlaGlnAlaLeuLeuGlyAlaGluGlnArgLysValGluIleAlaPheTy 99
Qy 301 CGGAAGAGCGGCTCCCGTCTGCTGCTCTGATGTGATACCCATTAAGATGAGAAA 360
Db 100 ArgLysAspGlySerCysPheLeuCysLeuValAspValValProValLysAsnGluAsp 119
Qy 361 GGGAGGTGCTCTCTCTCTA-----GTCTCTCACAGGACATC----- 399
Db 120 GlyAlaValIleMetPheIleLeuAsnPheGluValValMetGluLysAspMetValGly 139
Qy 400 -----ACGAAACCAAGACCGAGGGGCGCCGACACATGG----- 435
Db 140 SerProAlaHisAspThrAsnHisArgGlyProProThrSerTrpLeuAlaProGlyArg 159
Qy 435 ----- 435
Db 160 AlaLysThrPheArgLeuLysLeuProAlaLeuLeuAlaLeuThrAlaArgGluSerSer 179

QY	436	---	AAGGACACAGGTGGTGGCCGGCCGCATATGGCCGGSC---	ACGATCCAAAGCCTTC	489
Db	180	ValArgSerGlyGlyAlaGly-GlyAlaGlyAla-ProGlyAlaValValAspValA	199	503	
QY	490	AATGCCAACCGCGC	503		
Db	199	spLeuThrProAlaAlaProSerSerGluSerLeuAlaLeuAspGluValThrAlaMetA	219		
QY	504	-----GCGGACCGCGCGTCTCTA	524		
Db	219	spAsnHisValAlaGlyLeuGlyProAlaGluGluArgArgAlaLeuValGlyProGlyS	239		
QY	525	--CCACTGTGGGACCTGCAGACAGCAGCCCAAGGGCAAG--CACAAGCTCAAT--	576		
Db	239	erProProArgSerAlaProGlyGlnLeu-ProSerProArgAlaHisSerLeuAsnPro	258		
QY	576	-----	576		
Db	259	AspAlaSerGlySerSerCysSerLeuAlaArgThrArgSerArgGluSerCysAlaSer	278		
QY	577	-----AAGGGGGTGTTCGGGAG	594		
Db	279	ValArgArgAlaSerSerAlaAspAspIleGluAlaMetArgAlaGlyValLeuPro	298		
QY	595	AAACCAAC	603		
Db	299	ProProArgHisAlaSerThrGlyAlaMethHisProLeuArgSerGlyLeuLeuAsnSer	318		
QY	603	-----	603		
Db	319	ThrSerAspSerAspLeuValArgTyrArgThrIleSerLysIleProGlnIleThrLeu	338		
QY	603	-----	603		
Db	339	AsnPheValAspLeuLysGlyAspProPheLeuAlaSerProThrSerAspArgLulle	358		
QY	603	-----	603		
Db	359	IleAlaProLysIleLysGluArgThrHisAsnValThrGluLysValThrGlnValLeu	378		
QY	604	-----TTGCCTGAGTACAAAGTAGCGCCATCCGGAAGTCGCCCTTC	645		
Db	379	SerLeuGlyAlaAspValLeuProGluTyrIlysLeuGlnAlaProArgIleHisArgTrp	398		
QY	646	ATCCTGTTCACATGTGGGCACCTCAGAGCCACCTGGGATGCTTCATCCCTGCTGCCACA	705		
Db	399	ThrIleLeuHisTyrSerSerProPheLysAlaValTrpAspTrpLeuIleLeuLeuVal	418		
QY	706	CTCTATGTGGCTGTCACTGTGCCCTCAGCGGTGTGTGTG-----AGCACAGCAGG	756		
Db	419	IleTyrThrAlaValPheThrProTyrSerAlaAlaPheLeuLeuLysGluThrGluGlu	438		
QY	757	GACCCAGTGCC-----GCCCGCGCGCCGACGCTGTGACCTGGCC	801		
Db	439	GlyProProAlaThrGluCysGlyTyrAlaCysGlnProLeuAlaValValAspLeuIle	458		
QY	802	GTGAGGTCTCTTCATCCCTGCATTTGCTGAATTCGTAATTCGCATCCATTCGTGTCCAAG	861		
Db	459	ValAspIleMetPheIleValAspIleLeuIleAsnPheArgThrThrTyrValAsnAla	478		
QY	862	TCGGGCCAGGTGGTGTGGCCCCAAAGTCCATTGCTCCACTACGTCACCCACTGGTTC	921		
Db	479	AsnGluGluValValSerHisProGlyArgIleAlaValHisTyrPheLysGlyTrpPhe	498		
QY	922	CTGCTGGATGTCATCGCAGCGCTGCCCTTTGACCTGTCTACATGCTTCAAAGGTCAACGTG	981		
Db	499	LeuIleAspMetValAlaAlaIleProPheAspLeuLeu-----	511		
QY	982	TACTCTGGGGCC-----CATCTGCTGAAGCGGTGGCGCTGCTGCGC	1023		
Db	512	IlePheGlySerGlySerGluGluLeuIleGlyLeuLeuLysThrAlaArgLeuLeuArg	531		

QY	1024	CTGCTGGCGCTGCTTC	CGCGCTCGACGGTACTCG	CAGTACACGCGCGTGTCTG	CACA	1083
Db	532	LeuValArgValAlaArgLysLeuAspArgTyrSerGluTyrGlyAlaAlaValLeuPhe	551			
QY	1084	CTGCTCATGGCGGTTC	CGCCCTCTCGCGCACTGGGT	CGCTCGCTCGTCTGGTTACATT	1143	
Db	552	LeuLeuMetCysThrPheAlaLeuAlaHisTrpLeuAlaCysIleTrpTyrAlaIle	571			
QY	1144	GGCCAGCGCGAGATCG	AGACGAGCGCAATCCG	AGCTGCCTCGAGATTGCTGGCTCGCAGG	1203	
Db	572	GlyAsnMetGluGlnProHisMetAspSer	588			
QY	1204	CTGGCCCCCGCACTG	AGACATCCCTACTAC	TGTTGGCGCGAGCTGGAGGGAAC	1263	
Db	589	LeuGlyAspGlnIleGlyLysProTyr	598			
QY	1264	AGCTCCGGCCAGATG	CACTGACGACGACGAGCG	AGCGGCAACGGACGGGCTGGAG	1323	
Db	599	SerSerGly	601			
QY	1324	CTGCTGGCGCGCCGT	CGCTGCGCAGCGCCTAC	ATCACCTCCCTCTACTTTCGCAC	1383	
Db	602	--LeuGlyGlyProSerIleLysAspLysTyrValThrAlaLeuTyrPheThrPheSer	620			
QY	1384	AGCTCACAGCGTGGCT	TCGGAACAGTTCGCGCAACACG	CACACCGACACCGAGAAGATCTTC	1443	
Db	621	SerLeuThrSerValGlyPheGlyAsnValSerProAsnThrAsnSerGluLysIlePhe	640			
QY	1444	TCCATCTGCACCATCT	CATCGCGCCCTGATCG	ACGCGTGTGTTCGGAACTGACG	1503	
Db	641	SerIleCysValMetLeuIleGlySerLeuMetTyrAlaSerIlePheGlyAsnValSer	660			
QY	1504	GCCATCATCCAGCGCAT	GACGCGCGCTTCTCTAC	CACAGCGCACGCGCGACCTG	1563	
Db	661	AlaIleIleGlnArgLeuTyrSerGlyThrAlaArgTyrHisThrGlnMetLeuArgVal	680			
QY	1564	CGCACTACATCCGCAT	CCACCGTATCCCCAAGCCCTCA	AGCAGCGCATGTCTGGAGTAC	1623	
Db	681	ArgGluPheIleArgPheHisGlnIleProAsnProLeuArgGlnArgLeuGluTyr	700			
QY	1624	TTCAGGCCACCTGGCG	GTGAACATGGCATGCAC	CACCGAGTGTCTGCAGACCTTC	1683	
Db	701	PheGlnHisAlaTrpSerTyrThrAsnGlyIleAspMetAsnAlaValLeuLysGlyPhe	720			
QY	1684	CCTGACGAGTCGCGC	GACATCGCCATGCGCATCTGC	ACAAAGAGTCTCTGCAG--CTG	1740	
Db	721	ProGluCysLeuGlnAlaAspIleCysLeuHisLeuAsnArgSerLeuLeuGlnHisCys	740			
QY	1741	CCACTGTTTGAGCG	CCACGCGCTCGCTCGCGCACTGTCT	CTGCGCCCTGCGGCGCC	1800	
Db	741	LysProPheArgGlyAlaThrLysGlyCysLeuArgAlaLeuAlaMetLysPheLysThr	760			
QY	1801	GCCTTCTGCACCGCG	GAGTACTCTCATCCCAAGCGATGCC	CTGCAGGCCCTCTAC	1860	
Db	761	ThrHisAlaProProGlyAspThrLeuValHisAlaGlyAspLeuLeuThrAlaLeuTyr	780			
QY	1861	TTTGTCTGCTCTGCT	CTCATGGGTCTCAAGGTGGC	ACCGTCTCGCCATCTCTAGGG	1920	
Db	781	PheIleSerArgGlySerIleGluIleLeuArgGlyAspValValAlaIleLeuGly	800			
QY	1921	AAGGGCGACTGATCG	GTGTGAGTGTCCCGCGGAGCAGGT	GTTAAAGCCCAATGCC	1980	
Db	801	LysAsnAspIlePheGlyGluProLeuAsnLeuTyrAlaArgProGlyLysSerAsnGly	820			
QY	1981	GAGGTCAAGGGGCT	GACGTACTGCTCTCTG	CAGTGTCTGAGTGGCTGCAGCAC	2040	
Db	821	AspValArgAlaLeuThrTyrCysAspLeuHisLysIleHisArgAspAspLeuLeuGlu	840			
QY	2041	AGCCTTCGCTGTAC	CCCGAGTTTCCCGCGCTT	CAGTCTCGTCCCTCCGAGGAGCTC	2100	
Db	841	ValLeuAspMetTyrProGluPheSerAspHisPheTrpSerSerLeu-----GluIle	858			
QY	2101	AGCTACAACCTG-----	GGTGTGGGGGAGGCTCTG	CAGAGCTGCAC	2142	

859	ThrPheAsnLeuArgAspThrAsnMetIleProGlySerProGlySerProGlySerThrGluLeuGlu	878
2143	ACAGCTCCCTGAGCGGGACAATACCTTATGTCACCGCTGGAGGAGAAGAGACAGAT	2202
879	GlyGlyPheSerArgGlnArgIysArgIysLeuSerPheArgArgThrAspLysAsp	898
2203	GGGAGCAGGGCCCCACGGTCTCCCGAGCCCGACGCTGATGAGCCCTCCACGCCCTGTG	2262
899	ThrGluGln	901
2263	TCGCTGGCTGCACCTCTCTCATCTCAGCTGCCAAGCTGCTATCCCACTGCACAGCA	2322
902	--ProGlyGluValSerAla--	914
2323	CCCGGGCTCGTCTAGTGGCAGGGAGCCAGGCGGAGGCGGCTTTGAAGGCTGAG	2382
915	AlaGlyPro--SerSerArgGlyArgProGlyGlyProThrGlyGluSerProSer	932
2383	GTGCGGCCCTCTGCTCCGCCA--	2418
933	SerGlyProSerSerProGluSerSerGluAspGluGlyProGlyArgSerSerPro	952
2419	CTACGGCTG--	2466
953	LeuArgLeuValProPheSerSerProGlyGluProGlyGlyGluPro	972
2467	AGGTAGTAGTCATGCAATGAAGCGCTGGCTCGACCCAGCCCAAG--	2514
973	--LeuMetGluAspCysGluLysSerSerAspThrCysAsnProLeuSerGlyAlaPhe	991
2515	-----TTCTCTTTC-----	2538
992	SerGlyValSerAsnIlePheSerPheThrProGlyAspSerArgGlyArgGlnTyrGlu	1011
2539	GGCCCGGAATGTAGCAGAGCCCTCCCTGGACAGAGAGCGGCTGTCTACTGT--	2595
1012	LeuProArgCys-----ProAlaProThrProSerLeuLeuAsnIlePro	1026
2596	-----CCCCATGGGCCAGCGGACAGGACAGGACACAGACACACTG	2634
1027	LeuSerSerProGlyArgArgProArgGlyAspValGluSerArg--	1042
2635	GACAAGCTTCGGCAGCGGTGCACAGAGCTGTGCAGACAGGTG--CTGCAGATCGCGGAA	2691
1043	AspAlaLeuGlnArgGlnLeuAsnArgLeuGluThrArgLeuSerAlaAspMetAlaThr	1062
2692	GGACTGCAGTCACTTCGCCAGCGGTGTGCAGCTGTCTCTGGCGCCCCACAGGAGGTCG	2751
1063	ValLeuGlnLeuLeuGln-ArGlnMetThrLeu--	1073
2752	TGCCCTCGGGATCGGAGAGGGCGCTGCCAGCCAGCACTCCGGGCTTCTGCAGCCT	2811
1074	-----ValProAlaIysSerAla--	1080
2812	CTGTGTGTGGACATCGGGGCATCTCTTACTGCTGCAGCCCCCAGCTGCTGTCTGT	2871
1081	---ValThrThrProGlyProGlyProThrSerThrSerProLeuLeuProValSerPr	1099
2872	AGTGGAGTTGGCCCCACCTGCTCGTGGGGGCTCTCCCTCATGGCACCTCGCCCTGG	2931
1099	oLeu-----ProThrLeuThrLeuAspSerLeuSerGln-----	1110
2932	GGTCCCGCCAGCTCTC-----AGAGCTCCCCCTGCCTCGAGCCACAGCTTCTGTG	2982
1111	-ValSerGlnPheMetAlaCysGluGluLeuProGly---AlaProGluLeuProGln	1129
2983	ACCTCCACTCAGACTCAGAGGCCCTGCTCAGGAGACCTCTGCTGTGAGCCCGACACC	3042
1129	nGluGlyProThrArgArgLeuSerLeuProGlyGlnLeuGlyAlaLeuThrSerGlnPr	1149
3043	CCTG 3046	

Db 1149 oLeu 1150

RESULT 12

US-09-351-215-13

Sequence 13, Application US/09351215

Patent No. 6087488

GENERAL INFORMATION:

APPLICANT: Ganetzky, Barry S.

TITLE OF INVENTION: Polynucleotides Encoding Herg-3

FILE REFERENCE: 960296.94550

CURRENT APPLICATION NUMBER: US/09/351,215

CURRENT FILING DATE: 1999-07-12

EARLIER APPLICATION NUMBER: 08/956,242

EARLIER FILING DATE: 1997-10-22

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 13

LENGTH: 1159

TYPE: PRT

ORGANISM: Homo sapien

US-09-351-215-13

Alignment Scores:

Pred. No.:	2,41e-93	Length:	1159
Score:	1551.00	Matches:	424
Percent Similarity:	44.86%	Conservative:	143
Best Local Similarity:	33.54%	Mismatches:	337
Query Match:	25.47%	Indels:	360
DB:	3	Gaps:	38

US-09-965-830-1_COPY_6_3257 (1-3252) x US-09-351-215-13 (1-1159)

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QY	61	CGCTTCAGCGCACGACAGTAACCTCGTGTGGCAAGCCACAGGTGGCGGGCTCTTC	120
Db	21	LysPheGluGlyGlnSerArgLysPheIleleAlaAsnAlaArgValGluAsnCys---	39
QY	121	CCCGTGGTCTACTGCTCTGTAGTGGCTTCTGTACCTCAGCGGCTTCTCCCGGGCTGAGTC	180
Db	40	AlaValIleTyrCysAsnAspGlyPheCysGluLeuCysGlyTyrSerArgAlaGluVal	59
QY	181	ATCAGCGGGGCTGTGCTGTCT	240
Db	60	MetGlnArgProCysThrCysAspPheLeuHisGlyProArgThrGlnArgAlaAla	79
QY	241	CAACAGATCCGCAAGGCCCTCGACGACACAGGAGTTCAAGGCTGAGCTGATCTGTATC	300
Db	80	AlaGlnIleAlaGlnAlaLeuLeuGlyAlaGluArgLysValGluIleAlaPheTyr	99
QY	301	CGGAAGAGCGGCTCCCT	360
Db	100	ArgLysAspGlySerCysPheLeuCysLeuValAspValProValLysAsnGluAsp	119
QY	361	GGGAGGTGGCT	399
Db	120	GlyAlaValIleMetPheIleLeuAsnPheGluValValMetGluLysAspMetValGly	139
QY	400	-----ACGGAACCAAGAACCGAGGGGCCCGACAGATGG-----GTCTCTCAAGGACATC-	435
Db	140	SerProAlaHisAspThrAsnHisArgGlyProProThrSerTyrLeuAlaProGlyArg	159
QY	435	-----	435
Db	160	AlaLysThrPheArgLeuLysLeuProAlaLeuLeuAlaLeuThrAlaArgGluSerSer	179
QY	436	----AAGGACAGGTGGTGGCCGGCCCGCATATGCCGGGC---ACGATCCAAAGCGCTTC	489
Db	180	ValArgSerGlyGlyValagly-GlyAlaGlyAla-ProGlyAlaValValValAspValA	199

QY 490 AATGCCAACCGCGC----- 503
Db 199 spLeuThrProAlaalaProSerSerGluSerLeuAlaLeuAspGluValThrAlaMetA 219
QY 504 -----GCGAGCGCGCGCGTCTCTA----- 524
Db 219 spAsnHisValAlaGlyLeuGlyProAlaGluGluArgAlaLeuValGlyProGlyS 239
QY 525 --CCACCTGTCCGGGCACCTGCAGAACAGCAGCCCAAGGCAAG--CACAACTCAAT--- 576
Db 239 erProProArgSerAlaProGlyGlnLeu-ProSerProArgAlaHisSerLeuAsnPro 258
QY 576 ----- 576
Db 259 AspAlaSerGlySerSerCysSerLeuAlaArgThrArgSerArgGluSerCysAlaSer 278
QY 577 -----AAGGGGGTGTTCGGGAG 594
Db 279 ValArgArgAlaSerSerAlaAspAspIleGluAlaMetArgAlaGlyValLeuPro 298
QY 595 AAACCAAAAC----- 603
Db 299 ProProArgHisAlaSerThrGlyAlaMetHisProLeuArgSerGlyLeuLeuAsnSer 318
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Db 319 ThrSerAspSerAspLeuValArgTyrArgThrIleSerLysIleProGlnIleThrLeu 338
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Db 339 AsnPheValAspLeuLysGlyAspPheLeuAlaSerProThrSerAspArgGluIle 358
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Db 359 IleAlaProLysIleLysGluArgThrHisAsnValThrGluLysValThrGlnValLeu 378
QY 604 -----TTGCTGTAGTACAAAGTAGCGCCATCCGGAAGTCGCCCTTC 645
Db 379 SerLeuGlyAlaAspValLeuProGluTyrLysLeuGlnAlaProArgIleHisArgTrp 398
QY 646 ATCCGTGTGACCTGTGGGGCACTCAGAGCCACTGGGATGCTTCATCCTGCTGCCACA 705
Db 399 ThrIleLeuHisTyrSerProPheLysAlaValTrpAspTrpLeuIleLeuLeuVal 418
QY 706 CTCATGTGGCTGTCACTGTGCCCTACAGCGTGTGTGTG-----AGCACAGCAGG 756
Db 419 IleTyrThrAlaValPheThrProTyrSerAlaAlaPheLeuLeuLysGluThrGlu 438
QY 757 GAGCCCAAGTGC-----GCCGGCGCGCGCCAGCGTCTGTGACCTGGCC 801
Db 439 GlyProProAlaThrGluCysGlyTyrAlaCysGlnProLeuAlaValValAspLeuIle 458
QY 802 GTGAGGTCTCTTCATCTGTGATGTGCTGAATTCGTACCAATTCGTGTCCAAAG 861
Db 459 ValAspIleMetPheIleValAspIleLeuIleAsnPheArgThrThrValAsnAla 478
QY 862 TCGGGCAGGTGTGTGTGCCCCAAAGTCCATTTGCTCCACTACGTCACCACTGGTTC 921
Db 479 AsnGluGluValValSerHisProGlyArgIleAlaValHisTyrPheLysGlyTrpPhe 498
QY 922 CTGCTGGATGTATCGAGCGTGCCTTTGACCTGTACATCGCTTCAAGGTCAACGTG 981
Db 499 LeuIleAspMetValAlaAlaIleProPheAspLeuLeu----- 511
QY 982 TACTTCGGGGCC-----CATCTGCTGAAGACGGTGGCGCTGTGCGC 1023
Db 512 IlePheGlySerGlySerGluGluLeuIleGlyLeuLeuLysThrAlaArgLeuLeuArg 531
QY 1024 CTGCTCGCTGTCTCCGGGTGGACCGGTACTCGCAGTACAGCCCGTGTGTGCTGACA 1083
Db 532 LeuValArgValAlaArgLysLeuAspArgTyrSerGluTyrGlyAlaAlaValPhe 551
QY 1084 CTGCTCATGGCGGTGTTCGCCCTGTCTCGCGCACTGGGTGCGCTGTGCTGTGTTTACATT 1143

Db 552 LeuLeuMetCysThrPheAlaLeuIleAlaHisTrpLeuAlaCysIleTrpTyrAlaIle 571
QY 1144 GCGCAGCGGAGATCGAGAGCAGCAATCCGAGCTGCCTGAGATTGGCTGGCTGCAGGAG 1203
Db 572 GlyAsnMetGluGlnProHisMetAspSer-----ArgIleGlyTrpLeuHisAsn 588
QY 1204 CTGGCCCGCGGACTCGAGACTCCCTACTACCTGTGGTGGCGGAGGCCAGCTCGAGGGAAC 1263
Db 589 LeuGlyAspGlnIleGlyLysProTyr-----Asn 598
QY 1264 AGCTCCGCGCAGAGTGCACACTGCAGCAGCAGCAGGAGCCACGCGGAGCGGCTGGAG 1323
Db 599 SerSerGly----- 601
QY 1324 CTGCTGGCGCGCCCTGCTGCGCAGCGCTACATCCTCCTCTACTTGCACCTCAGC 1383
Db 602 ---LeuGlyGlyProSerIleLysAspLysTyrValThrAlaLeuTyrPheThrPheSer 620
QY 1384 AGCTCACCAGCGTGGCTTCGGCAACGTGTCGCCAACACCGACACCGAGAAGATCTTC 1443
Db 621 SerLeuThrSerValGlyPheGlyAsnValSerProAsnThrAsnSerGluLysIlePhe 640
QY 1444 TCCATCTGCACCATGCTCATCGCGCCTGATGCACCGGTGTGTGGGAACGTGAGC 1503
Db 641 SerIleCysValMetLeuIleGlySerLeuMetTyrAlaSerIlePheGlyAsnValSer 660
QY 1504 GCCATCATCCAGCGCATGTACGCCCGCGCTTCTGTACACACAGCGCGCAGCGCTG 1563
Db 661 AlaIleIleGlnArgLeuTyrSerGlyThrAlaArgTyrHisThrGlnMetLeuArgVal 680
QY 1564 GCGACATACATCCGCATCCCGCTATCCCAAGCCCTCAAGCAGCGCATCTGGAGTAC 1623
Db 681 ArgGluPheIleArgPheHisGlnIleProAsnProLeuArgGlnArgLeuGluGluTyr 700
QY 1624 TTCAGCGCCACCTGGCGGTGCACAAATGGATGCACACCCAGCGAGCTGCTCAGAGCCTC 1683
Db 701 PheGlnHisAlaTrpSerTyrThrAsnGlyIleAspMetAsnAlaValLeuLysGlyPhe 720
QY 1684 CTGACAGAGTGGCGCAGACATCGCCATGCACCTGCACAGGAGGTCTCTGAG---CTG 1740
Db 721 ProGluCysLeuGlnAlaAspIleCysLeuHisLeuAsnArgSerLeuLeuGlnHisCys 740
QY 1741 CCATGTTTGGCGGCGCAGCGCGCTGCTCGGCGCTGCTGCGCCCTGCGCCCTC 1800
Db 741 LysProPheArgGlyAlaThrLysGlyCysLeuArgAlaLeuAlaMetLysPheLysThr 760
QY 1801 GCCTTCTGCAGCGCGGAGTACCTCATCCACCAAGCGCATGCCCTGCGAGGCTCTAC 1860
Db 761 ThrHisAlaProProGlyAspThrLeuValHisAlaGlyAspLeuLeuThrAlaLeuTyr 780
QY 1861 TTTGCTGCTCTGCTCCATGAGGTGCTCAAGGTGGCGCCGTCTGCGCATCTCCTAGG 1920
Db 781 PheIleSerArgGlySerIleGluIleLeuArgGlyAspValValValAlaIleLeuGly 800
QY 1921 AAGGGCAGCTGATCGCTGTGAGTGCCTCGCGCGGAGCAGGTGTGTAAGGCCAATGCC 1980
Db 801 LysAsnAspIlePheGlyGluProLeuAsnLeuTyrAlaArgProGlyLysSerAsnGly 820
QY 1981 GAGCTCAAGGGGTGACGTACTCGCTCCTGACGTGTCTGCAGCTGCTGCGCTGCGCTGAC 2040
Db 821 AspValArgAlaLeuThrTyrCysAspLeuHisLysIleHisArgAspAspLeuGlu 840
QY 2041 AGCTTGTGCTGTACCCCGAGTTTGCCTCGCTTCTCAGTGTGCGCTCCGAGGGAGCTC 2100
Db 841 ValLeuAspMetTyrProGluPheSerAspHisPheTrpSerSerLeu-----GluIle 858
QY 2101 AGCTACAACTG-----GGTGTGGGGGAGGCTCTCAGAGGTGGAC 2142
Db 859 ThrPheAsnLeuArgAspThrAsnMetIleProGlySerProGlySerThrGluLeuGlu 878
QY 2143 ACCAGTCTCCTGAGCGCGCACAATACCTTATGTCCAGCTGGAGGAGAGAGACAGAT 2202

879 GlyGlyPheSerArgGlnArgLysLeuSerPheArgArgThrAspLysAsp 898
2203 GGGAGCAGGGCCCCACGGTCTCCAGCCAGCTGATGAGCCCTCCAGCCCTGCTG 2262
899 ThrGluGln----- 901
2263 TCCCTGCTGACCTCCTCATCTCTCAGTGCACAGCTGCTATCCCACTGCAACACA 2322
902 ---ProGlyGluValSerAla-----LeuGlyProGlyArgAlaGly 914
2323 CCCCCTGCTGCTAGTGGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2382
915 AlaGlyPro-----SerSerArgGlyArgProGlyGlyProGlyGluSerProSer 932
2383 GGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2418
933 SerGlyProSerSerProGluSerSerGluAspGluGlyProGlyArgSerSerPro 952
2419 CTACGCTG-----CCCCCATGCGCATGGAATGTGCCCCCAGATCTGAGCCCT 2466
953 LeuArgLeuValProPheSerSerProArgProGlyGluProGlyGlyGluPro 972
2467 AGGTAGTAGAGGATTAAGACGGCTGTGCTCGACACGCCCAAG----- 2514
973 ---LeuMetGluAspCysGluLysSerSerAspThrCysAsnProLeuSerGlyAlaPhe 991
2515 -----TTCTCTTTC-----CGCGTGGGCCAGTCT 2538
992 SerGlyValSerAsnIlePheSerPheTrpGlyAspSerArgGlyArgGlnTyrGlnGlu 1011
2539 GGGCCCGAATGATGACGAGCAGCCCTCCCTGACACGAGCGCTGCTCACTGTT--- 2595
1012 LeuProArgCys-----ProAlaProThrProSerLeuLeuAsnIlePro 1026
2596 -----CCCATGGCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2634
1027 LeuSerSerProGlyArgArgProArgGlyAspValGluSerArg-----Leu 1042
2635 GACAAGCTTCGGAGCGGTGACAGAGCTGTACAGAGCAGGTG---CTGCAGATGCGGAA 2691
1043 AspAlaLeuGlnArgGlnLeuAsnArgLeuGluThrArgLeuSerAlaAspMetAlaThr 1062
2692 GGAAGTCACTTCCGACAGGCTGTGACAGTCTGCTGCTGCTGCTGCTGCTGCTGCT 2751
1063 ValLeuGlnLeuLeuGln-ArgGlnMetThrLeu----- 1073
2752 TGCCCTCGGCATCGGAGAGGGCCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2811
1074 -----ValProAlaTyrSerAla-- 1080
2812 CTGTGTGGACACTGGGGCATCCTCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2871
1081 ---ValThrThrProGlyProGlyProThrSerThrSerProLeuLeuProValSerPr 1099
2872 AGTGGAGCTTGGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2931
1099 oLeu-----ProThrLeuThrLeuAspSerLeuSerGln----- 1110
2932 GGTCCCCCAGGTCTC-----AGAGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 2982
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2983 ACCTCCACCTCAGACTCAGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3042
1129 nGluGlyProThrArgArgLeuSerLeuProGlyGlnLeuGlyAlaLeuThrSerGlnPr 1149
3043 CCTG 3046
1149 oLeu 1150

RESULT 13

US-09-226-012-2

; Sequence 2, Application US/09226012

Patent No. 6207383
GENERAL INFORMATION: Mark T.
APPLICANT: Keating, Igor
TITLE OF INVENTION: MUTATIONS IN AND GENOMIC STRUCTURE OF HERG - A LONG QT
SYNDROME GENE
FILE REFERENCE: 2323-136
CURRENT APPLICATION NUMBER: US/09/226,012
EARLIER FILING DATE: 1999-01-06
EARLIER APPLICATION NUMBER: 09/122,847
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 1159
TYPE: PRT
ORGANISM: Homo sapiens
US-09-226-012-2

Alignment Scores:
Pred. No.: 2,41e-93 Length: 1159
Score: 1551.00 Matches: 424
Percent Similarity: 44.86% Conservative: 143
Best Local Similarity: 33.54% Mismatches: 337
Query Match: 25.47% Indels: 360
DB: 3 Gaps: 38

US-09-965-830-1_COPY_6_3257 (1-3252) x US-09-226-012-2 (1-1159)

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DB 21 LysPheGluGlyGlnSerArgLysPheIleIleAlaAsnAlaArgValGluAsnCys--- 39
QY 121 CCGTGTCTACTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
DB 40 AlaValIleTyrCysAsnAspGlyPheCysGluLeuCysGlyTyrSerArgAlaGluVal 59
QY 181 ATCAGCGCGGCTGCTGCT 240
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QY 241 CAACACATCGCAAGCGCTGAGCAGACCAAGAGTTCAGCGTCAAGCTGAGCTGCTGCTAC 300
DB 80 AlaGlnIleAlaGlnAlaLeuLeuGlyAlaGluGluArgLysValGluIleAlaPheTyr 99
QY 301 CGGAAGAGCGGCTCCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
DB 100 ArgLysAspGlySerCysPheLeuCysLeuValAspValProValLysAsnGluAsp 119
QY 361 GGGGAGGTGCT 399
DB 120 GlyAlaValIleMetPheIleLeuAsnPheGluValValMetGluLysAspMetValGly 139
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DB 140 SerProAlaHisAspThrAsnHisArgGlyProProThrSerTrpLeuAlaProGlyArg 159
QY 435 ----- 435
DB 160 AlaLysThrPheArgLeuLysLeuProAlaLeuLeuAlaLeuThrAlaArgGluSerSer 179
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QY 490 AATGCCAACCGGCG----- 503
DB 199 spLeuThrProAlaAlaProSerSerGluSerLeuAlaLeuAspGluValThrAlaMetAla 219

RESULT 15
US-09-358-383C-10
; Sequence 10, Application US/09358383C
; Patent No. 6518398
; GENERAL INFORMATION:
; APPLICANT: CURTIS, ROY A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-055CP
; CURRENT APPLICATION NUMBER: US/09/358,383C
; CURRENT FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: USSN 09/119,855

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; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1159
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-358-383C-10

Alignment Scores:
Pred. No.: 2,41e-93 Length: 1159
Score: 1551.00 Matches: 424
Percent Similarity: 44.86% Conservative: 143
Best Local Similarity: 33.54% Mismatches: 337
Query Match: 25.47% Indels: 360
DB: 4 Gaps: 38

US-09-965-930-1_COPY_6_3257 (1-3252) x US-09-358-383C-10 (1-1159)

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QY 61 CGCTTCGACGCGCAGCAGCAGTAACCTCTGCTGGGCAAGCCGACGTCGGGGCTCTTC 120
Db ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 21 LysPheGluGlyGlnSerArgLysPheIlelleAlaAsnAlaArgValGluAsnCys 39
QY 121 CCCGTGTCTACTCTCTGATGGCTTCTGTGACCTTCACGCGGTCTTCTCCGGGCTGAGGTC 180
Db ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 40 AlaValIleTyrcysAsnAspGlyPheCysGluLeuCysGlyTyrcysArgAlaGluVal 59
QY 181 ATGACGCGGGCTGTGCGCTCTCTCTCTTATGGCCACAGACCAGTCGAGCTCGTCCGC 240
Db ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
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QY 241 CAACAGATCCGCAAGGCCTCGGACGACCAAGGAGTTCAAGGCTGAGCTGATCCGTGATC 300
Db ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 80 AlaGlnIleAlaGlnAlaLeuLeuGlyAlaGluGluArgLysValGluIleAlaPheTy 99
QY 301 CGGAAGAGCGGGCTCCCGTCTGTGTCTCTCTGGATGTATACCCATAAGATGAGAA 360
Db ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 100 ArgLysAspGlySerCysPheLeuCysLeuValAspValProValLysAsnGluAsp 119
QY 361 GGGGAGGTGGCTCTCTCTCTA-----GTCTCTCACAGGACATC----- 399
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QY 120 GlyAlaValIleMetPheIleLeuAsnPheGluValValMetGluLysAspMetValGly 139
QY 400 -----AGCAACCAAGAACCGAGGGGGCCGACAGATGG----- 435
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QY 140 SerProAlaHisAspThrAsnHisArgGlyProProThrSerTrpLeuAlaProGlyArg 159
QY 435 ----- 435
Db ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 160 AlaLysThrPheArgLeuLysLeuProAlaLeuAlaLeuThrAlaArgGluSerSer 179
QY 436 ---AAGGACAGGTGGTGGCGCGCCCGATATGGCGGGC---ACGATCCAAGGCTTC 489
Db ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 180 ValArgSerGlyGlyAlaGly-GlyAlaGlyAla-ProGlyAlaValValValAspVal 199
QY 490 AATGCCAACCGGG----- 503
Db ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 199 spLeuThrProAlaAlaProSerSerGluSerLeuAlaLeuAspGluValThrAlaMeta 219
QY 504 -----GCGAGCGGGCGCGTGTCTA----- 521
Db ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 219 spAsnHisValAlaGlyLeuGlyProAlaGluGluArgArgAlaLeuValGlyProGly 233
QY 525 ---CCACCTGTCCGGGCACTGTGACAGACGCCCAAGGCGCAAG---CACAGCTCAAT--- 571
Db ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 239 erProArgSerAlaProGlyGlnLeu-ProSerProArgAlaHisSerLeuAsnPro 251
QY 576 ----- 576

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Db 259 AspAlaSerGlySerSerCysSerLeuAlaArgThrArgSerArgGluSerCysAlaSer 278
QY 577 -----AAGGGGGTGTGGGGAG 594
Db 279 ValArgArgAlaSerSerAlaAspAspIleGluAlaMetArgAlaGlyValLeuProPro 298
QY 595 AAACCAAC----- 603
Db 299 ProProArgHisAlaSerThrGlyAlaMetHisProLeuArgSerGlyLeuLeuAsnSer 318
QY 603 ----- 603
Db 319 ThrSerAspSerAspLeuValArgTyrArgThrIleSerLysIleProGlnIleThrLeu 338
QY 603 ----- 603
Db 339 AsnPheValAspLeuLysGlyAspProPheLeuAlaSerProThrSerAspArgGluIle 358
QY 603 ----- 603
Db 359 IleAlaProLysIleLysGluArgThrHisAsnValThrGluLysValThrGlnValLeu 378
QY 604 -----TTGCGCTGAGTACAAAGTAGCCCGCCATCCGGAAGTCGCCCTTC 645
Db 379 SerLeuGlyAlaAspValLeuProGluTyrLysLeuGlnAlaProArgIleHisArgTrp 398
QY 646 ATCCCTGTTCCACTGTGGGCACTGAGACCACTGGGATGGCTTCATCTGCTCGCCACA 705
Db 399 ThrIleLeuHisTyrSerProPheLysAlaValTrpAspTrpLeuIleLeuLeuVal 418
QY 706 CTCATGTGGCTGCTACCTGCGCTACAGCGGTGTGTGTG-----AGCACGACGCG 756
Db 419 IleTyrThrAlaValPheThrProTyrSerAlaAlaPheLeuLeuLysGluThrGluGlu 438
QY 757 GAGCCAGTGCC-----GCCCGCGCGCCCGCCAGCGTGTGACCTGGCC 801
Db 439 GlyProProAlaThrGluCysGlyTyrAlaCysGlnProLeuAlaValAspLeuIle 458
QY 802 GTGGAGGTCTCTTCATCTGACATGTGTGTAATTTCCGACCACATTCGTGCCAAG 861
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QY 862 TCGGCCAGGTGGTGTGGCCCAAGTCCATTTGCCCTCCACTAGTCACCACTGGTTC 921
Db 479 AsnGluGluValSerHisProGlyArgIleAlaValHisTyrPheLysGlyTrpPhe 498
QY 922 CTGCTGATGTATCGCAGCGCTGCGCTTTCACCTGCTACATGCTTCAAGTCACGTG 981
Db 499 LeuIleAspMetValAlaAlaIleProPheAspLeuLeu----- 511
QY 982 TACTCGGGGCG-----CATCTGTGAAGCGGTGCGCTGTCGCGC 1023
Db 512 IlePheGlySerGlySerGluGluLeuIleGlyLeuLeuLysThrAlaArgLeuLeuArg 531
QY 1024 CTGCTGCGCGCTGCTCCGCGCTGACCGGTACTGCGAGTACAGCGCGGTGCTGACA 1083
Db 532 LeuValArgValAlaArgLysLeuAspArgTyrSerGluTyrGlyAlaAlaValLeuPhe 551
QY 1084 CTGCTCATGGCGGTGTGGCGCTGCTCGCGCAGTGGTGGCTGCTGCTGTTTACAT 1143
Db 552 LeuLeuMetCysThrPheAlaLeuIleAlaHisTrpLeuAlaCysIleTrpTyrAlaIle 571
QY 1144 GCGCAGCGGAGATCGAGACGAGCGAAATCCGAGCTGCTGAGATTGCTGCTCAGGAG 1203
Db 572 GlyAsnMetGluGlnProHisMetAspSer-----ArgIleGlyTrpLeuHisAsn 588
QY 1204 CTGCGCGCGAGTGGAGACTCCCTACTACTGCTGGCGCGGAGCCAGCTGGAGGAAC 1263
Db 589 LeuGlyAspGlnIleGlyLysProTyr----- 598
QY 1264 AGCTCCGCGCGAGTGAACACTGACGACGACGACGAGCGCAACGCGGCGGTGGAG 1323
Db 599 SerSerGly----- 601

QY 1324 CTGCTGGGCGCGCTGCTGCGCAGCGCTACATCACTCCCTCTACTTCGCACTCAGC 1383
Db 602 ---LeuGlyGlyProSerIleLysAspLysTyrValThrAlaLeuTyrPheThrPheSer 620
QY 1384 AGCTCACACAGCTGGGCTTGGCAAGCTGTCCGCCAACACGACACCGAGAAATCTTC 1443
Db 621 SerLeuThrSerValGlyPheGlyAsnValSerProAsnThrAsnSerGluLysIlePhe 640
QY 1444 TCATCTGCACCACTGCTCATCGCGCGCTGATCAGCGGTGTGTGTGGAGAGTGCACG 1503
Db 641 SerIleCysValMetLeuIleGlySerLeuMetTyrAlaSerIlePheGlyAsnValSer 660
QY 1504 GCATCATTCAGCGCATGACGCCCGCGCTTCTGTACACAGCGCACGCGACCTG 1563
Db 661 AlaIleIleGlnArgLeuTyrSerGlyThrAlaArgTyrHisThrGlnMetLeuArgVal 680
QY 1564 CGCGACTACATCCGATCCACCGTATCCCCAGCCCCCTCAAGCAGCGCATGTGGAGTAC 1623
Db 681 ArgGluPheIleArgPheHisGlnIleProAsnProLeuArgGlnArgLeuGluTyr 700
QY 1624 TTCCAGGCCACCTGGCGCGTGAACAATGGCATCGACACACCGAGCTGTGCAGAGCCCTC 1683
Db 701 PheGlnHisAlaTrpSerTyrThrAsnGlyIleAspMetAsnAlaValLeuLysGlyPhe 720
QY 1684 CTGAGAGCTGCGCGCAGACATCGCCATCGACCTGACACAGGAGTCTCTGAG--CTG 1740
Db 721 ProGluCysLeuGlnAlaAspIleCysLeuHisLeuAsnArgSerLeuLeuGlnHisCys 740
QY 1741 CCACCTGTTGAGCGCGCGCAGCGCGCTGCGCGGCACTGTCTCTGCGCCCTGGCGCC 1800
Db 741 LysProPheArgGlyAlaThrLysGlyCysLeuArgAlaLeuAlaMetLysPheLysThr 760
QY 1801 GCCTTCTGCAGCGCGCGGAGTACCTCATCCACCAAGCGGATGCCCTGCGAGCCCTCTAC 1860
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QY 1861 TTTGCTCTGCTGCTCCATCGAGGTGTCAAGGTGGCACCCTGCTGCCATCTCAGG 1920
Db 781 PheIleSerArgGlySerIleGluIleLeuArgGlyAspValValAlaIleLeuGly 800
QY 1921 AAGGCGACCTGATCGGCTGTGAGCTGCCCGCGGAGCAGGTGGTAAAGCCCAATGCC 1980
Db 801 LysAsnAspIlePheGlyGluProLeuAsnLeuTyrAlaArgProGlyLysSerAsnGly 820
QY 1981 GACGTGAAGGGGCTGACGTACTGCTGCTGCTGAGTGTCTGCGAGTGGCTGGCTGCACGAC 2040
Db 821 AspValArgAlaLeuThrTyrCysAspLeuHisLysIleHisArgAspAspLeuLeuGlu 840
QY 2041 AGCCTTGGCTGTACCCCGAGTTTGGCGCGCTTCAGTCTGCGCTCCGAGGGGAGCTC 2100
Db 841 ValLeuAspMetTyrProGluPheSerAspHisPheTrpSerSerLeu-----GluIle 858
QY 2101 AGCTACAACTG-----GGTCTGGGGAGGCTCTGCAGAGTGCAC 2142
Db 859 ThrPheAsnLeuArgAspThrAsnMetIleProGlySerProGlySerThrGluLeuGlu 878
QY 2143 ACCAGCTCCCTGAGCGCGACAATACCTTATGTCCACGCTGGAGGAGAGGACACAGAT 2202
Db 879 GlyGlyPheSerArgGlnArgLysArgLysLeuSerPheArgArgArgThrAspLysAsp 898
QY 2203 GGGGAGCAGGGCCCCACGGTCTCCCGAGCCCCAGCTGATGAGCCCTCCAGCCCCCTGCTG 2262
Db 899 ThrGluGln----- 901
QY 2263 TCCCTCTGGCTGACCTCTCATCTCAGCTGCCAAGCTGCTATCCCCACCTCGAAGCA 2322
Db 902 ---ProGlyGluValSerAla-----LeuGlyProGlyArgAlaGly 914
QY 2323 CCGCGCGCTCTAGTGTGGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2382
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Search completed: September 1, 2004, 16:07:05
Job time : 188 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 1, 2004, 15:01:21 ; Search time 315.5 Seconds
(without alignments)
5824.688 Million cell updates/sec

Title: US-09-965-830-1_COPY_6_3257

Perfect score: 6089

Sequence: 1 atgcgcgcacatgggggcct.....aagaagcgcacaggggtctga 3252

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 3172214

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=A_Geneseq_29Jan04 -Qfmt=faстан -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001s.*
- 5: Geneseq2002s.*
- 6: Geneseq2003as.*
- 7: Geneseq2003bs.*
- 8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	5704	93.7	1083	7	Adc47040 BECI pota
3	5704	93.7	1083	7	Ade55604 Human Pro
4	5698	93.6	1083	3	AAY44778 Human Elk
5	5697	93.6	1083	3	AAY44779 Human Elk
6	5696	93.5	1083	3	AAY44780 Human Elk
7	5695	93.5	1083	3	AAY44781 Human Elk
8	5695	93.5	1083	3	AAY44835
9	5688	93.4	1080	3	AAY77738 Human ESK
10	5675	93.2	1083	3	AAY44904 Monkey po

11	5675	93.2	1083	6	ABU61670
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13	5649.5	92.8	1082	2	AAY34128
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16	2529.5	41.5	1107	6	ABU61677
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18	2515	41.3	1102	3	AAY83028
19	2515	41.3	1102	6	ABU61692
20	2515	41.3	1102	7	ADB66823
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22	2347	38.5	457	3	AAY77739
23	1901	31.2	1284	6	ABU61674
24	1901	31.2	1284	7	ADB66801
25	1901	31.2	1311	4	ABU61234
26	1835.5	30.1	542	6	ABU61671
27	1835.5	30.1	542	7	ADB66797
28	1832.5	30.1	542	3	AAY44905
29	1551	25.5	1159	2	AAY32020
30	1551	25.5	1159	3	AAY85405
31	1551	25.5	1159	4	AAB70939
32	1551	25.5	1159	4	AAM51812
33	1551	25.5	1159	5	AAU99167
34	1551	25.5	1159	6	ABP71697
35	1551	25.5	1159	6	ABU61673
36	1551	25.5	1159	6	ABP71255
37	1551	25.5	1159	7	ADB66800
38	1551	25.5	1159	7	ADD02769
39	1550	25.5	1159	3	AAY85406
40	1537.5	25.3	1163	7	ADD45069
41	1533.5	25.2	1163	3	AAY83031
42	1509.5	24.8	994	7	ADB68018
43	1508.5	24.8	994	5	ABG31253
44	1487	24.4	290	6	ABU61672
45	1487	24.4	290	7	ADB66799

ALIGNMENTS

RESULT 1

AAY22426

ID AAY22426 standard; protein; 1083 AA.

AC AAY22426;

XX

DT 28-SEP-1999 (first entry)

XX

DE Human brain specific potassium channel protein sequence.

XX

KW Brain specific potassium channel; human; central nervous system disorder;

XX

XX dementia; cerebral ischaemic sclerosis; therapy.

OS Homo sapiens.

XX

PN WO9937677-A1.

XX

PD 29-JUL-1999.

XX

PF 20-JAN-1999; 99WO-JF000190.

XX

PR 23-JAN-1998; 98JP-00011434.

XX

PR 04-DEC-1998; 98JP-00346198.

XX

PA (YAMA) YAMANOUCHI PHARM CO LTD.

 XX || PI | Miyake A, Mochizuki S, Yokoi H; |
DR	WPI; 1999-458663/38.
DR	N-PSDB; AAX84910.
XX	
PT	Potassium channel protein expressed specifically in brain tissue and
XX	method for its production.
XX	

PS Claim 1; Page 33-39; 63pp; English.

XX This sequence is the potassium channel protein of the invention, that is
 CC expressed specifically in brain tissue. The protein is used to treat and
 CC investigate disorders of the central nervous system such as dementia and
 CC cerebral ischaemic sclerosis

XX SQ Sequence 1083 AA;

Alignment Scores:
 Pred. No.: 0 Length: 1083
 Score: 5704.00 Matches: 1083
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 93.68% Indels: 0
 DB: 2 Gaps: 0

US-09-965-830-1_COPY_6_3257 (1-3252) x ANY22426 (1-1083)

QY 1 ATGCGCGGCATCGGGGCTCTGCGCTCGAAGACACACCTTCTGGACACCATCGCTACG 60
 DB 1 MetProAlaMetArgGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20

QY 61 CGCTTCGACGGCAGCAGTAACTTCGTGCTGGGCAAGCCCGAGTGGGGGCTCTTC 120
 DB 21 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnValAlaGlyLeuPhe 40

QY 121 CCGGTGCTTACTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 DB 41 ProValValTyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal 60

QY 181 ATGACGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 DB 61 MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArg 80

QY 241 CAACAGATCCGAAGCCCTCGACGACGACAGAGTTCAGGCTCAAGCTGAGTCTGCTGCTAC 300
 DB 81 GlnGlnIleArgGlyAlaLeuAspGluHisLysGluPheLysAlaGluLeuLeuTyr 100

QY 301 CGSAGAGCGGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 DB 101 ArgLysSerGlyLeuProPheTrpCysLeuLeuAspValIleProIleLysAsnGluLys 120

QY 361 GGGAGGTGGCT 420
 DB 121 GlyGluValAlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGly 140

QY 421 GGGCCGACAGATGGAAGAGACAGTGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
 DB 141 GlyProAspArgTrpLysGluThrGlyGlyArgArgArgTrpGlyArgAlaArgSer 160

QY 481 AAAGGCTTCAATGCCAACCG 540
 DB 161 LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis 180

QY 541 CTGCAAGCAGCCCAAGGGCAAGCACAAGCTCAATAAGGGGTGTTGGGGAGAACCA 600
 DB 181 LeuGlnLysGlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyGluLysPro 200

QY 601 AACTGCTGAGTACAAAGTAGCGGCGCATCCGGAAGTCGCGCTTCATCTGTTGCACTGT 660
 DB 201 AsnLeuProGluTyrLysValAlaAlaIleArgLysSerProPheIleLeuLeuHisCys 220

QY 661 GGGGCACTGAGACCTCGGATGGCTTCATCTGCTCGCCACACTCTATGTGGCTGTC 720
 DB 221 GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal 240

QY 721 ACTGTGCTTACAGCGT 780
 DB 241 ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro 260

QY 781 CCCAGCCTCTGTGACCTGGCGGTGGAGTCTCTTCATCTGACATTGCTGAATTC 840

DB 261 ProSerValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPhe 280

QY 841 CQTACCATTCGTCTCCAAGTCGGGCGCAGGTGGTGTGTGGCCCCAAAGTCATTGTCCTC 900

DB 281 ArgThrThrPheValSerLysSerGlyGlnValValPheAlaProLysSerIleCysLeu 300

QY 901 CACTACGTCAACACCTGGTTCCTGCTGATGTCATCGCAGCGCTGCCCTTCACCTGCTCA 960

DB 301 HistyrValThrThrTrpPheLeuLeuAspValIleAlaAlaLeuProPheAspLeuLeu 320

QY 961 CATGCTTCAAGTCAAGTCAAGTCTCGGGGCCCATCTGCTGAAGACGGTGGCGCTGCTG 1020

DB 321 HisAlaPheLysValAsnValTyrPheGlyAlaHisLeuLeuLysThrValArgLeuLeu 340

QY 1021 CGCTGCTGCGCTGCTCTCCGCGGTGGACCGGTACTCGACATCAGACGCGCTGGTGGCTG 1080

DB 341 ArgLeuLeuArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValValLeu 360

QY 1081 ACACGTCTCATGCGCGTGTTCGCTGCTGCGGCACTGGTGGCTGCGCTGCTGCTGCTTTAC 1140

DB 361 ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr 380

QY 1141 ATTGGCCAGCGGAGATCGAGACGCAATCCGAGTCCCTGAGTCCCTGAGTTCGGTGGCTG 1200

DB 381 IleGlyGlnArgGluIleGluSerSerGluSerGluLeuProGluIleGlyTrpLeuGln 400

QY 1201 GAGTGGCGCGCGCTGAGACTCCCTACTACTGCTGGTGGCGGGAGGCGGCTGAGGG 1260

DB 401 GluLeuAlaArgArgLeuGluThrProTyrTyrLeuValGlyArgArgProAlaGlyGly 420

QY 1261 ACAGCTCCGGCGAGGTGACAACTGACAGCAGCAGCAGGAGGAGGAGGAGGAGGAGGAG 1320

DB 421 AsnSerSerGlyGlnSerAspAsnCysSerSerSerSerSerSerSerSerSerSerSer 440

QY 1321 GAGTGTCTGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380

DB 441 GluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeu 460

QY 1381 AGCAGCTCACGAGCTGGCTGGCAACGCTGTCGCGCAACACGACACCGGAGAGATC 1440

DB 461 SerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGluLysIle 480

QY 1441 TTCTCCATCTGACCATGCTCATCGCGCGCTGATGCTGCTGCTGCTGCTGCTGCTGCTG 1500

DB 481 PheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValValPheGlyAsnVal 500

QY 1501 ACGGCTCATCATCGCGCATGTACGCGCGCGCTTCTGTGTACACACCGCGCACCGCGCAC 1560

DB 501 ThrAlaIleIleGlnArgMetTyrAlaArgPheLeuTyrHisSerArgThrArgAsp 520

QY 1561 CTGCGGACTTACATCCGATCCACCGTATCCCGAGCCCTCAAGCAGCGCATGCTGGAG 1620

DB 521 LeuArgAspTyrIleArgIleHisArgIleProLysProLysGlnArgMetLeuGlu 540

QY 1621 TACTTCCAGGCCACCTGGCGGTGAACATGGATGCGACACCGAGCTGCTGCGAGAGC 1680

DB 541 TyrPheGlnAlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeuGlnSer 560

QY 1681 CTCCTGTGACGAGTGGCGGACATCGCATCGCATCGCATCGCATCGCATCGCATCGCATCG 1740

DB 561 LeuProAspGluLeuArgAlaAspIleAlaMetHisLeuHisLysGluValLeuGlnLeu 580

QY 1741 CCACTGTTGAGCGCGCGCGCTGCTGCGGGGCTGCTGCGGGGCTGCTGCGGGGCTGCGGG 1800

DB 581 ProLeuPheGluAlaAlaSerArgGlyCysLeuArgAlaLeuSerLeuAlaLeuArgPro 600

QY 1801 GCCTTCTGACGCGCGCGGAGTACCTCATCCCAAGCGCATCCCTGCGAGGCGCTCTAC 1860

DB 601 AlaPheCysThrProGlyGluTyrLeuIleHisGlnGlyAspAlaLeuAlaLeuTyr 620

QY 1861 TTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920

DB 621 PheValCysSerGlySerMetGluValLeuLysGlyGlyThrValLeuAlaIleLeuGly 640

US-09-965-830-1_COPY_6_3257 (1-3252) x ADC47040 (1-1083)

QY 1 ATGCCGGCCTGCGGGGCTCTGCGGCTCAGAACACCTTCCTGGACACCATCGCTACG 60
 Db 1 MetProAlaMetArgGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20
 QY 61 CGCTTCGACGGCAGCACAGTAACCTTCGTGCTGGCGCAACCGCCAGTGGCGGGCTCTTC 120
 Db 21 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnValAlaGlyLeuPhe 40
 QY 121 CCCGTGGTCTACTGCTCTGATGGCTTCGTGACCTCACGGGCTTCCTCCGGGCTGAGTTC 180
 Db 41 ProValValTyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal 60
 QY 181 ATGACGGGGCTGCTGCTGCT 240
 Db 61 MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArg 80
 QY 241 CACAGATCCGCAAGGCCCTGACGAGCAGCAGAGGAGTTCAGAGGCTGAGCTGATCTCTGTAC 300
 Db 81 GlnGlnIleArgLysAlaLeuAspGluHisLysGluPheLysAlaGluLeuIleLeuTyr 100
 QY 301 CGGAAGAGGGGCTCCGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
 Db 101 ArgLysSerGlyLeuProPheTrpCysLeuLeuAspValIleProIleLysAsnGluLys 120
 QY 361 GGGGAGGTGGCT 420
 Db 121 GlyGluValAlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGly 140
 QY 421 GGGCCCGCAGATGAGAGAGACAGGTGGTGGCGCGCGCGATATGATCCCGGGCACGATCC 480
 Db 141 GlyProAspArgTrpLysGluThrGlyGlyArgArgGlyValPheGlyGluLysPro 200
 QY 481 AARGGCTTCAATGCAACCGCGGCGAGCGGGCGGTCTCTACCACTCTCGGGCAC 540
 Db 161 LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis 180
 QY 541 CTCGAGNAGCCAGGCGCAGCACAAGCTCAATAAGGGGNGTTGGGGAGAAACCA 600
 Db 181 LeuGlnLysGlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyGluLysPro 200
 QY 601 AACTTGCTCAGTACAAAGTAGCGCCATCCGGAAGTCCGCTTCATCTCTGTTCATCTGT 660
 Db 201 AsnLeuProGluTyrLysValAlaAlaIleArgLysSerProPheIleLeuLeuHisCys 220
 QY 661 GGGGCATGAGACCACTGGGATGGCTTATCTCTGCTCGCCACACTCTATGTGGCTGTC 720
 Db 221 GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal 240
 QY 721 ACTGTGCTTACAGCGTGTGTGAGCAGCAGCGGAGCCAGTGGCGCGCGCGCGCGCG 780
 Db 241 ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro 260
 QY 781 CCCAGCGTCTGTGACTGCGCGTGGAGTCTCTCTTCATCTTCATCTGCTGCTGCTGCT 840
 Db 261 ProSerValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPhe 280
 QY 841 CGTACCACTTCGTCGTCAGTCCGCGCCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 900
 Db 281 ArgThrThrPheValSerLysSerGlyGlnValPheAlaProLysSerIleCysLeu 300
 QY 901 CACTACGTCACACCTGCTCTCTGCTGATGTCATCGAGCGGCTGCCCTTTGACCTGTGTA 960
 Db 301 HisTyrValThrThrThrPheLeuLeuAspValIleAlaLeuProPheAspLeuLeu 320
 QY 961 CATGCTCTCAGAGTCAACGTGTACTTCGGGGCCCATCTGCTGAAGACGGTGGCGCTGTG 1020
 Db 321 HisAlaPheLysValAsnValTyrPheGlyAlaHisLeuLeuLysThrValArgLeuLeu 340
 QY 1021 CGCTGCTCGGCTGCTCTCGGGCTGGACCGGTACTCGCACTACAGCGCGCTGTGTGCTG 1080
 Db 341 ArgLeuLeuArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValValLeu 360

QY 1081 ACATGCTCATGCGCGCTGTTCCGCTCTCGGCACTGSGCTGCTGCTGCTGCTGCTGCTGCT 1140
 Db 361 ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr 380
 QY 1141 ATTGCGCAGCGGAGATCGAGAGCAGCAATCCGAGCTGCCTCGATGCTGCTGCTGCTGCTGCT 1200
 Db 381 IleGlyGlnArgGluIleSerSerGluSerGluLeuProGluIleGlyTrpLeuGln 400
 QY 1201 GAGCTGGCGCGCGACTGAGACTCCCTACTACTGCTGGCGCGGAGCGGCGGCGGAGG 1260
 Db 401 GluLeuAlaArgArgLeuGluThrProTyrTyrLeuValGlyArgArgProAlaGlyGly 420
 QY 1261 AACAGCTCCGCGCAGAGTGAACATGTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1320
 Db 421 AsnSerSerGlyGlnSerAspAsnCysSerSerSerSerSerSerSerSerSerSerSer 440
 QY 1321 GAGCTGCTGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
 Db 441 GluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeu 460
 QY 1381 AGCAGCTCACCCAGCGCTGGCTTCGGCAACGCTGTCGCCCAACACGACACCCGAGATC 1440
 Db 461 SerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGluLysIle 480
 QY 1441 TTCTCCATCTGCACCATGCTCATCGCGCGCTGATGACGCGGTGGTGGTGGTGGTGGTGG 1500
 Db 481 PheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValValPheGlyAsnVal 500
 QY 1501 ACGGCTCATCATCAGCGCATGTACGCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
 Db 501 ThrAlaIleIleGlnArgMetTyrAlaArgArgPheLeuTyrHisSerArgThrArgAsp 520
 QY 1561 CTCGCGCATACATCCGCTATCCAGCTATCCCAAGCCCTCAAGCAGCGCATGCTGGAG 1620
 Db 521 LeuArgAspTyrIleArgIleHisArgIleProLysProLeuLysGlnArgMetLeuGlu 540
 QY 1621 TACTTCCAGCCACCTGGCGGTGAACATGATGATGATGATGATGATGATGATGATGATGATG 1680
 Db 541 TyrPheGlnAlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeuLeuGlnSer 560
 QY 1681 CTCCTTACGAGCTGGCGCAGACATCGCCATCGACCTGACCAAGAGGTCTGTCAGCTG 1740
 Db 561 LeuProAspGluLeuArgAlaAspIleAlaMetHisLeuHisLysGluValLeuGlnLeu 580
 QY 1741 CCAGTGTTCAGCG 1800
 Db 581 ProLeuPheGluAlaAlaSerArgGlyCysLeuArgAlaLeuSerLeuAlaLeuArgPro 600
 QY 1801 GCCTTCTGCG 1860
 Db 601 AlaPheCysThrProGlyGlyTyrIleIleGlnGlyAspAlaLeuGlnAlaLeuTyr 620
 QY 1861 TTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
 Db 621 PheValCysSerGlySerMetGluValLeuLysGlyGlyThrValLeuAlaIleLeuGly 640
 QY 1921 AAGCGGACCTGATCGGCTGTGAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1980
 Db 641 LysGlyAspLeuIleGlyCysGluLeuProArgGluGlnValValLysAlaAsnAla 660
 QY 1981 GACGTGAGGGGCTGACCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
 Db 661 AspValLysGlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGlyLeuHisAsp 680
 QY 2041 AGCTTGGCTGTATCCCGAGTTTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2100
 Db 681 SerLeuAlaLeuTyrProGluPheAlaProArgPheSerArgGlyLeuArgGlyGluLeu 700
 QY 2101 AGCTCAACCTGGTGGTGGGAGGCTGTCGAGAGGTGACACAGCTCCCTGCTGAGCGGC 2160
 Db 701 SerTyrAsnLeuGlyAlaGlyGlySerAlaGluValAspThrSerSerLeuSerGly 720

QY	2161	GACAA	TACCC	TTATGTCC	ACGCTGGAGG	AAGAGACAGATGGG	AGCAGGCGCC	CAACG	2220
DB	721	AspAsn	ThrLeu	MetSerThr	LeuGlu	GlySer	ThrLeu	AspGlyGlu	740
QY	2221	GNCTCC	CCAGCC	CCAGCTAT	GAGCC	TCCAGCC	CCCTGCTGT	CCCTCGCTGC	2280
DB	741	ValSer	ProAla	ProAla	AspGlu	ProSer	ProLeu	LeuSerPro	760
QY	2281	TCATCCT	CAGCTGC	CAAGCTGT	ATNCCC	CACTGTCG	ACACAC	CCCGCTCG	2340
DB	761	SerSer	SerAla	Ala	Leu	LeuSer	ProArg	ArgThrAla	780
QY	2341	GGCAG	AGGAG	CCCGCAGG	CAGGCG	CAGGGCTT	TGAAGCTG	AGGCTG	2400
DB	781	GlyA	ArgGly	ArgPro	GlyArg	Ala	GlyAla	Leu	800
QY	2401	CCACG	GGCCCT	TAGAGG	GCTAC	GGCTG	CCCCCAT	GTCATG	2460
DB	801	ProArg	Ala	Leu	Glu	GlyLeu	ArgLeu	ProMet	820
QY	2461	AGCCCC	CAGG	TAGTAG	TGGCAT	TGACAG	CGCTGT	GGCTCG	2520
DB	821	SerPro	ArgVal	Val	Asp	GlyLeu	AspGly	CysGly	840
QY	2521	TTCCG	CGTGG	CCAGTCT	TGGCC	CGGAAT	GTAGAC	AGCCCT	2580
DB	841	PheArg	ValGly	GlnSer	GlyPro	GluCys	SerSer	ProSer	860
QY	2581	GGCCT	GTCACT	GTTC	CCCAT	TGGCC	CAGCG	AGCAG	2640
DB	861	GlyLeu	LeuThr	Val	Pro	His	GlyPro	SerGlu	880
QY	2641	CTTCG	GAGCG	GTGAC	AGACTGT	CGAC	AGCTGT	CGAC	2700
DB	881	LeuArg	GlnAla	ValThr	GluLeu	SerGlu	GlnVal	LeuGln	900
QY	2701	TCATT	TCGCC	AGGTGT	GCAGCT	TGTCT	CGGCC	CCACAG	2760
DB	901	SerLeu	ArgGln	AlaVal	GlnLeu	ValLeu	AlaPro	His	920
QY	2761	GCATC	GGGAG	AGGGCG	GTGCC	CAGC	AGCACT	CCGGCT	2820
DB	921	AlaSer	GlyGlu	GlyPro	CysPro	AlaSer	ThrSer	GlyLeu	940
QY	2821	GACACT	GGGC	CATN	CTCT	ACTGCT	CGAC	CCCGC	2880
DB	941	AspThr	GlyAla	SerTyr	CysLeu	GlnPro	ProAla	GlySer	960
QY	2881	TGCCCC	ACCCCT	CGTCCG	GGGCTCT	CTCCCT	CATGG	CACCTG	2940
DB	961	TrpPro	HisPro	ArgPro	GlyPro	ProPro	LeuMet	AlaPro	980
QY	2941	GGCTCT	CAGAGT	TC	CCCTGG	CGCTCG	AGCC	CAGCTT	3000
DB	981	AlaSer	GlnSer	SerPro	TrpPro	ArgAla	ThrAla	PheTrp	1000
QY	3001	GAGC	CCCTG	CGCTC	AGGAC	CTCTG	CTGTAG	CCCGC	3060
DB	1001	GluPro	ProAla	SerGly	AspLeu	CysSer	GluPro	SerThr	1020
QY	3061	TC	TGAG	GAAG	GGGCTAG	GA	CTGGG	CGCCCTG	3120
DB	1021	SerGlu	GluGly	Ala	ArgThr	GlyPro	AlaGlu	ProVal	1040
QY	3121	ACT	GAG	AGC	CCCC	AC	AGGTC	AGGCG	3180
DB	1041	ThrGly	GluPro	ProPro	GlySer	GlyLeu	AlaLeu	ProTrp	1060
QY	3181	GAG	ATG	GTCT	TAT	TGGCTG	CCATGG	CTCTG	3240
DB	1061	GluMet	ValLeu	Leu	Leu	Leu	Leu	Leu	1080
QY	3241	AC	AGG	GGT	C	3249			

REF ID: A66991 3243

Alignment Scores:

Db	1081	ThrGlyVal	1083
RESULT 3			
ADRS5604			
ID	ADRS5604	standard; protein; 1083	AA.
XX			
AC	ADE5604;		
XX			
DT	29-JAN-2004	(first entry)	
XX			
DE	Human Protein XP_035483,	SEQ ID NO 1423.	
XX			
KW	Human; pain; neuronal tissue; gene therapy;		
KW	spinal segmental nerve injury; chronic constriction injury; CCI;		
KW	spared nerve injury; SNI; Chung.		
XX			
OS	Homo sapiens.		
XX			
PN	WO2003016475-A2.		
XX			
PD	27-FEB-2003.		
XX			
PF	14-AUG-2002; 2002WO-US025765.		
XX			
PR	14-AUG-2001; 2001US-0312147P.		
PR	01-NOV-2001; 2001US-0346382P.		
PR	26-NOV-2001; 2001US-033347P.		
XX			
PA	(GEO) GEN HOSPITAL CORP.		
PA	(FARB) BAYER AG.		
XX			
PI	Woolf C, D'urso D, Befort K, Costigan M;		
XX			
DR	WPI; 2003-268312/26.		
DR	GENBANK; XP_035483.		
XX			
PT	New composition comprising two or more isolated polypeptides, useful for		
PT	preparing a medicament for treating pain in an animal.		
XX			
PS	Claim 1; Page; 1017pp; English.		
XX			
CC	The invention discloses a composition comprising two or more isolated rat		
CC	or human polynucleotides or a polynucleotide which represents a fragment,		
CC	derivative or allelic variation of the nucleic acid sequence. Also		
CC	claimed are a vector comprising the novel polynucleotide, a host cell		
CC	comprising the vector, a method for identifying a nucleotide sequence		
CC	which is differentially regulated in an animal subjected to pain and a		
CC	kit to perform the method, an array, a method for identifying an agent		
CC	that increases or decreases the expression of the polynucleotide sequence		
CC	that is differentially expressed in neuronal tissue of a first animal		
CC	subjected to pain, a method for identifying a compound which regulates		
CC	the expression of a polynucleotide sequence which is differentially		
CC	expressed in an animal subjected to pain, a method for identifying a		
CC	compound that regulates the activity of one or more of the		
CC	polynucleotides, a method for producing a pharmaceutical composition, a		
CC	method for identifying a compound or small molecule that regulates the		
CC	activity in an animal of one or more of the polypeptides given in the		
CC	specification, a method for identifying a compound useful in treating		
CC	pain and a pharmaceutical composition comprising the one or more		
CC	polypeptides or their antibodies. The polynucleotide or the compound that		
CC	modulates its activity is useful for preparing a medicament for treating		
CC	pain (e.g. spinal segmental nerve injury (Chung), chronic constriction		
CC	injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene		
CC	therapy). The sequence presented is a human protein (shown in Table 2 of		
CC	the specification) which is differentially expressed during pain. Note:		
CC	The sequence data for this patent did not form part of the printed		
CC	specification, but was obtained in electronic form directly from WIPO at		
CC	ftp.wipo.int/pub/published_pct_sequences.		
XX			
SQ	Sequence 1083	AA:	

Db 681 SerLeuAlaLeuTyrProGluPheAlaProArgPheSerArgGlyLeuArgGlyGluLeu 700
QY 2101 AGCTACACCTGGGTGCTGGGAGAGTCTGCAGAGTGGACACCACTCCCTGAGCGC 2160
Db 701 SerTyrAsnLeuGlyAlaGlyGlySerAlaGluValAspThrSerLeuSerGly 720
QY 2161 GACATACCTTTATGTCACGCTGGAGGAGAGACAGATGGGAGCAGGCGCCACG 2220
Db 721 AspAsnThrLeuMetSerThrLeuGluGlyValThrAspGlyGluGlnGlyProThr 740
QY 2221 GTCTCCCGAGCCAGCTGATGAGCCCTCCAGCCCTGCTGTCCTGCTGCTCCTCC 2280
Db 741 ValSerProAlaProAlaAspGluProSerSerProLeuLeuSerProGlyCysThrSer 760
QY 2281 TCATCTCAGCTGCCAAGCTGTATCCCAAGCTGCGAGCAGCAGCCCGGCTGCTAGGT 2340
Db 761 SerSerSerAlaAlaLysLeuLeuSerProArgArgThrAlaProArgProArgLeuGly 780
QY 2341 GGCAGAGGAGCCAGGCGAGGCGGCTTTGAAGCTGAGCTGCGCCCTCTGCTCC 2400
Db 781 GlyArgGlyArgProGlyArgAlaGlyAlaLeuLysAlaGluAlaGlyProSerAlaPro 800
QY 2401 CCACGGCCCTAGAGGGCTAGGCTGCGCCCTCCATGCCATGGAATGTCCTCCAGATCG 2460
Db 801 ProArgAlaLeuGluGlyLeuArgLeuProProMetProTrpAsnValProProAspLeu 820
QY 2461 AGCCCCAGGCTAGTAGTGGCATTCAGACGCTGTGGCTCGACAGCCCAAGTCTCT 2520
Db 821 SerProArgValValAspGlyLeuAspGlyCysGlySerAspGlnProLysPheSer 840
QY 2521 TTCGCGTGGGCGCTGCGCCCGAATGTAGCAGCAGCCCTCCCTCGACAGAGAGC 2580
Db 841 PheArgValGlyGlnSerGlyProGlyCysSerSerProSerProGlyProGluSer 860
QY 2581 GGCCTGCTCACTGTTCCCATGGGCGCCAGGCAAGAAACACAGACACATGACACAG 2640
Db 861 GlyLeuLeuThrValProHisGlyProSerGluAlaArgAsnThrAspThrLeuAspLys 880
QY 2641 CTTGGCAGGGCGTGACAGAGCTGTGACAGAGGTGTGACAGATCGGAGAGGAGCTCG 2700
Db 881 LeuArgGlnAlaValThrGluLeuSerGluGlnValLeuGlnMetArgGluGlyLeuGln 900
QY 2701 TCATCTGCCAGGCTGTCAGCTGTCTGCGCGCCACAGGGGTCCTGCGCTCGG 2760
Db 901 SerLeuArgGlnAlaValGlnLeuValLeuAlaProHisArgGluGlyProCysProArg 920
QY 2761 GCATCGGAGAGGGCGTGCAGCCAGCAGCCTCCGGCTTCTGACGCTCTGTGTGTG 2820
Db 921 AlaSerGlyGluGlyProCysProAlaSerThrSerGlyLeuLeuGlnProLeuCysVal 940
QY 2821 GACACTGGGCGATCTCTCTACTGCTGAGCCCGCCAGCTGCTGCTGCTGAGTGGGACT 2880
Db 941 AspThrGlyAlaSerSerTyrCysLeuGlnProProAlaGlySerValLeuSerGlyThr 960
QY 2881 TGGCCCAACCTCTGCTGGGCGCTCTCCCTCATGGCACCTCGCCCTGGGGTCCCCCA 2940
Db 961 TrpProHisProArgProGlyProProProLeuMetAlaProTrpProTrpGlyProPro 980
QY 2941 GCGTCTCAGAGTCCCTGCTGCGCCAGCCAGCAGCTTCTGGACCTCCACTCAGATCA 3000
Db 981 AlaSerGlnSerProTrpProArgAlaThrAlaPheTrpThrSerThrSerAspSer 1000
QY 3001 GAGCCCTCTGCTCAGGAGACTCTGCTGAGCCCGACAGCCCTGCTGCTGCTGCTGCT 3060
Db 1001 GluProProAlaSerGlyAspLeuCysSerGluProSerThrProAlaSerProProPro 1020
QY 3061 TCTGAGGAGGGCTAGGATGGGCGCCGACAGCTGTGAGCCAGGCTGAGGCTTACGAGC 3120
Db 1021 SerGluGluGlyAlaArgThrGlyProAlaGluProValSerGlnAlaGluAlaThrSer 1040
QY 3121 ACTGGAGAGCCCGACAGAGGTGAGGGGCTGCGCTTGGCGTGGGACCCCGACAGCTG 3180

Db 1041 ThrGlyGluProProGlySerGlyGlyLeuAlaLeuProTrpAspProHisSerLeu 1060
QY 3181 GAGATGGTGTATTGCTGCCATGGCTCTGGCACAGTCCAGTGGACCCAGGAAGAGGC 3240
Db 1061 GluMetValLeuIleGlyCysHisGlySerGlyThrValGlnTrpThrGlnGluGly 1080
QY 3241 ACAGGGGTC 3249
Db 1081 ThrGlyVal 1083
RESULT 4
ID AAY44778
XX AAY44778 standard; protein; 1083 AA.
AC AAY44778;
XX
DT 04-MAY-2000 (first entry)
XX
DE Human Elk voltage gated potassium channel subunit monomer.
KW Voltage gated potassium channel subunit; VGPCs; hElk; human; stroke;
KW Kv superfamily; Bag family; ether a go-go; Elk subfamily; modulator;
KW chromosome 12q13; resting potential; cell excitability; seizure; CNS;
KW migraine; psychotic; anticonvulsant; neuroprotective; ion flux disorder;
KW reporter molecule; detection; gene therapy; antimigrane;
KW neuroprotective; antipsychotic.
XX
OS Homo sapiens.
FH
FH Key Location/Qualifiers
Region 452..710
FT /label= Extended P-S6 region
FT /note= "Extended Pore-S6 region with conserved amino
FT acids"
FT Region 452..514
FT /label= P-S6 region
FT /note= "Pore-S6 region with conserved amino acids"
FT Misc-difference 965
FT /note= "Encoded by CGT"
PN WO200001819-A1.
XX
XX 13-JAN-2000.
PD
PF 30-JUN-1999; 99WO-US014944.
XX
PR 01-JUL-1998; 98US-0091469P.
PR 21-JAN-1999; 99US-0116621P.
XX
PA (ICAG-) ICAGEN INC.
XX
PI Jegla TJ, Wickenden A;
XX
XX WPI; 2000-182114/16.
DR N-PSDB; AAZ50119.
XX
XX Novel polynucleotides and polypeptides of human ELK, a voltage-gated
XX potassium channel subunit useful for treating ELK miss-expression and to
XX screen for inhibitors and activators of such channels.
PS Claim 13; Page 62; 79pp; English.
XX
CC The present sequence is the human ELK (hElk) polypeptide monomer,
CC comprising an alpha subunit of the voltage-gated potassium channel
CC (VGPCs). It is a member of the Kv (Voltage gated potassium) superfamily,
CC Bag (ether a go-go) family and Elk subfamily of potassium channel
CC monomers. hElk gene is mapped to chromosome 12q13. It is isolated from
CC brain and maintains the resting potential and controls excitability of
CC the cell. It has antimigrane, cerebroprotective, antipsychotic,
CC neuroprotective and anticonvulsant activity. The hElk polypeptide can be
CC used to screen for modulators of VGPCs, that are useful for treating
CC abnormal ion flux disorders, CNS disorders such as migraines, hearing and
CC vision problems, seizures, psychotic disorders and to prevent strokes. It

CC can be used as a marker for diagnosis of diseases linked to this gene and
 CC also as reporter molecule in detection systems. The polynucleotide is
 CC useful for gene therapy, to rectify Elk expression
 XX
 SQ Sequence 1083 AA;

Alignment Scores:
 Pred. No.: 0 Length: 1083
 Score: 5698.00 Matches: 1082
 Percent Similarity: 99.91% Conservative: 0
 Best Local Similarity: 99.91% Mismatches: 1
 Query Match: 93.58% Indels: 0
 DB: 3 Gaps: 0

US-09-965-830-1_COPY_6_3257 (1-3252) x AAY44778 (1-1083)

QY	1	ATGCGCGCATCGGGGCTCTGCGGCTCAGAACACCTTCTGACACCATCGCTACG	60
DB	1	MetProAlaMetArgGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr	20
QY	61	CGCTTCGACGGCAGCACAGTAATCTGCTCGGCAACGCCAGGTGGGGGCTCTTC	120
DB	21	ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnValAlaGlyLeuPhe	40
QY	121	CCCGTGTCTACTGCTCTGATGGCTTCTGTACCTCACGGGCTTCTCCGGCTGAGGTC	180
DB	41	ProValValTyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal	60
QY	181	ATCAGCGGGCTGTGCTCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	240
DB	61	MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArg	80
QY	241	CAACAGATCGCAGGCGCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	300
DB	81	GlnGlnIleArgLysAlaLeuAspGluHisLysGlnPheLysAlaGluLeuLeuTyr	100
QY	301	CGGAAGAGCGGCTCCGCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	360
DB	101	ArgLysSerGlyLeuProPheTyrCysLeuLeuAspValIleProLysAsnGluLys	120
QY	361	GGGAGGTGGCTCTCTCTAGTCTCTCAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	420
DB	121	GlyGlnValAlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGly	140
QY	421	GGCCCCGACAGATGAGGACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	480
DB	141	GlyProAspArgTyrLysGlnThrGlyGlyArgArgArgTyrGlyArgAlaArgSer	160
QY	481	AAAGCTTCAATGCAACCGCGGCGAGCGGCGGCTGCTCTACCACTGCTCGGGGAC	540
DB	161	LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis	180
QY	541	CTGAGAAGCGCCCAAGGGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	600
DB	181	LeuGlnLysGlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyGluLysPro	200
QY	601	AACCTGCTGAGTCAAAAGTACCGCCATCCGAGTCCGCTCTCATCTGTTGCACTGT	660
DB	201	AsnLeuProGluTyrLysValAlaAlaIleArgLysSerProPheLeuLeuHisCys	220
QY	661	GGGGCACTGAGAGCCACTGGGATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	720
DB	221	GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal	240
QY	721	ACTGTGCCCTACAGGT	780
DB	241	ThrValProTyrSerValCysValSerThrAlaArgLysSerProPheLeuLeuHisCys	260
QY	781	CCGAGCGCTGTGACCTGCGCGGTGAGGTCTCTTTCATCTTTCATCTTTCATCTTTCAT	840
DB	261	ProSerValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPhe	280
QY	841	CGTACACATTCGTGTCCAAAGTGGGCGCAGGTGTGTGTGTGTGTGTGTGTGTGTGTGT	900

DB	281	ArgThrThrPheValSerLysSerGlyGlnValValPheAlaProLysSerIleCysLeu	300
QY	901	CACTACGTCAACACCTGTTCTCTGATGATGATGATGATGATGATGATGATGATGATGAT	960
DB	301	HisTyrValThrThrPheLeuLeuAspValIleAlaLeuProPheAspLeuLeu	320
QY	961	CATGCTTCAAGGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT	1020
DB	321	HisAlaPheLysValAsnValTyrPheGlyAlaHisLeuLeuLysThrValArgLeuLeu	340
QY	1021	CGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1080
DB	341	ArgLeuLeuArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValLeuLeu	360
QY	1081	ACACTGCTCATGCGCGTGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1140
DB	361	ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr	380
QY	1141	ATTGGCCAGCGGAGATCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	1200
DB	381	IleGlyGlnArgGluIleGluSerGluSerGluLeuProGluIleGlyTrpLeuGln	400
QY	1201	GAGCTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1260
DB	401	GluLeuAlaArgArgLeuGluThrProTyrTyrLeuValGlyArgArgProAlaGlyGly	420
QY	1261	AACAGCTCCGCGCAGAGTGACAACTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	1320
DB	421	AsnSerSerGlyGlnSerAspAsnCysSerSerSerSerGluAlaAsnGlyThrGlyLeu	440
QY	1321	GAGCTGCTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1380
DB	441	GluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeu	460
QY	1381	AGCAGCTCACAGCGTGGCTTCGCGCAACGTGTCCGCCAACACCGACACCGAGAGATC	1440
DB	461	SerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGluLysIle	480
QY	1441	TTCCTCATGTGACCATGCTCATCGCGCGCTGATGACGCGGTGGTGGTGGTGGTGGT	1500
DB	481	PheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValPheGlyAsnVal	500
QY	1501	ACGCCCATCATCCAGCGCATGTACCGCGCGCTTCTGTACCAACAGCGCGCGCGGAC	1560
DB	501	ThrAlaIleIleGlnArgMetTyrAlaArgArgPheLeuTyrHisSerArgThrArgAsp	520
QY	1561	CTGCGGCACTACATCCGCGCATCCACCGTATCCCGCGCGCTTCAAGCGCGCTCAAG	1620
DB	521	LeuArgAspTyrIleArgIleHisArgIleProLysProLeuLysGlnArgMetLeuGlu	540
QY	1621	TACTTCCAGGCGCATCGCGCGGTGAACATGGCATCGACACACCGAGCTGCTGAGAGC	1680
DB	541	TyrPheGlnAlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeuLeuGlnSer	560
QY	1681	CTCCCTGACGAGCTGGCGGAGACATCGCCATGACCTGACACCAAGAGGCTCTGAGAGT	1740
DB	561	LeuProAspGluLeuArgAlaAspIleAlaMetHisLeuHisLysGluValLeuGlnLeu	580
QY	1741	CCACTGTTTGAAGGCGCGCGCGGTGCTGCTGCGGGGCACTGTCTCTGCGCGCGCGCC	1800
DB	581	ProLeuPheGluAlaAlaSerArgGlyCysLeuArgAlaLeuSerLeuAlaLeuArgPro	600
QY	1801	GCCTTCTGACCGCGCGGAGTACTCATCCACCAAGCGGATGCCCTCAGCGCCCTCTAC	1860
DB	601	AlaPheCysThrProGlyGluTyrLeuIleHisGlnGlyAspAlaLeuGlnAlaLeuTyr	620
QY	1861	TTCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1920
DB	621	PheValCysSerGlySerMetGluValLeuLysGlyGlyThrValLeuAlaIleLeuGly	640
QY	1921	AAGGGCGACCTGATCGGCTGTGAGTGTGCGCGCGGAGCAGGTGTGTGTGTGTGTGTGT	1980

CC Bag (ether a 90-90) family and Elk subfamily of potassium channel
 CC monomers. hElk gene is mapped to chromosome 12q13. It is isolated from
 CC brain and maintains the resting potential and controls excitability of
 CC the cell. It has antimigraine, cerebroprotective, antipsychotic,
 CC neuroprotective and anticonvulsant activity. The hElk polypeptide can be
 CC used to screen for modulators of VGPCs, that are useful for treating
 CC abnormal ion flux disorders, CNS disorders such as migraines, hearing and
 CC vision problems, seizures, psychotic disorders and to prevent strokes. It
 CC can be used as a marker for diagnosis of diseases linked to this gene and
 CC also as reporter molecule in detection systems. The polynucleotide is
 CC useful for gene therapy, to rectify ELK expression. Note: The present
 CC sequence is not found in the specification, but is derived from hELK
 CC amino acid sequence found in page 62
 XX
 SQ

Sequence 1083 AA;

Alignment Scores:
 Pred. No.: 0 Length: 1083
 Score: 5697.00 Matches: 1081
 Percent Similarity: 99.91% Conservative: 1
 Best Local Similarity: 99.82% Mismatches: 1
 Query Match: 93.56% Indels: 0
 DB: 3 Gaps: 0

US-09-965-830-1_COPY_6_3257 (1-3252) x AAY44779 (1-1083)

QY	1	ATGCGCGCATCGGGGCTCTGGCGCTCAGACACCTTCTGGACACCATCGCTACG	60
DB	1	MetProAlaMetArgGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr	20
QY	61	CGCTTCGACGGCAGCACAGTAACTTCGTCTGGGCAACGCCAGGTGGCGGGCTCTTC	120
DB	21	ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnValAlaGlyLeuPhe	40
QY	121	CCGCTGGTCTACGTCTGTATGGCTTCTGTGACTCAGCGGCTCTCCGGGCTGAGTTC	180
DB	41	ProValValTyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal	60
QY	181	ATCAGGGGGCTGCTGCTGCTCTCTCTCTTTATGGGCGACACCATCGAGTCTGTCGCG	240
DB	61	MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArg	80
QY	241	CAACAGATCCGCAAGGCTCGGACGACGACCAAGAGTTCAGGCTGAGTCTGCTCTAC	300
DB	81	GlnGlnIleArgIysAlaLeuAspGluHisIysGluPheIysAlaGluLeuLeuTyr	100
QY	301	CGGAAGACGGGCTCCGGTCTGTGTCTCTGTGTGTATGATCCATCCATTAAGAAATGAAA	360
DB	101	ArgIysSerGlyLeuProPheTrpCysLeuLeuAspValIleProIleLysAsnGluLys	120
QY	361	GGGAGGTGGCTCTCTCTAGTCTCTCACAGGACATCAGCGAAACCAAGAACCGAGGG	420
DB	121	GlyGluValAlaLeuPheLeuValSerHisIysAspIleSerGluThrLysAsnArgGly	140
QY	421	GGCCCCCAGACAGATGAAGGACAGGTGGTGGCGGCGCGCATATGGCGGGCAGATCC	480
DB	141	GlyProAspArgTrpIysGluThrGlyGlyArgArgArgGlyArgAlaArgSer	160
QY	481	AAAGCTTCAATGCAACCGCGCGGAGCGCGGCGGTCTTACCACCTCTCGGGGAC	540
DB	161	LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis	180
QY	541	CTGCAGAGACGCCCAAGGCAAGCAGAGTCAATAAGGGGTGTTTGGGGAGAAACCA	600
DB	181	LeuGlnIysGlnProIysGlyIysHisIysLeuAsnIysGlyValPheGlyGluLysPro	200
QY	601	AACCTTGCCTGAGTCAAAAGTAGCCCATCCGGAAGTCCGCTTTCATCTGTGTGACGTG	660
DB	201	AsnLeuProGluTyrLysValAlaAlaIleArgIysSerProPheIleLeuLeuHisCys	220
QY	661	GGGGCAGTACAGACCATCGGATGGCTTCTCTGCTGCGCACACTCTATGTGCTGTC	720
DB	221	GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal	240

QY	721	ACTGTGCTTACAGCGTGTGTGTGAGCACAGCAGGAGCCAGTCCGCGCGCGCCCG	780
DB	241	ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro	260
QY	781	CCCAGCTGTGTGACCTGGCGGTGAGGTCTCTTTCATCTTGCATTTGTGTGATTTTC	840
DB	261	ProSerValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPhe	280
QY	841	CQTACACATTCGTCTCCAAAGTCGCGGCCAGGTGGTGTGGTGGTGGTGGTGGTGGT	900
DB	281	ArgThrThrPheValSerIysSerGlyGlnValValPheAlaProIysSerIleCysLeu	300
QY	901	CATACGTCCACCATCTGGTTCCTGTGATGTGCATCGCAGCGCTGCCCTTTCACCTGCTA	960
DB	301	HisTyrValThrTrpPheLeuLeuAspValIleAlaAlaLeuProPheAspLeuLeu	320
QY	961	CATGCTTCAAGGTCAAGTGTCTCGGGGCCATCTGCTGAAGACGGTGGCGCTGCTG	1020
DB	321	HisAlaPheLysValAsnValTyrPheGlyAlaHisLeuLeuLysThrValArgLeuLeu	340
QY	1021	CGCTTGTGCTGCTGCTTCCCGGGTGGACCGGTACTCGAGTACGACGCGCGTGGTGGT	1080
DB	341	ArgLeuLeuArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValValLeu	360
QY	1081	ACATGCTCATGCGCGTGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1140
DB	361	ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr	380
QY	1141	ATTGGCCAGCGGAGATCGAGCAGCAGCAATCCGAGTCTGCTGAGATGCTGCTGCTG	1200
DB	381	IleGlyGlnArgGluLeuGluSerSerGluSerGluLeuProGluLeuGlyTrpLeuGln	400
QY	1201	GAGTGTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1260
DB	401	GluLeuAlaArgArgLeuGluThrProTyrTyrLeuValGlyArgArgProAlaGlyGly	420
QY	1261	AACAGTCTCGCGCGCAGGTGACACTGACGAGCAGCAGCAGCAGCAGCAGCAGCAGC	1320
DB	421	AsnSerSerGlyGlnSerAspAsnCysSerSerSerSerGluAlaAsnGlyThrGlyLeu	440
QY	1321	GAGTGTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1380
DB	441	GluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeu	460
QY	1381	AGCAGCTCACCGAGTGGGCTTCGGCAACGTGTCCGCCAACACGACGACGACGACG	1440
DB	461	SerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGluLysIle	480
QY	1441	TTCTCCATCTGCACCATGCTCATCGCGCGCTGATGACGCGGTGGTGGTGGTGGTGG	1500
DB	481	PheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValValPheGlyAsnVal	500
QY	1501	ACGCGCATCATCCAGCGCATGTACCGCGCGCTTCTGTACCAACGACGCGCGCGGAC	1560
DB	501	ThrAlaIleIleGlnArgMetTyrAlaArgArgPheLeuTyrHisSerArgThrArgAsp	520
QY	1561	CTGCGCGCATCATCCGCGCATCCACCGTATCCCGAACCGCTCAGCAGCGCATCGGAG	1620
DB	521	LeuArgAspTyrIleArgIleHisArgIleProIysProLeuLysGlnArgMetLeuGlu	540
QY	1621	TACTTCCAGGCCACTGGCGGTGACCAATGCGATCGACACCGAGCTGCTGCGAGC	1680
DB	541	TyrPheGlnAlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeuLeuGlnSer	560
QY	1681	CTCCTGTACGAGTCTGCGCGCAGACATCGCCATGCACTGTGCAAGAGGCTCTGCGAGT	1740
DB	561	LeuProAspGluLeuArgAlaAspIleAlaMetHisLeuHisLysGluValLeuGlnLeu	580
QY	1741	COACTGTTTGGAGCGCGCGCGCTGCTGCGCGCAGTCTGCTGCTGCTGCTGCTGCTG	1800
DB	581	ProLeuPheGluAlaAlaSerArgGlyCysLeuArgAlaLeuSerLeuAlaLeuArgPro	600

1801 GCCTTCTGACGCGCGGAGTACCTCATCAACAGGCGATGCCCTCAGGCGCTCTAC 1860
601 AlaPheCysThrProGlyGluTyrLeuIleHisGlnGlyAspAlaLeuGlnAlaLeuTyr 620
1861 TTTTCTGCTCTGCTCATGAGTGTCTCAAGGTTGGCACCCTGCTGCCATCTAGGG 1920
621 PheValCysSerGlySerMetGluValLeuIleGlyGlyThrValLeuAlaIleLeuGly 640
1921 AAGGCGACCTGATCGGCTGTGAGTGCCTCCGCGGGAGCAGGTGCTAAAGGCCAATGCC 1980
641 LysGlyAspLeuIleGlyCysGluLeuProArgGluGlnValValAlaAsnAla 660
1981 GACGTGAAGGGGCTCACTACTGCTCCTGAGTGTCTGACGCTGCTGGCTGCACGAC 2040
661 AspValIysGlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGlyLeuHisAsp 680
2041 AGCCTTGGCTGTACCCGAGTTTGGCCCGGCTTCACTGCTGGCTCCGAGGGAGCTC 2100
681 SerLeuAlaLeuTyrProGluPheAlaProArgPheSerArgGlyLeuArgGlyGluLeu 700
2101 AGCTACAACCTGGTGTGGGGGAGGCTCTGCAGAGTGGACACAGCTCCCTCAGCGGC 2160
701 SerTyrAsnLeuGlyAlaGlyGlySerAlaGluValAspThrSerSerLeuSerGly 720
2161 GACATACCTTATGTCCAGCTCGAGGAGAGAGACAGATGGGAGCGGCCACG 2220
721 AspAsnThrLeuMetSerThrLeuGluGluIysGluThrAspGlyGluGlnGlyProThr 740
2221 GTCTCCCGAGCCAGCTGATGACCTCTCAGCCCTCTGCTGCTCCCTGGCTGCACCTCC 2280
741 ValSerProAlaProAlaAspGluProSerSerProLeuLeuSerProGlyCysThrSer 760
2281 TCATCTCTCAGTGCCTCAAGCTGTATCCCGAGCTCGAAGCAGCACCCCGGCTCGTCTAGT 2340
761 SerSerSerAlaAlaIysLeuLeuSerProArgGlnThrAlaProArgProArgLeuGly 780
2341 GGCAGAGGAGCGCAGCGAGCGGCTTTGAAGCTGAGGCTGGCGCTCTGCTGCC 2400
781 GlyArgGlyArgProGlyArgAlaGlyAlaLeuIysAlaGluAlaGlyProSerAlaPro 800
2401 CCAGGCGCTAGAGGGCTACGGCTCCCGCCCATGTCATGGAATGTGCCCGCCAGATCTG 2460
801 ProArgAlaLeuGluGlyLeuArgLeuProProMetProTrpAsnValProProAspLeu 820
2461 AGCCCCAGGCTAGTAGTGCATTGAAGCGGCTGTGCTCGACAGCCAGCCAGTCTCTCT 2520
821 SerProArgValValAspGlyIleGluAspGlyCysGlySerAspGlnProIysPheSer 840
2521 TTCGGCTGGCGAGTGTGCGCCGGAATGTAGCAGCAGCCCTCCCTGGACACAGAGAGC 2580
841 PheArgValGlyGlnSerGlyProGluCysSerSerSerProSerProGlyProGluSer 860
2581 GGCCTGCTCACTGTCCCGATGGCGCCAGCGAGGCAAGGAACACAGACACTGGACAAG 2640
861 GlyLeuLeuThrValProHisGlyProSerGluAlaArgAsnThrAspThrLeuAspLys 880
2641 CTTCCGCGAGCGGTGACAGAGCTGTACAGACAGTGTCTGAGATGGCGGAAGACTGCAG 2700
881 LeuArgGlnAlaValThrGluLeuSerGluGlnValLeuGlnMetArgGluGlyLeuGln 900
2701 TCATCTGCGCAGCTGTGACGTGTCTGCTGGCGCCCGACAGGAGGCTCCGTCGCTCCG 2760
901 SerLeuArgGlnAlaValGlnLeuValLeuAlaProHisArgGluGlyProCysProArg 920
2761 GCATCGGAGAGGGCGGTGCCAGCAGCACTCTCGGGCTTCTGACGCTCTGTGTGTG 2820
921 AlaSerGlyGluGlyProCysProAlaSerThrSerGlyLeuLeuGlnProLeuCysVal 940
2821 GACACTGGGCGATCTCTCTACTGCTGACGCGCCCGAGCTGGCTGTCTGTGAGTGGACT 2880
941 AspThrGlyAlaSerSerTyrCysLeuGlnProProAlaGlySerValLeuSerGlyThr 960
2881 TGGCCCCACCTCTGTCGCGGGCGCTCTCTCCCTCATGCGCACCTCGGCGCTCCGCCA 2940

961 TrpProHisProAlaProGlyProProLeuMetAlaProTrpProTrpGlyProPro 980
2941 CGCTCTCAGAGCTCCCTCGCTCGAGCCACAGCTTTCTGGACCTCCACCTCAGACTCA 3000
981 AlaSerGlnSerSerProTrpProArgAlaThrAlaPheTrpThrSerThrSerAspSer 1000
3001 GAGCCCTCTGCTCAGAGACTCTGCTGTAGCCACAGCACCTGCTCCCTCTCTCTCT 3060
1001 GluProProAlaSerGlyAspLeuCysSerGluProSerThrProAlaSerProProPro 1020
3061 TCTCAGGAAGGGCTAGACTGGCCCGCAGAGCTGTGAGCCAGGCTGAGGCTACCGC 3120
1021 SerGluGluGlyAlaArgThrGlyProAlaGluProValSerGlnAlaGluAlaThrSer 1040
3121 ACTCGAGAGCCCGCCACAGGGTCTCAGGGGCTGCTGCTGGCTGGACCCCGCAGCCTG 3180
1041 ThrGlyGluProProProGlySerGlyGlyLeuAlaLeuProTrpAspProHisSerLeu 1060
3181 GAGATGCTGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3240
1061 GluMetValLeuValGlyCysHisGlySerGlyThrValGlnTrpThrGlnGluGly 1080
3241 ACAGGGGCTC 3249
1081 ThrGlyVal 1083
RESULT 6
AAY44780
ID AAY44780 standard; protein; 1083 AA.
XX
AC AAY44780;
XX
DT 04-MAY-2000 (first entry)
XX
DE Human Elk voltage gated potassium channel monomer variant #2.
XX
KW Voltage gated potassium channel subunit; VGPCs; helk; human; stroke;
KW Kv superfamily; Eag family; ether a go-go; Elk subfamily; modulator;
KW chromosome 12q13; resting potential; cell excitability; seizure; marker;
KW CNS; migraine; treat; hearing/vision problem; psychotic; anticonvulsant;
KW ion flux disorder; reporter molecule; detection; gene therapy;
KW antimitigane; cerebroprotective; neuroprotective; antipsychotic.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 452..710
FT /label= Extended P-S6 region
FT /note= "Extended Pore-S6 region with conserved amino
FT acids"
FT Region 452..514
FT /label= P-S6 region
FT /note= "Pore-S6 region with conserved amino acids"
FT Misc-difference 1060
FT /note= "Wild type Leu substituted with Ile"
XX
PN W0200001819-A1.
XX
XX 13-JAN-2000.
XX
XX 30-JUN-1999; 99WO-US014944.
XX
XX 01-JUL-1998; 98US-0091469P.
XX 21-JAN-1999; 99US-0116621P.
XX
XX (ICAG-) ICAGEN INC.
XX
XX Jegla TU, Wickenden A;
XX WPI; 2000-182114/16.
XX

PT Novel polynucleotides and polypeptides of human ELK, a voltage-gated
 PT potassium channel subunit useful for treating ELK miss-expression and to
 PT screen for inhibitors and activators of such channels.
 XX
 PS Disclosure; Page: 79pp; English.

XX The present sequence is the human ELK (hELK) polypeptide variant #2,
 CC comprising an alpha subunit of the voltage-gated potassium channel
 CC (VGPCs). It is a member of the Kv (voltage-gated potassium) superfamily,
 CC Eag (eether a go-go) family and Elk subfamily of potassium channel
 CC monomers. hELK gene is mapped to chromosome 12q13. It is isolated from
 CC brain and maintains the resting potential and controls excitability of
 CC the cell. It has antimigraine, cerebroprotective, antipsychotic,
 CC neuroprotective and anticonvulsant activity. The hELK polypeptide can be
 CC used to screen for modulators of VGPCs, that are useful for treating
 CC abnormal ion flux disorders, CNS disorders such as migraines, hearing and
 CC vision problems, seizures, psychotic disorders and to prevent strokes. It
 CC can be used as a marker for diagnosis of diseases linked to this gene and
 CC also as reporter molecule in detection systems. The polynucleotide is
 CC useful for gene therapy, to rectify ELK expression. Note: The present
 CC sequence is not found in the specification but derived from hELK amino
 CC acid sequence found in page 62

XX Sequence 1083 AA;

Alignment Scores:
 Pred. No.: 0 Length: 1083
 Score: 5696.00 Matches: 1081
 Percent Similarity: 99.91% Conservative: 1
 Best Local Similarity: 99.82% Mismatches: 1
 Query Match: 93.55% Indels: 0
 DB: 3 Gaps: 0

US-09-965-830-1_COPY_6_3257 (1-3252) x AAY44780 (1-1083)

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 QY 121 CCCTGCTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCGGGCTGAGTTC 180
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 DB 81 GlnGlnIleArgLysAlaLeuAspGluHisLysGluPheLysAlaGluLeuIleLeuTyr 100
 QY 301 CGGAAGAGCGGGCTCCCGTTCCTGGTCTCTCTGATGTGATCCCATAAAGATGAGAAA 360
 DB 101 ArgLysSerGlyLeuProPheTyrCysLeuLeuAspValIleProIleLysAsnGluLys 120
 QY 361 GGGGAGTGGCTCTCTCTCTAGTCTCTCACAGGACATCAGCAACCAAGACCGAGGG 420
 DB 121 GlyGluValAlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGly 140
 QY 421 GGGCCCCACAGATGGAAGAGACAGGTGGTGGCGCGCGCATATGCGCGGACCATCC 480
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 QY 481 AAAGGCTTCAATGCAACCGGGCGGAGCGGGCGCTGTCTACACCTGTCTCGGGCAC 540
 DB 161 LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis 180
 QY 541 CTGCAGAGCAGCCCAAGGCGACAGCAAGCTCAATAAGGGGGTGTGGGAGAAACCA 600

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 QY 661 GGGGACTGAGAGCCACTGGGATGGCTTCATCTCTGCTCGCCACACTTATGTGTGCTGC 720
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 QY 841 GGTACCATCTGCTGTCAAGTGGCGGCGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGG 900
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1681 CTCCTGACGAGTGGCGCAGACATCGCCATGCACTGACACAGAGGTCTCTGAGCTG 1740
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 1741 CCACCTGTTTGGCGCGCAGCGCGCTGCTGCGCGCACTGCTCTGCGCTCGCGCC 1800
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 601 AlaPheCysThrProGlyGluTyrLeuIleHisGlnGlyAspAlaLeuGlnAlaLeuTyr 620
 1861 TTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920
 621 PheValCysSerGlySerMetGluValLeuLeuGlyGlyThrValLeuAlaIleLeuGly 640
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 661 AspValLysGlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGlyLeuHisAsp 680
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 681 SerLeuAlaLeuTyrProGluPheAlaProArgPheSerArgGlyLeuArgGlyGluLeu 700
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 701 SerTyrAsnLeuGlyAlaGlyGlySerAlaGluValAspThrSerSerLeuSerGly 720
 2161 GACATATACCTTATGTCCACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2220
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 761 SerSerSerAlaAlaLysLeuLeuSerProArgThrAlaProArgProArgLeuGly 780
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 781 GlyArgGlyArgProGlyArgAlaGlyAlaLeuLysAlaGluAlaGlyProSerAlaPro 800
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 2521 TTCGCGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2580
 841 PheArgValGlyGlnSerGlyProGluCysSerSerSerProSerProGlyProGluSer 860
 2581 GGCCTGCTACTGTTCCCATGGCCCGCAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2640
 861 GlyLeuLeuThrValProHisGlyProSerGluAlaArgAsnThrAspThrLeuAspLys 880
 2641 CTTTGGCAGCGCTGACAGCTGCTGACAGCAGCTGCTGACAGCAGCTGCTGACAGCAGCTG 2700
 881 LeuArgGlnAlaValThrGluLeuSerGluGlnValLeuGlnMetArgGluGlyLeuGln 900
 2701 TCATTTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2760
 901 SerLeuArgGlnAlaValGlnLeuValLeuAlaProHisArgGluGlyProCysProArg 920

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 2821 GACACTGGGGCATCTCTCTACTGCTGAGCGCCAGCGCGCTGCTGCTGCTGCTGCTGCTG 2880
 941 AspThrGlyAlaSerSerTyrCysLeuGlnProProAlaGlySerValLeuSerGlyThr 960
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 2941 GGTCTCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3000
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 1041 ThrGlyGluProProProGlySerGlyGlyLeuAlaLeuProTrpAspProHisSerIle 1060
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 1061 GluMetValLeuIleGlyCysHisGlySerGlyThrValGlnTrpThrGlnGluGly 1080
 3241 ACAGGGGCTC 3249
 1081 ThrGlyVal 1083

RESULT 7
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 ID AAY44781 standard; protein; 1083 AA.
 XX AAY44781;
 AC AAY44781;
 DT 04-MAY-2000 (first entry)
 XX Human Elk voltage gated potassium channel monomer variant #3.
 DE Voltage gated potassium channel subunit; VGPCs; hElk; human; stroke;
 KW Kv superfamily; Eag family; ether a go-go; Elk subfamily; modulator;
 KW chromosome 12q13; resting potential; cell excitability; seizure; marker;
 KW CNS; migraine; treat; hearing/vision problem; psychotic; anticonvulsant;
 KW ion flux disorder; reporter molecule; detection; gene therapy;
 KW antimigrane; cerebroprotective; neuroprotective; antipsychotic.
 XX Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 452..710
 FT /label= Extended P-S6 region
 FT /note= "Extended Pore-S6 region with conserved amino
 FT acids"
 FT Region 452..514
 FT /label= P-S6 region
 FT /note= "Pore-S6 region with conserved amino acids"
 FT Misc-difference 744
 FT /note= "Wild type Ala substituted with Ser"
 XX WO200001819-A1.
 XX 13-JAN-2000.
 XX 30-JUN-1999; 99WO-US014944.
 XX

PR 01-JUL-1998; 9RUS-0091469P.
 PR 21-JAN-1999; 9RUS-0116621P.
 XX (ICAG-) ICAGEN INC.
 XX Jegla TJ, Wickenden A;
 PI WPI; 2000-182114/16.
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 XX Disclosure; Page; 79pp; English.
 XX The present sequence is the human ELK (hELK) polypeptide variant #3,
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 CC monomers. hELK gene is mapped to chromosome 12q13. It is isolated from
 CC brain and maintains the resting potential and controls excitability of
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 CC used to screen for modulators of VGPCs, that are useful for treating
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 CC vision problems, seizures, psychotic disorders and to prevent strokes. It
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 CC also as reporter molecule in detection systems. The polynucleotide is
 CC useful for gene therapy, to rectify ELK expression. Note: The present
 CC sequence is not found in the specification but derived from hELK amino
 CC acid sequence found in page 62
 XX SQ Sequence 1083 AA;

Alignment Scores:
 Pred. No.: 0 Length: 1083
 Score: 5695.00 Matches: 1081
 Percent Similarity: 99.91% Conservatives: 1
 Best Local Similarity: 99.82% Mismatches: 1
 Query Match: 93.53% Indels: 0
 DB: 3 Gaps: 0

US-09-965-830-1_COPY_6_3257 (1-3252) x AAY44781 (1-1083)

Qy 1 ATCCGGCCATGGGGCCCTCTCGCCCTCAGAACACCTCTCTCGACACCATCGCTACG 60
 Db 1 MetProAlaMetArgGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20
 Qy 61 CGCTTCGACGCGCAGCAGTAACCTTCGTCTGGCCAAACGCCAGGTGGCGGGCTCTTC 120
 Db 21 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnValAlaGlyLeuPhe 40
 Qy 121 CCCGTGTCTACTCTCTGTGCTGTGACCTCAGGCTTCTCCCGGCTGAGTTC 180
 Db 41 ProValValTyCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal 60
 Qy 181 ATGCAGCGGGCTGTCT 240
 Db 61 MetGlnArgGlyCysAlaCysSerPheLeuTyGlyProAspThrSerGluLeuValArg 80
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 Qy 661 GGGGCACTGAGAGCCACCTGGATGGTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
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 Qy 1381 AGCAGCTCACCAGGTGGGT 1440
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QY 3061 TCTCAGGAAGGGGTAGGACTGGCGCGCAGAGCTGTGAGCCGAGCCCTGGAGCCCTG 3120
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QY 3121 ACTGGAGAGCCCCACAGGCTCAGGGGCTGAGGGCTGCTGCTGCTGCTGCTGCTGCTG 3180
Db 1041 ThrGlyGluProProProGlySerGlyGlyLeuAlaLeuProTrpAspProHisSerLeu 1060
QY 3181 GAGATGCTGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3240
Db 1061 GluMetValLeuIleGlyCysHisGlySerGlyThrValGlnTrpThrGlnGluGly 1080
QY 3241 ACAGGGGTC 3249
Db 1081 ThrGlyVal 1083
RESULT 8
AA84835
ID AAY84835 standard; protein; 1083 AA.
AC AAY84835;
XX
DT 08-AUG-2000 (first entry)
XX
DE Herg4, a potassium channel protein of the ERG family.
XX Human; potassium channel protein; Herg4; human erg related gene 4;
KW epilepsy; migraine; cell proliferation disorder; cancer;
KW compartmental trouble; neurotransmitter; hormone; ischemia;
KW brain disease; cardiac disease; inflammation; pain.
XX Homo sapiens.
XX WO200022001-A2.
XX 20-APR-2000.
XX 13-OCT-1999; 99WO-BP007671.
XX 13-OCT-1998; 98EP-00402540.
XX (SNFI) SANOFI -SYNTHELABO.
XX Renard S, Avenet P;
PI

XX	WFI: 2000-317948/27.
DR	N-PSDB: AAA14893.
DR	
XX	
XX	Novel herg4 polypeptide of human erg potassium channel family useful for
PT	treatment of epilepsy, migraine, cell proliferation.
PT	
XX	
XX	Claim 11: Page 45-48; 48pp; English.
PS	
XX	
CC	The present sequence represents a human potassium channel protein of the
CC	ERG family, which is designated Herg4 (human erg related gene 4). The
CC	Herg4 polypeptides and polynucleotides are useful in the treatment of
CC	epilepsy, migraine, cell proliferation disorders, cancer, comportemental
CC	troubles, and to prevent or alter the effect of endogenous
CC	neurotransmitters and hormones. Antibodies against Herg4 are also useful
CC	for the treatment of cerebral, cardiac and renal ischemias, brain and
CC	cardiac diseases, inflammation, pain, and to mimic or antagonize the
CC	effect of endogenous neurotransmitters and hormones
XX	
XX	Sequence 1083 AA;
SQ	

Alignment Scores:		
Pred. No.:	0	1083
Score:	5695.00	1081
Percent Similarity:	99.91%	
Best Local Similarity:	99.92%	
Indels:	0	
Query Match:	93.53%	
Gaps:	3	0
Length:		
Matches:		1081
Conservative:		1
Mismatches:		1
Indels:		0
Gaps:		0

IIS-09-965-830-1 COPY 6 3257 (1-3252) x AAY84835 (1-1083)

QY	1	ATGCGGCGCATCGGGGCGCTCTCGCGCTCAGAACACCTTCTCTGGACACCATCGCTACG	60
Db	1	MetProAlaMetArgGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr	20
QY	61	CGCTTCGACGGCAGCAGCAAGTAACCTTCGTGTGGCAACGCCACAGTGGCGGGCTCTTC	120
Db	21	ArgPheAspGlyThrHisSerAsnPheValIeuGlyAsnAlaGlnValAlaGlyLeuPhe	40
QY	121	CCCGTGTGCTACTGCTCTCATGGCTCTGTGACCTCACCGGCTTCTCCGGGCTGAGGTC	180
Db	41	ProValValTyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal	60
QY	181	ATGCAGCGGGCTGTGCTGTCTCTCTCTTATGGCCGACACACAGTAGCTGCTCCGC	240
Db	61	MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArg	80
QY	241	CAACAGATCCGCAAGGCCCTGCACGACGACCAAGGAGTTCAAGGCTGAGCTGATCTGTAC	300
Db	81	GlnGlnIleArgLysAlaLeuAspGluHisLysGluPheLysAlaGluLeuIleLeuTyr	100
QY	301	CGGAGAGCGGGCTCCGTTCTGGTGTCTCTCGGATGTGATACCCATAAAGAAATCAGAAA	360
Db	101	ArgLysSerGlyLeuProPheTrpCysLeuLeuAspValIleProIleLysAsnGluLys	120
QY	361	GGGGAGTGGCTCTCTTCTAGTCTCTCAAGGACATCAGCGAAACCAAGAACCGAGG	420
Db	121	GlyGluValAlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGly	140
QY	421	GGCCCCAGATGGAAGGAGACAGTGTGTGGCGCGCGCGATATGCCCGGCGACAGATCC	480
Db	141	GlyProAspArgTrpLysGluThrGlyGlyArgArgTyrGlyArgAlaArgSer	160
QY	481	AAAGGCTTCAATGCCAACCGGCGGAGCGGGCCGTCTTACCACCTGTCCGGGAC	540
Db	161	LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis	180
QY	541	CTGCAGAAGCAGCCCCAAGGCGACGACAGCTCAATAAGGGGTGTTCGGGAGAAACCA	600
Db	181	LeuGlnLysGlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyGluLysPro	200
QY	601	AACCTTGCTGATACAAAGTAGCGGCATCCGGAAGTCGCGCTTCATCTGTGTGCACTGT	660

QY	1741	CCACTGTTTGAGCGCGCGCCAGCGCGCTCCCTGCGGGCACATGTTCTCTGGCCCTCGCGGCC	1801
Db	581	ProLeuPheGluAlaAlaSerArgGlyCysLeuArgAlaLeuSerLeuAlaLeuArgPro	600
QY	1801	GCCTTCTGACGCGCGGGGAGTACCTCATCCACCAAGCGCATGCCCTGCGAGGCCCTCTAC	1860
Db	601	AlaPheCysThrProGlyGluThrLeuIleHisGlnGlyAspAlaLeuGlnAlaLeuTyr	620
QY	1861	TTTGTCTCTCTGGCTCCATCGAGGTGCTCAAGGTTGGCACCCTGCTGCGCATCTCTAGGG	1920
Db	621	PheValCysSerGlyPheMetGluValLeuLysGlyGlyThrValLeuAlaIleLeuGly	640
QY	1921	AAGGCGCACTCATCGGCTGTGAGTGCCTCCGCGGAGCAGAGGTGTATAAGGCCAATGCC	1980
Db	641	LysGlyAspLeuIleGlyCysGluLeuProArgArgGluGlnValValYsAlaAsnAla	660
QY	1981	GACGTGAAGGGCTGACGTACTCGTCTCTGAGTGTCTGACGTGTGCTGCGCTGCACGAC	2040
Db	661	AspValLysGlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGlyLeuHisAsp	680
QY	2041	AGCCTTGGCTGTACCCCGAGTTTGGCCGCTTCAGTCTGCTGCGCTCCGAGGGGAGCTC	2100
Db	681	SerLeuAlaLeuTyrProGluPheAlaProArgPheSerArgGlyLeuArgGlyGluLeu	700
QY	2101	AGCTACAACCTGGTGTGGGGAGGTCTGCAAGGTGCACACCACTCCCTGAGCGGC	2160
Db	701	SerTyrAsnLeuGlyAlaGlyGlySerAlaGluValAspThrSerSerLeuSerGly	720
QY	2161	GACATACCTTATGTCAGCTGGAGGAGAAGAGACAGATGGGAGCAGGCCCCACG	2220
Db	721	AspAsnThrLeuMetSerThrLeuGluGluLysGluThrAspGlyGluGlnGlyProThr	740
QY	2221	GTCTCCCGCAGCCCGAGCTGATGACCCCTCCAGCCCTCTGCTGCTCCCTGGCTGCACCTCC	2280
Db	741	ValSerProAlaProAlaAspGluProSerSerProLeuLeuSerProGlyCysThrSer	760
QY	2281	TCATCTCAGCTGCCAAGCTGCTATCCCACTGCAACACAGCACCCCGGCTGTCTAGGT	2340
Db	761	SerSerSerAlaAlaLysLeuLeuSerProArgThrAlaProArgProArgLeuGly	780
QY	2341	GGCAGAGGGAGGCCAGCAGCGGAGGGGCTTTGAAGCTGAGGCTGGCCCTCTGCTCCC	2400
Db	781	GlyArgGlyArgProGlyArgAlaGlyAlaLeuLysAlaGluAlaGlyProSerAlaPro	800
QY	2401	CCACGGGCCCTAGAGGGCTTACGGCTGCCCCCATGCTGAAATGTAATGTCGCCCACTGTG	2460
Db	801	ProArgAlaLeuGluGlyLeuArgLeuProMetProTyrPasnValProProAspLeu	820
QY	2461	AGCCCCAGGTAGTAGATGTCATTGAAGACGGGTGTGGCTCGGACCGAGCCCAAGTTCTCT	2520
Db	821	SerProArgValValAspGlyIleGluAspGlyCysGlySerAspGlnProLysPheSer	840
QY	2521	TTCCGGGTGGCCAGTCTGGCCCGGATGTAGGAGCAGGCCCTCCCTCGGACGAGAGC	2580
Db	841	PheArgValGlyGlnSerGlyProGluCysSerSerSerProSerProGlyProLysSer	860
QY	2581	GGCTCTCTCACTGTTCCCATGGCCACGAGGCAAGAAACACACACACTGCACAAAG	2640
Db	861	GlyLeuLeuThrValProHisGlyProSerGluAlaArgAsnThrAspThrLeuAspLys	880
QY	2641	CTTGGCAGCGGTGACAGAGCTGTGACAGCAGGTGCTGCAGATCGCGAAGGACTGCAG	2700
Db	881	LeuArgGlnAlaValThrGluLeuSerGluGlnValLeuGlnMetArgGluGlyLeuGln	900
QY	2701	TCACTTGGCCAGGCTGTGAGCTTGTCTGGCGCCCCACAGGAGGGTCCGTGCCCTCGG	2760
Db	901	SerLeuArgGlnAlaValGlnLeuValLeuAlaProHisArgGluGlyProCysProArg	920
QY	2761	GCATCGGAGAGGGGCCGTGCCAGCACCTCCGGGCTTCTGCACGCTCTGTGTGTG	2820
Db	921	AlaSerGlyGluGlyProCysProAlaSerThrSerGlyLeuLeuGlnProLeuCysLeu	940

QY	2821	GACATGGGGCATCTCTACTGCTGCAGCCCCCAGCTGCTGTGTCTTGAAGTGGCACT	2880
Dd	941	AspThrGlyAlaSerSerTyxCysLeuGlnProProAlaGlySerValLeuSerGlyThr	960
QY	2881	TGGCCCCCACCCTCGPCGGGGCCTCCCTCCCTCATGGCACCCCTGGCCCTGGGGTCCTCCCA	2940
Dd	961	TtpProHisProAArgproGlyProProProLeuMetAlaProTrpProTrpGlyProPro	980
QY	2941	GGTCTCAGAGCTCCCCCTGCCCTCGAGCCACACAGCTTTCTTGACCTCCACTCAGACTCA	3000
Dd	981	AlaSerGlnSerSerProTrpProArgAlaThraPheTrpThrSerThrSerAspSer	1000
QY	3001	GAGCCCCCTGCTCAGAGAGACCTTGCTCTGAGCCAGCACCCCTGCCTCCCTTCCTTCCT	3060
Dd	1001	GluProProAlaSerGlyAspLeuCysSerGluProProSerThrProAlaSerProProPro	1020
QY	3061	TCTGAGGAAGGGCTAGGACTTGGGCCCGCAGAGCCTGTGAGCCAGGCTGAGGCTACAGC	3120
Dd	1021	SerGluGluGlyAlaArgThrGlyProAlaGluProValSerGlnAlaGluAlaThrSer	1040
QY	3121	ACTGGAGAGCCCCCACCAGGGCTCAGGGGGCCTGGCCCTTGCTGGGACCCCCACAGCCTG	3180
Dd	1041	ThrGlyGluProProProGlySerGlyGlyLeuAlaLeuProTrpAspProHisSerLeu	1060
QY	3181	GAGATGGTGTTATTGGCTGCCATGGCTCTGGCACAGTCCAGTGGACCCAGGAAGAAGGC	3240
Dd	1061	GluMetValLeuIleGlyCysHisGlySerGlyThrValGlnTrpThrGlnGluGly	1080
QY	3241	ACAGGGGTC	3249
Dd	1081	ThrGlyVal	1083
 RESULT 9 AAV77738			
ID	AAV77738	standard; protein; 1080 AA.	
XX			
AC	AAV77738;		
XX			
DT	19-MAY-2000	(first entry)	
DE	Human ESK1 (hESK1) protein.		
KW	ESK1; eag similar K+ channel; potassium channel associated disorder;		
KW	neurological; Alzheimer's disease; anxiety; panic; autism; hyperactivity;		
KW	obsessive-compulsive disorder; schizophrenia; Huntington's disease;		
KW	epilepsy; cardiovascular; musculoskeletal; proliferative; cancer;		
KW	ESK channel blocker; nootropic; neuroprotective; antidepressant;		
KW	tranquilizer; neuroleptic; antiparkinsonian; cardiant; cytostatic;		
XX	anticconvulsant.		
OS	Homo sapiens.		
XX			
Key	Location/Qualifiers		
FH	Domain	212..239	
FT	/note= "potential transmembrane domain S1"		
FT	Domain	259..277	
FT	/note= "potential transmembrane domain S2"		
FT	Domain	297..320	
FT	/note= "potential transmembrane domain S3"		
FT	Domain	329..349	
FT	/note= "potential transmembrane domain S4"		
FT	Domain	356..378	
FT	/note= "potential transmembrane domain S5"		
Modified-site	418		
FT	/note= "potential N-glycosylation site"		
FT	Modified-site	425	
FT	/note= "potential N-glycosylation site"		
FT	Modified-site	433	
FT	/note= "potential N-glycosylation site"		
Domain	449..468		
FT	/note= "potential pore-forming P domain"		
FT	Modified-site	467	
FT	/note= "potential N-glycosylation site"		

PT Domain 477..501
/note= "potential transmembrane domain S6"
FT Modified-site 496
/note= "potential N-glycosylation site"
FT Domain 601..668
/note= "putative cyclic nucleotide binding domain (cNBD)"
XX WO200009534-A1.
XX 24-FEB-2000.
XX 13-AUG-1999; 99WO-US018556.
XX 14-AUG-1998; 98US-0096570P.
XX (ELAN-) ELAN PHARM INC.
XX Forsayeth JR, Zhao BB;
XX WPI; 2000-224270/19.
XX N-PSDB; AA287712.
XX Novel eag similar potassium channel polypeptide useful for treating
PT various neurological, cardiovascular, musculoskeletal and proliferative
PT disorders.
XX Claim 3; Fig 1A-E; 52pp; English.
XX This represents a eag similar K+ channel (ESK) polypeptide (hESK1). The
CC hESK1 protein can be expressed by standard recombinant methodology. The
CC ESK polypeptide, polynucleotides and antibodies are useful for treating
CC and diagnosing various potassium channel associated disorders such as
CC neurological disorders, e.g. Alzheimer's disease, depression, anxiety,
CC panic, obsessive-compulsive disorders, attention deficit, epilepsy;
CC hyperactivity disorders, autism, schizophrenia, Huntington's disease and
CC Parkinson's disease, cardiovascular disorders, musculoskeletal disorders
CC and proliferative disorders such as cancer. The ESK polynucleotide is
CC also useful for synthesis of ESK and gene mapping. The polypeptide can be
CC used in an assay to identify molecules such as synthetic drugs,
CC antibodies, peptides or other molecules which have an effect on the
CC activity of the ESK channel
XX
XX Sequence 1080 AA;

Alignment Scores:
Pred. No.: 0 Length: 1080
Score: 5688.00 Matches: 1080
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 93.41% Indels: 0
DB: 3 Gaps: 0

US-09-965-830-1_COPY_6_3257 (1-3252) x RAY77738 (1-1080)

QY 10 ATGGGGGGCTCTGGGGCTCTGAGACACCTTCTGGACACCATCGCTACGGCTTCGAC 69
Db 1 MetArgGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThrArgPheAsp 20
QY 70 GGACGACGAGTAATCTGCTGGGCAAGCCAGCTGGGGGGCTCTTCCCGTGGTC 129
Db 21 GlyThrHisSerAsnPheValLeuGlyAsnAlaGlnValAlaGlyLeuPheProValVal 40
QY 130 TACTGCTCTATGGCTTCTGTGACCTCACGGGCTTCTCCGGGCTGAGGTCAATCAGCGG 189
Db 41 TyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluValMetGlnArg 60
QY 190 GGCTGTGCTCTCTCTTCTTATGGCCAGACACAGTAGCTGCTCCCGCCACAGATC 249
Db 61 GlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArgGlnGlnIle 80
QY 250 CGCAGGCGCTGGAGGACCAAGAGTTCAAGGCTGAGCTGATCTCTTACCGGAAGAGC 309
Db 81 ArgLysAlaLeuAspGluHisLysGluPheLysAlaGluLeuIleLeuTyrArgLysSer 100

QY 310 GGGCTCCGGTCTCTGCTCTCTGATGATCCCATAAAGATGAGAAAGGGAGGTG 369
Db 101 GlyLeuProPheTrpCysLeuLeuAspValIleProIleLysAsnGluLysGlyGluVal 120
QY 370 GCTCTCTCTCTAGTCTCTCAAGGACATCAGCGAAACCAAGAACCGAGGGGGCCCGAC 429
Db 121 AlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGlyProAsp 140
QY 430 AGATGGAAGGAGACAGGTGGTGGCGCGCGATATGCGCGGACGATCCAAAGGCTTC 489
Db 141 ArgTrpLysGluThrGlyGlyArgArgTrpGlyArgAlaArgSerLysGlyPhe 160
QY 490 AATGCCAACCGCGCGGAGCGCGCGCTGCTTACCACTGTCTCGGCGACCTGCGAGAAG 549
Db 161 AsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHisLeuGlnLys 180
QY 550 CAGCCCAAGGGCAAGCACAAAGCTCAATAAGGGGTGTTTGGGGAGAAACCAAACTTGCT 609
Db 181 GlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyGluLysProAsnLeuPro 200
QY 610 GAGTCAAGTAGCGCCCATCCGGAAGTCGCCCTTCATCCTCTGCTGCTGGGCACATG 669
Db 201 GluTyrLysValAlaAlaIleArgLysSerProPheIleLeuLeuHisCysGlyAlaLeu 220
QY 670 AGAGCCACTGGATGGCTTCTATCTGCTCGCACACTTCTATGCTGCTGCTCACTGTGCC 729
Db 221 ArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaValThrValPro 240
QY 730 TACAGCTGTGTGTGAGCACACAGCGGAGCCAGTGGCGCGCGCGCGCGCCAGCGTC 789
Db 241 TyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyProSerVal 260
QY 790 TGTGACCTGGCGGTGAGGTCTCTTCATCTCTGACATCTGCTGCTGATTTCCGTACACCA 849
Db 261 CysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPheArgThrThr 280
QY 850 TTCGTGTCAAGTCGGCGCGAGTGTGTTTGGCCAAAGTCCATTTGCTTCCACTACGTC 909
Db 281 PheValSerLysSerGlyGlnValPheAlaProLysSerIleCysLeuHisTyrVal 300
QY 910 ACCACCTGCTTCTGCTGATGTCTATCGCAGCGCTGCCCTTTGACCTGCTACATGCTTC 969
Db 301 ThrThrTrpPheLeuLeuAspValIleAlaLeuProPheAspLeuLeuHisAlaPhe 320
QY 970 AAGTCAACGTGTACTTCCGGGGCCCATCTGCTCAAGCGTGGCGCTGCGCGCTGCTG 1029
Db 321 LysValAsnValTyrPheGlyAlaHisLeuLeuLysThrValArgLeuLeuArgLeuLeu 340
QY 1030 CGCTGCTTCCGGCGGTGGACCGGTACTGCGAGTACAGCGCGCTGGTGTGACATGCTC 1089
Db 341 ArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValValLeuThrLeuLeu 360
QY 1090 ATGCGCGTGTTCCTGCTGCTGCGGCACTGGGTGCGCTGCTGCTGTTTACATGTCGAG 1149
Db 361 MetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyrIleGlyGln 380
QY 1150 CGGAGATCAGAGCAGCGAATCGAGCTGCTGAGATTGCTGCTGCTGCGAGGAGCTGCC 1209
Db 381 ArgGluIleGluSerSerGluSerGluLeuProGluIleGlyTrpLeuGlnGluLeuAla 400
QY 1210 CGCGACTGAGACTCCCTACTACTGCTGGCGCGAGGCGGAGCTGAGGAGAAACAGCTCC 1269
Db 401 ArgArgLeuGluThrProTyrTyrLeuValGlyArgArgProAlaGlyGlyAsnSerSer 420
QY 1270 GGCCAGAGTGCACAACTCAGCAGCAGCAGCGAGGCCAAACGGGACGGGGCTGGAGCTGCTG 1329
Db 421 GlyGlnSerAspAsnCysSerSerSerSerSerGluAlaAsnGlyThrGlyLeuGluLeuLeu 440
QY 1330 GGGCGCGCTGCTGCGCAGCGCTTACATCCTCTCTTCTGCGACTCAGCAGCGCTC 1389
Db 441 GlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeuSerSerLeu 460

QY	1390	ACCAGCGTGGCTTCGGCAACGTGTCCGCAACACGGAACCGAGAGATCTTCTCCATC	1449	Db	821	ValValAspGlyIleGluAspGlyCysGlySerAspGlnProlyPheSerPheArgVal	840
Db	461	ThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGluIysIlePheSerIle	480	QY	2530	GCCAGCTCTGGCCCGAATGTAGCAGCAGCCCTCCCTCGGACGAGAGCGCTGCTC	2589
QY	1450	TGCACCATGCTATCCGCGCCCTGTATGCAGCGGTGGTGTGGGAACGTGACGGCCATC	1509	Db	841	GlyGlnSerGlyProGluCysSerSerProSerProGlyProGluSerGlyLeuLeu	860
Db	481	CysThrMetLeuIleGlyAlaLeuMetHisAlaValPheGlyAsnValThrAlaIle	500	QY	2590	ACTGTTCCCATCGGCGCCAGCGAGCAAGAACACAGACACTGACAGCTTCCGCGAG	2649
QY	1510	ATCAGCGCATGTACCCCGCCCTTCTGTACACAGCGCGACGCGCGACCTGCGCGAC	1569	Db	861	ThrValProHisGlyProSerGluAlaArgAsnThrAspThrLeuAspLysLeuArgGln	880
Db	501	IleGlnArgMetTyrAlaArgPheLeuTyrHisSerArgThrArgAspLeuArgAsp	520	QY	2650	GCAGTCAAGAGCTGTACAGCAGAGTGTCTGCAGATCGGGAGGACTGACAGTTCCTGC	2709
QY	1570	TACATCCGATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGTCTGGAGTACTTCCAG	1629	Db	881	AlaValThrGluLeuSerGluGlnValLeuGlnMetArgGluGlyLeuGlnSerLeuArg	900
Db	521	TyrIleArgIleHisArgIleProLysProLeuLysGlnArgMetLeuGluTyrPheGln	540	QY	2710	CAGCTGTGCAGCTGTCTCTGGCGCCCAAGCGAGGCTCGTCCCTCGGGCATTCGGGA	2769
QY	1630	GCCACTGGCGGTGAACATGATCGACACACCGAGCTGTCTGCAGAGCTCCCTGCAC	1689	Db	901	GlnAlaValGlnLeuValLeuAlaProHisArgGluGlyProCysProArgAlaSerGly	920
Db	541	AlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeuLeuGlnSerLeuProAsp	560	QY	2770	GAGGGCGGTGCGCCAGCAGCAGCTCCGGGCTTCTGCAGCTCTGTGTGTGGACACTGGG	2829
QY	1690	GAGTGGCGCAGACATCGCATCGCATCCCTGCACCAAGGAGTCTCTGCAGCTGCCACTGTTT	1749	Db	921	GluGlyProCysProAlaSerThrSerGlyLeuLeuGlnProLeuCysValAspThrGly	940
Db	561	GluLeuArgAlaAspIleAlaMetHisLeuHisLysGluValLeuGlnLeuProLeuPhe	580	QY	2830	GCATCTCTCTACTCTGCTGCAGCCCGCCAGCTGGCTGTCTGTAGTGGAGCTTGGCCCCAC	2889
QY	1750	GAGCGCGCCAGCGCGGTGCTCGGGCACTGTCTCTGGCCCTGCGGCCCGCTTCTGC	1809	Db	941	AlaSerSerTyrCysLeuGlnProProAlaGlySerValLeuSerGlyThrTrpProHis	960
Db	581	GluAlaAlaSerArgGlyCysLeuArgAlaLeuSerLeuAlaLeuArgProAlaPheCys	600	QY	2890	CCTCGTCCGGGCGCTCTCTCCCTCATGGCACCTCTGGGCTCGGGTCCCGAGCGTCTCAG	2949
QY	1810	ACGCGCGCGAGTACTCTATCCACCAAGCGATGCCCTGCGAGGCTCTACTTTGTCTGC	1869	Db	961	ProArgProGlyProProProLeuMetAlaProTrpProTrpGlyProProAlaSerGln	980
Db	601	ThrProGlyGluTyrLeuIleHisGlnGlyAspAlaLeuGlnAlaLeuTyrPheValCys	620	QY	2950	AGCTCCCGCTCGGCTCGAGCCACAGCTTCTGGACCTCCACTCAGACTCAGAGCCCTCT	3009
QY	1870	TCTGGCTCCATGGAGGTCTCAAGGTGCGCACCGTCTCGCCATCTAGGGAGGCGGAC	1929	Db	981	SerSerProTrpProArgAlaThrAlaPheTrpThrSerThrSerAspSerGluProPro	1000
Db	621	SerGlySerMetGluValLeuLysGlyGlyThrValLeuAlaIleLeuGlyLysGlyAsp	640	QY	3010	GCCTCAGAGAGCTTGTCTGTAGCCCGCAGCCCTGCTGCTCCCTCTCTCTCTCTGAGGAA	3069
QY	1930	CTGATCGGTGTGAGTGTCCCGCGGAGCAGGTGTAAAGCCAAATGCCGACCTGAG	1989	Db	1001	AlaSerGlyAspLeuCysSerGluProSerThrProAlaSerProProSerGluGlu	1020
Db	641	LeuIleGlyCysGluLeuProArgGluGlnValValLysAlaAsnAlaAspValLys	660	QY	3070	GGGCTAGGACTGGCCCGCAGAGCTGTGAGCCAGGCTAGGCTACAGCCTCGAGAG	3129
QY	1990	GGGCTGACGATCTGGCTCTGAGTGTCTGAGTGTGGCTGCTGCAAGCAGCTTGGCG	2049	Db	1021	GlyAlaArgThrGlyProAlaGluProValSerGlnAlaGluAlaThrSerThrGlyGlu	1040
Db	661	GlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGlyLeuHisAspSerLeuAla	680	QY	3130	CCCCCAGCAGGTTCAGGGGCTGCGCTTGGCCCTGGACCCCGCCAGCCTGGAGATGTG	3189
QY	2050	CTGTACCCCGAGTTTCCCGCGCTTCAGTCTGGTGGCTCCGAGGGAGCTCAGCTACAAC	2109	Db	1041	ProProProGlySerGlyGlyLeuAlaLeuProTrpAspProHisSerLeuGluMetVal	1060
Db	681	LeuTyrProGluPheAlaProArgPheSerArgGlyLeuArgGlyGluLeuSerTyrAsn	700	QY	3190	CTTATTGGCTGCATGGCTCTGCGCAGTCCAGTGCACCCAGGAGCAAGAGGCAAGGGGTC	3249
QY	2110	CTGGGTGCTGGGGAGGCTCTGAGAGGTGGACACAGCTCTCTGAGCGCGCAATACC	2169	Db	1061	LeuIleGlyCysHisGlySerGlyThrValGlnTrpThrGlnGluGlyThrGlyVal	1080
Db	701	LeuGlyAlaGlyGlyGlySerAlaGluValAspThrSerSerLeuSerGlyAspAsnThr	720	RESULT 10			
QY	2170	CTTATGTCCACGCTGGAGGAGAGGACAGATGGGGAGCAGGCGCCCGCTCCCGCA	2229	AAV44904			
Db	721	LeuMetSerThrLeuGluGluLysGluThrAspGlyGluGlnGlyProThrValSerPro	740	ID AAY44904 standard; protein; 1083 AA.			
QY	2230	GCCTCAGCTCATGAGCCTCCAGCCCGCTGTCTGTCTGCTGCTGCTGCTGCTGCTGCT	2289	XX AAY44904;			
Db	741	AlaProAlaAspGluProSerSerProLeuLeuSerProGlyCysThrSerSerSer	760	XX 18-MAY-2000 (first entry)			
QY	2290	GCTGCCAAGCTGTATCCCAAGTCAAGCAGCAGCCCGGCTGTCTAGTGGCAGAGGG	2349	DE Monkey potassium channel molecule ERG-LP1.			
Db	761	AlaAlaLysLeuLeuSerProArgThrAlaProArgProArgLeuGlyGlyArgGly	780	XX Monkey; potassium channel molecule; ERG-like protein 1; ERG-LP1;			
QY	2350	AGGCCAGCAGGCGGGCTTTAAGCTCAGCTGAGCTGCGCCCTCTGTCTCCCGCCAGCGCC	2409	KW neuroprotective; antiParkinsonian; anticonvulsant; antidepressant;			
Db	781	ArgProGlyArgAlaGlyAlaLeuLysAlaGluAlaGlyProSerAlaProProArgAla	800	KW neuroleptic; nootropic; treatment; CNS disorder; central nervous system;			
QY	2410	CTAGAGGGGTACCGCTCCCGCCCATGCGATGTGCCCGCCAGATCTGAGCCCGCAGG	2469	KW potassium channel mediated disorder; epilepsy; Alzheimer's disease;			
Db	801	LeuGluGlyLeuArgLeuProMetProTrpAsnValProProAspLeuSerProArg	820	KW Parkinson's; multiple sclerosis; depression; schizophrenia; amnesia.			
QY	2470	GTAGTAGATGGCATTTGAAGACGGCTGTGGCTCGGACCGCCCAAGTTCTTCTCGCGTG	2529	XX Primates.			
				XX Key Location/Qualifiers			
				FH Modified-site 13..16			
				FT /note= "Casein kinase II phosphorylation site"			
				FT Modified-site 20..23			

Db 41 ProValValTyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal 60
 QY 181 ATGACGGGGCTGTGCTGCTCTCTCTTATGGGCGACACCAAGTGTGAGCTGTGCTCCG 240
 Db 61 MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArg 80
 QY 241 CAACAGATCCGGAAGCCCTGGAGCAGACCAAGAGTTCAAGGCTGAGCTGATCCCTGTAC 300
 Db 81 GlnGlnIleArgIysAlaLeuAspGluHisIysGluPheIysAlaGluLeuIleLeuTyr 100
 QY 301 CGAAGAGCGGGCTCCGGTCTGCTGCTCTCTGATGTATACCCATAAAGAATGAGAAA 360
 Db 101 ArgIysSerGlyLeuProPheTrpCysLeuLeuAspValIleProIleIysAsnGluIys 120
 QY 361 GGGAGGTGGCTCTCTTCTAGTCTCTCAAGAGCATCAGCGAACAACAGAACCGAGGG 420
 Db 121 GlyGluValAlaLeuPheLeuValSerHisIysAspIleSerGluThrLysAsnArgGly 140
 QY 421 GGGCGGACAGATGGAAGGAGACAGGTGGTGGCGGCGCATATGGCGGCACGATCC 480
 Db 141 GlyProAspArgTrpIysGluThrGlySerGlyArgArgTrpGlyIysAlaArgSer 160
 QY 481 AAGGCTTCAATGCAACCGCGCGAGCGCGCTGTCTTACCACTGTCTCGGGCAC 540
 Db 161 LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis 180
 QY 541 CTGCAAGAGCAGCCCAAGGGCAAGCAAGTCAATTAAGGGGTGTTGGGGAGAACCACCA 600
 Db 181 LeuGlnIysGlnProLysGlyLysHisIysLeuAsnIysGlyValPheGlyGluIysPro 200
 QY 601 AACTGGCTGAGTCAAGTAGCGCCATCCGGAAGTCGCCCTTCATCTGTGCTGCTGCT 660
 Db 201 AsnLeuProGluTyrLysValAlaAlaIleArgLysSerProPheIleLeuLeuHisCys 220
 QY 661 GGGCACTGAGCAGCACCTGGATGGCTTCACTGCTGCGCCACACTATGTGCTGCTC 720
 Db 221 GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal 240
 QY 721 ACTGTGCCCTACAGCGTGTGTGAGCAGACAGCGAGCGGAGCGGCGCGCGCGCG 780
 Db 241 ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro 260
 QY 781 CCCAGCGTGTGACCTGGCGGTGAGGTCTCTTCACTTCACTTGTGCTGCTGCTGCTGCT 840
 Db 261 ProSerValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPhe 280
 QY 841 CGTACCAATTGCTTCAAGTCGGCGCAGGTGGTGTGGTGGTGGTGGTGGTGGTGGTGGT 900
 Db 281 ArgThrThrPheValSerIysSerGlyGlnValValPheAlaProLysSerIleCysLeu 300
 QY 901 CACTACGTCACCACTGCTTCTGTGTGATGTCATCGAGCGCTGCGCTTGTGCTGCTGCT 960
 Db 301 HisTyrValThrTrpPheLeuLeuAspValIleAlaAlaLeuProPheAspLeuLeu 320
 QY 961 CATGCTTCAAGGTCAAGTGTACTTGGGCGCCATCTGCTCAAGACGCTGCGCTGCTGCTG 1020
 Db 321 HisAlaPheLysValAsnValTyrPheGlyAlaHisLeuLeuIysThrValArgLeuLeu 340
 QY 1021 CGCCTGCTGCGCTGCTTCCGGCTGGACCGGTACTCGCAGTACAGCGCGCTGCTGCTG 1080
 Db 341 ArgLeuLeuArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValValLeu 360
 QY 1081 ACACCTGCTCATGCGCTGTGCGCTGCTGCGCATGCGGTGCGCTGCTGCTGCTGCTGCT 1140
 Db 361 ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr 380
 QY 1141 ATTGGCCAGGGAGATCGAGACCGCAATCCGAGCTGCTGAGATTGCTGCTGCTGCTGCTG 1200
 Db 381 IleGlyGlnArgGluIleGluSerSerGluSerGluLeuProGluIleGlyTrpLeuGln 400
 QY 1201 GAGCTGCGCGCGCTGAGACTCCCTACTACTGCTGGTGGCGGAGGCGGAGCTGGAGGG 1260
 Db 401 GluLeuAlaArgArgLeuGluThrProTyrTyrLeuValGlyArgArgProAlaGlyGly 420

QY 1261 AACAGCTCCGGCCAGAGTGCACAACTGCAGCAGCAGCGAGCCCAACCGGACGGGGCTG 1320
 Db 421 AsnSerSerGlyGlnSerAspAsnCysSerSerSerGluAlaAsnGlyThrGlyLeu 440
 QY 1321 GAGCTCTGGGGCGGCGCTGCTGCGAGCGCTCATCATCCTCCCTCTACTTTCGCACTC 1380
 Db 441 GluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeu 460
 QY 1381 AGCAGCTCACAGCTGGGCTTGGCAACGCTGCGCCCAACACGAGACCGAGAGATC 1440
 Db 461 SerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGluLysIle 480
 QY 1441 TCTTCATCTGCACCATGCTCATCGCGCGCTCATGCACCGGTGGTGGTGGTGGTGGTGG 1500
 Db 481 PheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValValPheGlyAsnVal 500
 QY 1501 ACGCCCATCATCGAGCGCATGTACCGCGCGCTTCTGTACACACCGCGCGCGCGAC 1560
 Db 501 ThrAlaIleIleGlnArgMetTyrAlaArgArgPheLeuTyrHisSerArgThrArgAsp 520
 QY 1561 CTGGCGACTACATCCGATCCACCGTATCCCAAGCCCTCAAGCAGCGCATCTCGAG 1620
 Db 521 LeuArgAspTyrIleArgIleHisArgIleProLysProLeuLysGlnArgMetLeuGlu 540
 QY 1621 TACTTCAGGCGCACTGGCGGTGAACAATGGCATCGACACCGAGCTGCTGCGAGC 1680
 Db 541 TyrPheGlnAlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeuGlnSer 560
 QY 1681 CTCCTGACGAGCTGCGCGGAGCATCGCCATGACCTGCACAGAGGCTCCTCAGCTG 1740
 Db 561 LeuProAspGluLeuArgAlaAspIleAlaMetHisLeuHisIysGluValLeuGlnLeu 580
 QY 1741 CCCTGTTTGGGCGCGCGCGCTGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
 Db 581 ProLeuPheGluAlaAlaSerArgGlyCysLeuArgAlaLeuSerLeuAlaLeuArgPro 600
 QY 1801 GCCTTCTGCACCGCGCGAGTACTCATCCCAAGCGAGTGCCTCAGCGCTCCTCAGC 1860
 Db 601 AlaPheCysThrProGlyGluTyrLeuIleHisGlnGlyAspAlaLeuGlnAlaLeuTyr 620
 QY 1861 TTTGCTGCTCTGCTCCATGAGGTGCTCAAGGTGCACCGCTGCTGCCATCTCAGG 1920
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 QY 1921 AAGGCGCACTGATCGGCTGAGCTGCGCGCGGAGCAGTGGTAAAGCCCAATGCC 1980
 Db 641 LysGlyAspLeuIleGlyCysLeuProArgArgGluGlnValValLysAlaAsnAla 660
 QY 1981 GACGTGAAGGGGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
 Db 661 AspValLysGlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGlyLeuHisAsp 680
 QY 2041 AGCCTTGGCTGTACCCGAGTTTCCCGCTTTCAGTCTGCTGCTGCTGCTGCTGCTGCT 2100
 Db 681 SerLeuAlaLeuTyrProGluPheAlaProArgPheSerArgGlyLeuArgGlyGluLeu 700
 QY 2101 AGCTCAACCTGGGTGGGAGGCTCTGAGAGGTGCACACAGCTCCCTCGAGCGGC 2160
 Db 701 SerTyrAsnLeuGlyAlaGlyGlySerAlaGluValAspThrSerSerLeuSerGly 720
 QY 2161 GACATATCCCTTATGTCCACGCTGGAGGAGAGAGACAGATGGGAGCAGGCGCCACG 2220
 Db 721 AspAsnThrLeuMetSerThrLeuGluLysGluThrAspGlyGluGlnGlyProThr 740
 QY 2221 GTCTCCAGCGCCCGAGCTGATGAGCCCTCCAGCCCTGCTGCTGCTGCTGCTGCTGCT 2280
 Db 741 ValSerProAlaProAlaAspGluProSerSerProLeuLeuSerProGlyCysThrSer 760
 QY 2281 TCATCTGAGCTGCGAGCTGCTATCCCACTGCAACAGCAGCCCGGCTCGTCTAGGT 2340
 Db 761 SerSerSerAlaAlaLysLeuLeuSerProArgThrAlaProArgProArgLeuGly 780

181 ATGAGCGGGCTGCTGCTCTCTCTTATGGCCAGACACCACTGAGCTGCTCCGC 240
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61 MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArg 80
QY
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Db
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QY 2941 CGCTCTCAGAGCTCCCGCTGGCTCGAGCCACAGCTTTCTGGACCTCCACCTCAGACTCA 3000
Db 981 AlaSerGlnSerSerProTrpProArgAlaThrAlaPheTrpThrSerThrSerAspSer 1000
QY 3001 GAGCCCCCTGCTCAGAGACCTCTGCTTGAGCCAGCACCCCTGCTCCCTCCCTCTCTCT 3060
Db 1001 GluProProAlaSerGlyAspLeuCysSerGluProSerThrProAlaSerProProPro 1020
QY 3061 TCTGAGGAGGGCTAGGACTGGCCCGCAGAGCTGTGAGCCAGCTGAGCCAGGTACAGC 3120
Db 1021 SerGluGluGlyAlaArgThrGlyProProGluProValSerGlnAlaGluAlaThrSer 1040
QY 3121 ACTGAGAGAGCCCCACAGGCTCAGGGGCTGGCCCTGGCCCTGGGACCCACACAGCTG 3180
Db 1041 ThrGlyGluProProProValSerGlyGlyLeuAlaLeuProTrpAspProHisSerLeu 1060
QY 3181 GAGATGGTCTTATGGCTGCCATGGCTCTGGCACAGTCCAGTGACCCAGGGAAGAGGC 3240
Db 1061 GluMetValLeuIleGlyCysHisGlySerGlyThrValGlnTrpThrGlnGluGluGly 1080
QY 3241 ACAGGGGTC 3249
Db 1081 ThrGlyVal 1083
```

RESULT 13

AAY34128

ID AAY34128 standard; protein; 1082 AA.

XX AC AAY34128;

XX DT 30-NOV-1999 (first entry)

XX DE Human potassium channel K-Hnov14.

XX KW Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;
XX KW cardiovascular disorder; CNS disorder; renal disorder.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Misc-difference 22 /note= "Arg substituted by Cys in a variant form of
XX FT K-Hnov14"

XX FT WO9943696-A1.

QY 181 ATGCAGCGGGCTGTGCCTGTCTCTTATGATGCGCCAGACACAGTCAGTCGTCGCCG 240

XX PD

XX PF

XX XX

XX XX

XX XX

XX XX

XX XX

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XX 02-SEP-1999.

XX 22-FEB-1999; 99WO-US0003826.

XX 25-FEB-1998; 98US-0076687P.

XX 07-AUG-1998; 98US-0095836P.

XX 19-JAN-1999; 99US-0116448P.

XX (AXYS-) AXYS PHARM INC.

XX Miller AP, Curran ME, Hu P, Rutter M, Wang J;

XX WPI; 1999-527591/44.

XX N-PSDB; AA211906.

XX New nucleic acids encoding mammalian K-Hnov potassium channel proteins,

XX useful for the diagnosis and treatment of episodic ataxia with myokymia,

XX cardiac arrhythmia, epilepsy and Bartter's syndrome.

XX Claim 3; Page 77-79; 112pp; English.

XX This sequence represents the human K-Hnov14 potassium channel. K-Hnov

XX proteins have a high degree of homology to known potassium channels and

XX may be alpha subunits, which form the functional channel, or accessory

XX subunits that act to modulate the channel activity. K-Hnov14 is a 6

XX transmembrane domain, voltage gated potassium channel. The gene's

XX chromosomal location is 12q14, determined via PCR chromosomal

XX localisation using primers AA211928 and AA211929. K-Hnov cDNAs were

XX isolated by extension of expressed sequence tags (ESTs) which were

XX related but not identical to known human potassium channels. Potential

XX polymorphisms detected as sequence variants between multiple independent

XX clones. Potassium channels have critical roles in various cell types and

XX biochemical pathways. Defective potassium channels are known to cause

XX four human diseases: episodic ataxia with myokymia; cardiac arrhythmia

XX (long QT syndrome); epilepsy; and Bartter's syndrome. As potassium

XX channels are critical components of virtually all cells, it is likely

XX that abnormal potassium channels are also implicated in certain renal,

XX cardiovascular and central nervous system (CNS) disorders. Nucleotides

XX encoding K-Hnov proteins may be used for identifying homologous or

XX related proteins and the DNA sequences encoding them. They may be used to

XX produce compositions that modulate the biochemical pathways associated with

XX K-Hnov protein and in studying the recombinant production of K-Hnov

XX it. They may also be used for the recombinant production of K-Hnov

XX protein in fermentation cultures. Additionally, such nucleotides may be

XX used in gene therapy protocols for the treatment of diseases associated

XX with abnormal potassium channels

XX Sequence 1082 AA;

XX Alignment Scores:

XX Pred. No.: 0 Length: 1082

XX Score: 5649.50 Matches: 1076

XX Percent Similarity: 99.35% Conservative: 0

XX Best Local Similarity: 99.35% Mismatches: 6

XX Query Match: 92.78% Indels: 1

XX DB: 2 Gaps: 1

XX US-09-965-830-1_COPY_6_3257 (1-3252) x AAY34128 (1-1082)

XX QY 1 ATGCGCGCATGGGGCTCTCTGGCGCTCAGACACACCTCTCTGACACCATGCTAGC 60

XX Db 1 MetProAlaMetArgGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20

XX QY 61 CGCTTCGACGCGCACAGTAACTTCGTGGGCAACGCCAGGTGGCGGGCTCTTC 120

XX Db 21 ArgPheAspGlyThrHisSerAsnValLeuGlyAsnAlaSer---GlyGlyAlaLeu 39

XX QY 121 CCGGTGGTCTACTGCTCTCTGATGGCTTCTGTGACCTCAGGGGCTCTCCCGGGCTGAGTTC 180

XX Db 40 ProValValTyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal 59

60 MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArg 79
241 CAACAGATCCGACAGGCGCTCGACGACGACCAAGAGTTCAAGGCTGAGCTGATCCTGTAC 300
80 GlnGlnIleArgIysAlaLeuAspGluHisIysGluPheIysAlaGluLeuIleLeuTyr 99
301 CGGAAGAGCGGCTCCGCTCTCTGCTCTCTGCTCTGATGTATACCATTAAGAAGTACGAAA 360
100 ArgIysSerGlyLeuProPheThrPheCysLeuLeuAspValIlePheProIleIysAsnGluIys 119
361 GGGAGGTGGCTCTCTCTAGTCTCTCACAGGACATACGCGAAACCAAGAACCGAGGG 420
120 GlyGluValAlaLeuPheLeuValSerHisIysAspIleSerGluThrLysAsnArgGly 139
421 GGGCCCCACAGATGGAAGGACAGAGTGTGGCGCGCGCGCATATGCGCGGCGACGATCC 480
140 GlyProAspArgTrpLysGluThrGlyGlyArgArgArgTyrGlyArgAlaArgSer 159
481 AAGGCTTCAATGCCAACCGCGCGGAGCGCGCGCTGTCTACCACTCTCCGGGCGAC 540
160 LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis 179
541 CTGCAGAGCAGCCCAAGGCGCAAGCAAGCTCAATAAGGGGTGTTTGGGAGAAACCA 600
180 LeuGlnLysGlnProLysGlyLysHisIysLeuAsnLysGlyValPheGlyGluLysPro 199
601 AACTGCTGAGTACAAAGTAGCGGCATCGGGAAGTGGCCCTTCATCCTGTTGACTGT 660
200 AsnLeuProGluTyrLysValAlaAlaIleArgLysSerProPheIleLeuLeuHisCys 219
661 GGGCACTGAGAGCACCTGGATGGTCTTACTCTGTCGCCACACTCTATGTGCTGTC 720
220 GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal 239
721 ACTGTGCCCTACAGCGTGTGTGAGCACAGCACGGGAGCCAGTGGCGCGCGCGCGC 780
240 ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro 259
781 CCCAGCGTGTGACCTGGCGCGTGGAGGTCTCTTCTATCTTCATCTTGACATGTGCTGAATTTC 840
260 ProSerValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPhe 279
841 CGTACCACATTGCTGTGCTCAAGTCGGGCGAGGTGTGTTGCCCAAGTCCATTGCTC 900
280 ArgThrThrPheValSerLysSerGlyGlnValPheAlaProLysSerIleCysLeu 299
901 CACTACGTCACCACTGGTTCTCTGCTGATGTCATCGCAGCGCTGCCCTTTGACCTGCTA 960
300 HistyrValThrThrTrpPheLeuLeuAspValIleAlaLeuProPheAspLeuLeu 319
961 CATGCCCTCAAGTCAAGTGTACTTCGGGCGCATCTGTGAGACGGTGGCGCTGCTG 1020
320 HisAlaPheLysValAsnValTyrPheGlyAlaHisLeuLeuLysThrValArgLeuLeu 339
1021 CGCCTGTGCGCTGCTTCCGCGCTGACCGGCTACTCGCAGTACAGCGCGTGGTGTG 1080
340 ArgLeuLeuArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValValLeu 359
1081 ACATGCTCATGGCGGTGTTCCGCTGCTGCTGCGCACTGGGTGCGCTGCTGCTGTTTAC 1140
360 ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr 379
1141 ATTGGCCAGCGGAGATCGAGAGCAGGAATCCGAGCTGCTGATGATGGTGGCTGCG 1200
380 IleGlyGlnArgGluIleGluSerSerGluSerGluLeuProGluIleGlyTrpLeuGln 399
1201 GAGCTGGCGCGGACTGGAGACTCCCTACTACTGTGTGGGCGGAGCCAGCTGGAGGG 1260
400 GluLeuAlaArgLeuGluThrProTyrTyrLeuValGlyArgArgProAlaGlyGly 419
1261 AACAGCTCCGGCCAGAGTGACAACCTGCAGCAGCAGCAGCGAGGCCAACCGGACGGGGCTG 1320

420 AsnSerSerGlyGlnSerAspAsnCysSerSerSerGluAlaAsnGlyThrGlyLeu 439
1321 GAGCTGCTGGGCGCGCTGCTGCGCAGCGCTACATCACCTCCCTACTCTTGCACCTC 1380
440 GluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeu 459
1381 AGCAGCCTCACCAGCGTGGCTTCGGCAACGCTGTCGCCAACACCGACACCGAGAGATC 1440
460 SerSerLeuThrSerValGlyPheGlyAsnValSerAlaLeuThrAspThrGluLysIle 479
1441 TTCTCCATGTCACCATGCTCATCGGCGCCTGTATGCAOCGGTGGTGTGTTGGAAACGTG 1500
480 PheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValValPheGlyAsnVal 499
1501 ACGGCAATCATCCAGCGCATGTAGCGCGCGCTTCTGTACACACAGCGCGCAGCGGAC 1560
500 ThrAlaIleIleGlnArgMetTyrAlaArgArgPheLeuTyrHisSerArgThrArgAsp 519
1561 CTGGCGCACTACATCCGCATCCACCGTATCCCAAGCCCTTCAAGCAGCGCATGCTGGAG 1620
520 GlnArgAspTyrIleArgIleHisArgIleProLysProLeuLysGlnArgMetLeuGlu 539
1621 TACTTCAGGCGCACTCGGCGGTGAACAATGGCATCGACACACCGAGCTGCTCAGAGC 1680
540 TyrPheGlnAlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeuLeuGlnSer 559
1681 CTCCTCACGAGCTGCGCGCAGACATCGCCATGCACCTGCACAGGAGGTCTCTCAGCTG 1740
560 LeuProAspGluLeuArgAlaAspIleAlaMetHisLeuHisIysGluValLeuGlnLeu 579
1741 CCAGTGTTCAGGCGCGCAGCGCGCTGCTGCGGCGACTGTCTCTGGCGCTCGCGGCC 1800
580 ProLeuPheGluAlaIleAspArgGlyCysLeuArgAlaLeuSerLeuAlaLeuArgPro 599
1801 GCCTTCGACGCGCGCGAGTACTCATTCACCAAGCGGATGCCCTGCGAGGCCCTCTAC 1860
600 AlaPheCysThrProGlyGluTyrLeuIleHisGlnGlyAspAlaLeuGlnAlaLeuTyr 619
1861 TTTGTCTGCTGCTGCTCCATGGAGGTGCTCAAGGTGCGCCGCTGCTGCGCTCCTAGG 1920
620 PheValCysSerGlySerMetGluValLeuLysGlyGlyThrValLeuAlaIleLeuGly 639
1921 AAGGGCACCTGATCGGCTGTGAGTCCCGCGCGGAGGAGGTGTTAAAGGCCAATGCC 1980
640 LysGlyAspLeuIleGlyCysGluLeuProArgArgGluGlnValValLysAlaAsnAla 659
1981 GAGGTGAAGGGGTGACGTACTCGTCTCTGAGTGTCTGACGTGGCTGCGCTGCGACAC 2040
660 AspValLysGlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGlyLeuHisAsp 679
2041 AGCCTTGGCTGTACCGCGAGTTTGGCGGCTTTCAGTGTGCTGCGCTCGAGGGAGCTC 2100
680 SerLeuAlaLeuTyrProGluPheAlaProArgPheSerArgGlyLeuArgGlyGluLeu 699
2101 AGCTACAACTGGTGTCTGGGCGAGGCTCTGACAGGTGGACACCACTCTCTGAGCGGC 2160
700 SerTyrAsnLeuGlyAlaGlyGlySerAlaGluValAspThrSerSerLeuSerGly 719
2161 GACAATACCTTATGTCCAGCTGGAGGAGAGAGACAGATGGGAGCAGGGCCCCACG 2220
720 AspAsnThrLeuMetSerThrLeuGluLysGluThrAspGlyGluGlnGlyProThr 739
2221 GTCTCCCGACCGCTGATGAGCCCTCCAGCCCTGCTGTCTGCTGCTGCTGCTGCTGCTC 2280
740 ValSerProAlaProAlaAspGluProSerSerProLeuLeuSerProGlyCysThrSer 759
2281 TCATCTCAGTGTCAAGTGTCTATCCACGTCCGAACAGCACCGCCCGCTCGTCTAGGT 2340
760 SerSerSerAlaAlaLysLeuLeuSerProArgArgThrAlaProArgProArgLeuGly 779
2341 GGCAGAGGCGCGCAGCGGCGGCTTTGAAGCTGAGGCTGAGGCTGCCCTCTGCTCCC 2400
780 GlyArgGlyArgProGlyArgAlaGlyAlaLeuLysAlaGluAlaGlyProSerAlaPro 799

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QY 2401 CCACGGCCCTAGAGGGCTACGGCTGCCCCCATCGATGGAATGCCCCCAGATCTG 2460
Db      |||
QY 800  ProArgAlaLeuGluGlyLeuArgLeuProMetProTyrAsnValProProAspLeu 819
Db      |||
QY 2461 AGCCCCAGGGTAGATGCGCATGAAGCGGTGTGGCTCGGACCGCCAAAGTTCTCT 2520
Db      |||
QY 820  SerProArgValValAspGlyIleGluAspGlyCysGlySerAspGlnProLysPheSer 839
Db      |||
QY 2521 TTCCGGGTGGCCAGCTGGCCCGGAATGTAGCAGCAGCCCTCCCTGACCCAGAGAGC 2580
Db      |||
QY 840  PheArgValGlyGlnSerGlyProGluCysSerSerProSerProGlyProGluSer 859
Db      |||
QY 2581 GGCCTGCTCACTGTTCCCATGGGCCAGCGAGGCAAGGAACACAGACACTGGACAAG 2640
Db      |||
QY 860  GlyLeuLeuThrValProHisGlyProSerGluAlaArgAsnThrAspThrLeuAspLys 879
Db      |||
QY 2641 CTTGGCAGCGGTGACAGAGCTGTGACAGCAGGTGCTGACAGTGGGGAGACTGCAG 2700
Db      |||
QY 880  LeuArgGlnAlaValThrGluLeuSerGluGlnValLeuGlnMetArgGluGlyLeuGln 899
Db      |||
QY 2701 TCATCTGCGCAGGCTGTGAGCTGTGCTCGGCCCCACAGGAGGCTCGTCCCTCGG 2760
Db      |||
QY 900  SerLeuArgGlnAlaValGlnLeuValLeuAlaProHisArgGluGlyProCysProArg 919
Db      |||
QY 2761 GCATCGGGAGAGGGCGGTGCCAGCAGCACCTCCGGGCTCTGCAGGCTCTGTGTGTG 2820
Db      |||
QY 920  AlaSerGlyGluGlyProCysProAlaSerThrSerGlyLeuLeuGlnProLeuCysVal 939
Db      |||
QY 2821 GACACTGGGCATCTCTACTGCTGACGCCGCCAGCTGGCTGTGCTGTGAGTGGACT 2880
Db      |||
QY 940  AspThrGlyAlaSerSerTyrCysLeuGlnProProAlaGlySerValLeuSerGlyThr 959
Db      |||
QY 2881 TGCCCCCACCCTCGTCCGGGGCTCTCTCCCTCATGGCACCTCGGCGCTCGGCCA 2940
Db      |||
QY 960  TrpProHisProArgProGlyProProProLeuMetAlaProArgProTyrGlyProPro 979
Db      |||
QY 2941 GGTCTCAGAGCTCCCGCTGGCTCGAGCCACAGCTTTCTGGACCTCCACCTCAGACTCA 3000
Db      |||
QY 980  AlaSerGlnSerSerProTyrProArgAlaThrAlaPheTyrThrSerThrSerAspSer 999
Db      |||
QY 3001 GAGCCCCCTGCTCAGAGACTCTGCTGAGCCGACGACCCCTGCTCCCTCCCTCTCT 3060
Db      |||
QY 1000 GluProProAlaSerGlyAspLeuCysSerGluProSerThrThrProAlaSerProPro 1019
Db      |||
QY 3061 TCTGAGGAAGGGCTAGGACTGGGCCCGCAGAGCCTGTGAGCCAGGCTGAGGCTACGAG 3120
Db      |||
QY 1020 SerGluGluGlyAlaArgThrGlyProAlaGluProValSerGlnAlaThrSer 1039
Db      |||
QY 3121 ACTGGAGAGCCCCACAGGCTCAGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3180
Db      |||
QY 1040 ThrGlyGluProProProGlySerGlyGlyLeuAlaLeuProTyrAspProHisSerLeu 1059
Db      |||
QY 3181 GAGATGCTGCTATTGCTGCCATGCTCTGCGCACAGTCCAGTGGACCCAGGAGAGGC 3240
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QY 1060 GluMetValLeuIleGlyCysHisGlySerGlyThrValGlnThrThrGlnGluGly 1079
Db      |||
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RESULT 14

ADE55602
ID ADE55602 standard; protein; 1087 AA.

XX AC ADE55602;

XX AC ADE55602;

DT 29-JAN-2004 (first entry)

XX DE Rat Protein CAA07586, SEQ ID NO 1421.

XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;

XX KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX OS Rattus norvegicus.
XX PN WO2003016475-A2.
XX PD 27-FEB-2003.
XX PF 14-AUG-2002; 2002WO-US025765.
XX PR 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
XX (GEO) GEN HOSPITAL CORP.
XX (FARB) BAYER AG.
XX Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
XX GENBANK; CAA07586.
XX PT New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX PS Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially
XX expressed in an animal subjected to pain, a method for identifying a
XX compound that regulates the activity of one or more of the
XX polynucleotides, a method for producing a pharmaceutical composition, a
XX method for identifying a compound or small molecule that regulates the
XX activity in an animal of one or more of the polypeptides given in the
XX specification, a method for identifying a compound useful in treating
XX pain and a pharmaceutical composition comprising the one or more
XX polypeptides or their antibodies. The polynucleotide or the compound that
XX modulates its activity is useful for preparing a medicament for treating
XX pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene
XX injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
XX therapy). The sequence presented is a rat protein (shown in Table 2 of
XX the specification) which is differentially expressed during pain. Note:
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic form directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 1087 AA;

Alignment Scores:

Pred. No.: 0 Length: 1087
Score: 5428.00 Matches: 1039
Percent Similarity: 96.60% Conservative: 11
Best Local Similarity: 95.58% Mismatches: 33
Query Match: 89.14% Indels: 4
DB: 7 Gaps: 2

US-09-965-830-1_COPY_6_3257 (1-3252) x ADE55602 (1-1087)

QY 1 ATGCGGCGCATGGGGCTCTGGCGCTCAGACACCTCTCTGACACCATCGCTACG 60
Db 1 MetProAlaMetArgGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20
QY 61 CGCTTCGAGCGGACGACAGTAACTTCGTCTGGGCAAGCCAGGTCGGGGGCTCTTC 120
Db 21 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnValAlaGlyLeuPhe 40

316	LeuTyrAlaPheAsnValThrValValSerLeuValHisLeuLeuLysThrValArgLeu	335
1018	CTCGGCTGCTGGCGCTGCTTCCGGCGCTCGAGCCGGTACTCGCAGTACACGCCGCTGGTG	1077
336	LeuArgLeuLeuArgLeuLeuGlnLysLeuAspArgTyrSerGlnHisSerThrIleVal	355
1078	CTGACACTGCTCATGGCGGTGTTCGCCCTGCTCGCGCACTCGGGTCGCTCGCTGTGTT	1137
356	LeuThrLeuLeuMetSerMetPheAlaLeuLeuAlaHisTrpMetAlaCysIleTrpTyr	375
1138	TACATTGGCCAGCGGGAGATCGAGAGCGGAATCCGAGCTGGCTGAGATTGGCTGGCTG	1197
376	ValIleGlyLysMetGluArgGluAspAsnSerLeuLeuLysTrpGluValGlyTrpLeu	395
1198	CAGAGTGGCCCGCCGACTGGAGACTCCCTACTTACTCTGGTGGCGCGGACGCTGGA	1257
396	HisLeuLeuGlyLysArgLeuGluSerProTyrTyr	407
1258	GGGAACAGCTCCGGCCAGAGTGAACACTGCAGCAGCAGCAGCGAGGCCAACGGGACGGG	1317
408	GlyAsnAsnThr	411
1318	CTGAGACTGTGGCGGCCGCTGCTGCGGAGCGCCTACATCACTCCCTCTACTTCGCA	1377
412	-----LeuGlyGlyProSerIleArgSerAlaTyrIleAlaAlaLeuTyrPheThr	428
1378	CTCAGCAGCTCACACGCTGGCTTCGGCAAAGTGTCCGCCACACGGACACCGAGAAG	1437
429	LeuSerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspAlaGluLys	448
1438	ATCTTCTCCATCTGCACCATGCTCATCGGGGCCCTGATGCACGCGGTGTGTTGGGAAC	1497
449	IlePheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaLeuValPheGlyAsn	468
1498	GTGACGCCCATATCCAGCGCATATACGCCCGCGCTTCTGTACCAACACGCCGACGCGC	1557
469	ValThrAlaIleIleGlnArgMetTyrSerArgTrpSerLeuTyrHisThrArgThrLys	488
1558	GACCTGGCGACTACATCCGCATCCACGGTATCCCCAAGCCCCCTCAAGCAGCGCATCTG	1617
489	AspLeuLysAspPheIleArgValHisLeuProGlnGlnLeuLysGlnArgMetLeu	508
1618	GAGTACTTCAGAGGCACCTGGCGCGGTGAACAATGGCATCCACACCGAGTCTCTCGAG	1677
509	GluTyrPheGlnThrThrTrpSerValAsnAsnGlyIleAspSerAsnGluLeuLeuLys	528
1678	AGCTCTCTGACGAGCTGCGCGCAGACATCGCCATGCACCTGCAACAAGGAGTCTCTCGAG	1737
529	AspPheProAspGluLeuArgSerAspIleThrMetHisLeuAsnLysGluIleLeuGln	548
1738	CTGCCACTGTTTGAAGCGCCAGCGCGGTGCTCTGGCGGACACTGTCTCTGGCCCTCGG	1797
549	LeuSerLeuPheGluCysAlaSerArgGlyCysLeuArgSerLeuHisIleLys	568
1798	CCGCGCTTCTGCACGCGCGGGGAGTACTCTATCCACCAAGCGCATGCCCTGACGCGCTC	1857
569	ThrSerPheCysAlaProGlyGluTyrLeuLeuArgGlnGlyAspAlaLeuGlnIleLeu	588
1858	TACTTTTGTCTCTGCTCCATCGGAGGTGCTCAAGGGTGGCGACCGCTGCTGCCATCTTA	1917
589	TyrPheValCysSerGlySerMetGluValLeuLysAspSerMetValLeuAlaIleLeu	608
1918	GGGAAGGGCGACTGATCGGCTGTGAGCTGCCCGCGGGAGCAGGTGGTTAAGGCCAAT	1977
609	GlyLysGlyAspLeuIleGlyAlaAsnLeuSerIleLysAspGlnValIleLysThrAsn	628
1978	GCCGACGTGAAGGGCTGACTACTCGTCTCTGCAGTGTCTGCAGCTGGCTGGCTGCAC	2037
629	AlaAspValLysAlaLeuThrTyrCysAspLeuGlnCysIleIleLeuLysGlyLeuPhe	648
2038	GACAGCCTTGGCTGTATCCCGAGTTTGGCCCGCGCTTCAGTCTGGTGCCTCCGAGGGGAG	2097

[illegible]

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QY 2965 CGAGCCAGAGCTTCTGGACCTCCACCTCAGACTCAGAGCCCTGCTCAGGAGACTC 3024
Db   ::: |||
971 GlnArgThrGly-----AlaHisGluGlnAsnProAlaAspSerGluLeu 985
QY 3025 TGCTGTGAGCCAGACACCCCTGCTCCCT----- 3054
Db   |||||
986 TyrHisSerProSerLeuAspTyrSerProSerHisTyrGlnValGlnGluGlyHis 1005
QY 3055 -----CCTCTTCTGAGGAGGGCTAGACTGGGCCCGCAGAG 3093
Db   |||
1006 LeuGlnPheLeuArgCysIleSerProHisSerAspSerThrLeuThr---ProLeuGln 1024
QY 3094 CCTGTGAGCCAGGCTACGAGCACTGAGAGCCCCCAGGGTCAAGGGGCGCTG 3153
Db   ::::|
1025 SerIleSerAlaThrLeuSerSerSerValCysSerSerSerGluThrSerLeuHisLeu 1044
QY 3154 GCCTTGCCCTGGGACCCCAAGCCTGGAGATGGTGTTATGGTGCCATGGCTCTGGC 3213
Db   |||||
1045 ValLeuPro-----SerArgSerGluGlu-----GlySerPheSerGlnGly 1058
QY 3214 ACAGTC-----CAGTGCACCCAGGAA 3234
Db   |||||
1059 ThrValSerSerPheSerLeuGluAsnLeuProGlySerTrpAsnGlnGlu 1075
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Search completed: September 1, 2004, 16:05:29
Job time : 474.5 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 1, 2004, 14:38:36 ; Search time 161 Seconds
(without alignments)
11209.319 Million cell updates/sec

Title: US-09-965-830-1_COPY_6_3257
Perfect score: 3252
Sequence: 1 atccggccatgcggggcct.....aagaagcacacaggggtctga 3252

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3252	100.0	3323	4	US-09-600-776-1
2	3245.8	99.8	3249	4	US-09-343-494-2
3	3218	99.0	3257	4	US-09-336-643A-19
4	3156	97.0	3355	4	US-09-358-383C-1
5	3153	97.0	3249	4	US-09-358-383C-3
6	2664.8	81.9	3715	4	US-09-600-776-9
7	884.8	27.2	3064	4	US-09-600-776-5
8	869.8	26.7	3736	4	US-09-600-776-10
9	844.4	26.0	870	4	US-09-358-383C-9
10	844.4	26.0	1132	4	US-09-358-383C-7
11	761.2	23.4	3321	4	US-09-358-383C-17
12	761.2	23.4	5107	4	US-09-358-383C-15
13	572.8	17.6	1626	4	US-09-358-383C-6
14	572.8	17.6	2694	4	US-09-358-383C-4
15	572.8	17.6	5955	4	US-09-358-383C-14
16	361.6	11.1	3041	4	US-09-694-777A-19
17	353.6	10.9	3041	4	US-09-694-777A-20
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19	342.8	10.5	3950	3	US-09-226-012-3
20	303	9.3	2886	4	US-09-694-777A-13
21	303	9.3	3002	4	US-09-694-777A-1
22	281.2	8.6	2967	4	US-09-694-777A-14
23	281.2	8.6	3083	4	US-09-694-777A-2
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28	198.8	6.1	2967	4	US-10-162-012-6	Sequence 6, Appli
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ALIGNMENTS

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; Sequence 1, Application US/09600776
; Patent No. 6326168
; GENERAL INFORMATION:
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: A novel potassium channel protein
; FILE REFERENCE: Y9903-PCT
; CURRENT APPLICATION NUMBER: US/09/600,776
; CURRENT FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: JP P1998-011434
; PRIOR FILING DATE: 1998-01-23
; PRIOR APPLICATION NUMBER: JP P1998-346198
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3323
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6)..(3257)
; US-09-600-776-1

Query Match	100.0%;	Score 3252;	DB 4;	Length 3323;
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; Sequence 2, Application US/09343494
; Patent No. 6413741
; GENERAL INFORMATION:
; APPLICANT: Jeglia, Timothy J.
; APPLICANT: Wickenden, Alan
; TITLE OF INVENTION: Human Bk, a Voltage-Gated Potassium Channel Subunit
; FILE REFERENCE: 018512-001320US
; CURRENT APPLICATION NUMBER: US/09/343,494
; CURRENT FILING DATE: 1999-06-30
; EARLIER APPLICATION NUMBER: US 60/091,469
; EARLIER FILING DATE: 1998-07-01
; EARLIER APPLICATION NUMBER: US 60/116,621
; EARLIER FILING DATE: 1999-01-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
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; LENGTH: 3249
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3249)
; OTHER INFORMATION: helk
US-09-343-494-2
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 3247; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 3
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; Sequence 19, Application US/09336643A
; Patent No. 6399761
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. 6399761el Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643A
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 3857
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (249)....(3495)
; OTHER INFORMATION: K+Hnov14
US-09-336-643A-19

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Best Local Similarity 99.8%; Pred. No. 0;
Matches 3244; Conservative 0; Mismatches 5; Indels 3; Gaps 2;

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2821 GACACTGGGGCATCTCTCTACTGCTGCGAGCCCGCAGCTGGCTGTGTCTTGAAGTGGACT 2880
3066 GACACTGGGGCATCTCTCTACTGCTGCGAGCCCGCAGCTGGCTGTGTCTTGAAGTGGACT 3125
2881 TGGCCCGACCTCTGTCGCGGGCTCTCTCCCTCATGGCACCTTGGCCCTGGGGTCCCCCA 2940
3126 TGGCCCGACCTCTGTCGCGGGCTCTCTCCCTCATGGCACCTTGGGGTCCCCCA 3185
2941 GCGTCTCAGAGCTCCCTGCGCTCGAGCCAGCTTCTTGGACCTTCCACCTCAGACTCA 3000
3186 GCGTCTCAGAGCTCCCTGCGCTCGAGCCAGCTTCTTGGACCTTCCACCTCAGACTCA 3245
3001 GAGCCCCCTGCTCAGGAGACCTCTGCTCTGAGCCCGACACCTTGCCTTCCCTCTCTCT 3060
3246 GAGCCCCCTGCTCAGGAGACCTCTGCTCTGAGCCCGACACCTTGCCTTCCCTCTCTCT 3305
3061 TCTGAGGAGGGCTAGGACTTGGGGCCCGCAGAGCTGTGAGCAGGCTGAGGCTACCAAGC 3120
3306 TCTGAGGAGGGCTAGGACTTGGGGCCCGCAGAGCTGTGAGCAGGCTGAGGCTACCAAGC 3365
3121 ACTGAGAGCCCGCCACAGGCTCAGGGGCTTGGCTTGGCTTGGGACCCCGCAGGCTG 3180
3366 ACTGAGAGCCCGCCACAGGCTCAGGGGCTTGGCTTGGCTTGGGACCCCGCAGGCTG 3425
3181 GAGATGCTGCTTATTTGGCTGCCATGGCTCTTGGCAGTCTTGGCAGTCCAGTGAAGAGGC 3240
3426 GAGATGCTGCTTATTTGGCTGCCATGGCTCTTGGCAGTCTTGGCAGTCCAGTGAAGAGGC 3485
3241 ACAGGGGTCTGA 3252
3486 ACAGGGGTCTGA 3497

RESULT 4

US-09-358-383C-1
; Sequence 1, Application US/09358383C
; Patent No. 6518398
; GENERAL INFORMATION:
; APPLICANT: Curtis, RORY A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-055CP
; CURRENT APPLICATION NUMBER: US/09/358,383C
; CURRENT FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: USN 09/119,855
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3355
; TYPE: DNA
; ORGANISM: Macaca sp.
; FEATURE:
; NAME/KEY: CDS

; LOCATION: (104)..(3352)		
US-09-358-383C-1		
Query Match		97.0%; Score 3156; DB 4; Length 3355;
Best Local Similarity		98.2%; Pred. No. 0;
Matches 3192; Conservative		0; Mismatches 60; Indels 0; Gaps 0;
QY	1	ATGCCGGCCATGCGGGGCTCTCTGGGCGCTCAGAACACCTTCTGGACACCATCGCTACG 60
DB	104	ATGCCGGCCATGCGGGGCTCTCTGGGCGCGAGAAACCTTCTGGACACCATCGCTACG 163
QY	61	CGCTTCGAGCGGACGACAGTAACTTCGCTGGCGCAACGCCAGGTGGCGGGCTCTTC 120
DB	164	CGCTTCGAGCGGACGACAGTAACTTCGCTGGCGCAACGCCAGGTGGCGGGGCTCTTC 223
QY	121	CCGCTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCGGGCTGAGGTC 180
DB	224	CCGCTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCGGGCTGAGGTC 283
QY	181	ATGCAGCGGGGTGTGCTGCTCTCTTCTTATGGGCGAGACACAGTGAGCTCGTCCGC 240
DB	284	ATGCAGCGGGGTGTGCTGCTCTCTTCTTATGGGCGAGACACAGTGAGCTCGTCCGC 343
QY	241	CAACAGATCCGAAAGGCCCTGGACGAGACAGGAGTTCAAGGCTGAGCTGATCCTGTAC 300
DB	344	CAACAGATCCGAAAGGCCCTGGACGAGACAGGAGTTCAAGGCTGAGCTGATCCTGTAC 403
QY	301	CGGAAAGCGGGCTCCCGTTCCTGCTCTCTCTGGATGTATACCCATAAAGATGAGAAA 360
DB	404	CGGAAAGCGGGCTCCCGTTCCTGCTCTCTCTGGATGTATACCCATAAAGATGAGAAA 463
QY	361	GGGAGGTGGCTCTCTTCTCTAGTCTCTCAAGGACATCAGCGAAACCAAGAACCGAGGG 420
DB	464	GGGAGGTGGCTCTCTTCTCTAGTCTCTCAAGGACATCAGTGAACCAAGAACCGAGGG 523
QY	421	GGCCCGGACAGATGGAAGGAGACAGGTGTGGCGCGCGGCTGTCTTACCACTGTCCGGGCAC 540
DB	524	GGCCCTGACAGATGGAAGGAGACAGGTGTGGCGCGCGGCTGTCTTACCACTGTCCGGGCAC 583
QY	481	AAAGGCTTCAATGCCAACCGGCGGAGCGGCGGCTGTCTTACCACTGTCCGGGCAC 540
DB	584	AAAGGCTTCAATGCCAACCGGCGGAGCGGCGGCTGTCTTACCACTGTCCGGGCAC 643
QY	541	CTGCAGAGCAGCCCAAGGCGAAGCAAAAGCTCAATAAGGGGTGTTTGGGAGAAACCA 600
DB	644	CTGCAGAGCAGCCCAAGGCGAAGCAAAAGCTCAATAAGGGGTGTTTGGGAGAAACCA 703
QY	601	AACTTGGCTGAGTACAAAGTAGCGGCATCCGGAAGTCGCCCTTCATCTGTGCACTGT 660
DB	704	AACTTGGCTGAGTACAAAGTAGCTGCCATCCGGAAGTCGCCCTTCATCTGTGCACTGT 763
QY	661	GGGGCACTGAGAGCCACCTGGGATGGCTTCTATCTCTGCTGCGCACACTCTATGTGGCTGC 720
DB	764	GGGGCGCTGAGGGCCACCTGGGATGGCTTCTATCTCTGCTGCGCACAGCTCTATGTGGCTGC 823
QY	721	ACTGTGCCCTACAGCGTGTGTGAGCAGACAGCGGAGCCAGTGGCGGCGCGGGCCCG 780
DB	824	ACCGTGCCCTACAGCGTGTGTGAGCAGACAGCGGAGCCAGTGGCGGCGCGGGCCCA 883
QY	781	CCGACGCTCTGTGACCTGGCCGTGTGAGGTCTCTTCTTCACTTGAATGTGCTGAAATTC 840
DB	884	CCGACGCTCTGTGACCTGGCTGTGAGGTCTCTTCTTCACTTGAATGTGCTGAAATTC 943
QY	841	CGTACCAATTCGTGCCAAGTCGGGCGAGGTGG

Qy	3181	GAGATGGTCTTATTGCTGCCATGGCTCTGGCACACAGTCCAGTGGACCAGGGAAGAGGC	3244
Dd	3284	GAGATGGTCTTATTGCTGCCACGGCTCTGGCACAGTCCAGTGGACCAGGGAAGAGGC	3343
Qy	3241	ACAGGGGTCTGA	3252
Dd	3344	ACAGGGGTCTGA	3355
 RESULT 5 US-09-358-383C-3 ; Sequence 3, Application US/09358383C ; Patent No. 6518398 ; GENERAL INFORMATION: ; APPLICANT: Curtiss, Rory A.J. ; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR ; FILE REFERENCE: MWI-055CP ; CURRENT APPLICATION NUMBER: US/09/358,383C ; CURRENT FILING DATE: 1999-07-21 ; PRIOR APPLICATION NUMBER: USSN 09/119,855 ; PRIOR FILING DATE: 1998-07-21 ; NUMBER OF SEQ ID NOS: 36 ; SOFTWARE: PatentIn Ver. 2.0 ; SEQ ID NO 3 ; LENGTH: 3249 ; TYPE: DNA ; ORGANISM: Macaca sp. ; FEATURE: ; NAME/KEY: CDS ; LOCATION: (1)..(3249) US-09-358-383C-3			
 Query Match 97.0%; Score 3153; DB 4; Length 3249; Best Local Similarity 98.2%; Pred. No. 0; Matches 3189; Conservative 0; Mismatches 60; Indels 0; Gaps 0;			
Qy	1	ATGCGGCCCATGCGGGGCTTCCTGGCGCCTCAAGAACACTTCTTGACACCATCGCTACG	60
Dd	1	ATGCGGCCCATGCGGGGCTTCCTGGCGCCTCAAGAACACTTCTTGACACCATCGCTACG	60
Qy	61	CGTTTCAGCGCAGCAGCAGTAATCTGCTGCTGGGCAACGCCAGGTGGCGGGCTCTTC	120
Dd	61	CGTTTCAGCGCAGCAGCAGTAATCTGCTGCTGGGCAACGCCAGGTGGCGGGCTCTTC	120
Qy	121	CCGCTGCTTACTGCTCTGTAGGCTTCTGTACCTACCGGGTCTCCCCGGGCTGAGGTC	180
Dd	121	CCGCTGCTTACTGCTCTGTAGGCTTCTGTACCTACCGGGTCTCCCCGGGCTGAGGTC	180
Qy	181	ATGACGGGGGCTGTGCTCTGCTCTTCTTTATGGGCCAGACACCACTGAGCTCGTCCG	240
Dd	181	ATGACGGGGGCTGTGCTCTGCTCTTCTTTATGGGCCAGACACCACTGAGCTCGTCCG	240
Qy	241	CACACAGATCCGAAAGGCCCTGGACGACACAAGAGTTCGAAGGCTGAGCTGATCCTGTAC	300
Dd	241	CACACAGATCCGAAAGGCCCTGGACGACACAAGAGTTCGAAGGCTGAGCTGATCCTGTAC	300
Qy	301	CGGAAGAGCGGGCTCCCGTTCTGGTGTCTCTGGATGTGATACCCATAAAGAATGAAAA	360
Dd	301	CGGAAGAGCGGGCTCCCGTTCTGGTGTCTCTGGATGTGATACCCATAAAGAATGAAAA	360
Qy	361	GGGGAGGTGGCTCTCTTCTTAGTCTCTCAACAGGACATCAGCGAAAACCAAGAACCGAGGG	420
Dd	361	GGGGAGGTGGCTCTCTTCTTAGTCTCTCAACAGGACATCAGTGAACCAAGAACCGAGGG	420
Qy	421	GGCCCCGACAGATGGAAGGAGACAGGTGGTGGCGCGCGGATATGGCGGGGACGATCC	480
Dd	421	GGCCCCGACAGATGGAAGGAGACAGGTGGTGGCGCGCGGATATGGCGGGGACGATCC	480
Qy	481	AAGGGCTTCATATGCCAACCGCGCGGAGCCGGGCGGTGCTCTACCACTCTCCGGGCAC	540
Dd	481	AAGGGCTTCATATGCCAACCGCGCGGAGCCGGGCTGTGCTCTACCACTCTCCGGGCAC	540
Qy	541	CTGCAGAGCAGCCCAAGGGCAAGCAACAGCTCAATAAGGGGGGTGTTTTGGAGAAACCA	600

Db 541 CTGAGAGAGCCCAAGGCAAGCACAAAGCTCAATAAGGGGTGTTTGGGAGAGCCA 600
Qy 601 AACTTGGCTGAGTACAAAGTAGCCGCATCCGGAAGTGCCTTCATCTCTGTTGACATGT 660
Db 601 AACTTGGCTGAGTACAAAGTAGCTCCATCCGGAAGTGCCTTTTCATCTGTTGACATGT 660
Qy 661 GGGGCACTGAGAGCCACCTGGGATGAGTCTTCATCTCTGCTCGCCACACTCTATGTGCTGTC 720
Db 661 GGGGCGCTGAGGGCCACCTGGGATGAGTCTTCATCTCTGCTCGCCACACTCTATGTGCTGTC 720
Qy 721 ACTGTGCCCTACAGCGTGTGTGAGCACAGCACGCGGAGCCAGTCCGCGCCGCGCCCG 780
Db 721 ACCGTGCCCTACAGCGTGTGTGAGCACAGCACGCGGAGCCAGTCCGCGCCGCGCCCGCA 780
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Db 841 CGTACCAATTCGTCTCAAGTCCGAGTCCGAGTGTGTTTGGCCCAAGTCCATTTGCCCTC 900
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Db 1081 ACATGCTCATGGCCGTGTTTCCCTGCTCGCAGTGGTGGCTGCTGCTGCTGCTTTTAC 1140
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Db 1261 AACAGCTCCGGCCAGAGTGAACATGCGAGCAGCAGCGAGGCCAACGGGACGGGGCTG 1320
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Db 1501 ACGGCCATCATCCAGGCAATGACGCCCGCGCTTCTGTATCACAGCGGACGCGCGAC 1560
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Db 1621 TACTTCCAGGCACTGGCGGTGAACAAATGGCATCGACACCAACCGAGTGTGTCGAGAGC 1680
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Db 1741 CGCTGTTTGAAGGCGGCGCAGCGCGCTGCTGCGGCACTGTCTCTGCGCCCTGCGGCGC 1800
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1416 AACAGCTCTGGCCAGAGTGAACATGAGTAGCAGTGGCGGCGAGCAAGCAAGCGG 1475
1312 ACGGGGCTGAGAGTGTCTGGGCGGCGCGTGGCGCAGCGCTACATCACCTCCCTCTAC 1371
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1372 TTCGCATCTACAGAGCTACACAGCGTGGGCTTGGGCAAGCTGTCGCGCAACAGCGACAC 1431
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1432 GAGAGATCTTCCATCTGACCATGTCTATCGGCGCCCTGATGACGAGCGGTGGTGT 1491
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1716 ACCGCTGACCTGCGAGACTACATTCGATCCACCGCATCCCGAAGCCCTCAAGAGCGC 1775
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1672 CTGCAGAGCTTCCCTGACGAGCTGCGCGCAGACATCGCATTCGACCTCAACAGAGGTC 1731
1836 CTGCAGAGCTTCCCGATGAGCTTGCAGCAGACATCGCATTCGACCTCAACAGAGGTC 1895
1732 CTGCAGAGCTGCACTGTTTGAAGCGGCGCAGCGCGCTGCTGCGGCACTGTCTCTGCGC 1791
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1956 CTGAGGCGCGCGCTTCTGACGCGCGGCGAGTACCTCATCCACAGGCGATGCTCTCCAG 2015
1852 GCCCTCTACTTGTCTGCTGCGCTCCATGGAGTGTCTCAAGGCTGGCAGCGTGTCTGCC 1911
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2376 GGACACAGATCTACAGAGCCCGCAGACATGAGCCCTCCAGCCCTGCTGCTACCTGGC 2435
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2632 CTGCAAGCTTCCGCGAGGCGTGCAGAGCTGTCTGGCGGCCCCACAGGAGGAGGTCG 2691
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3336 CCCACAGCTGAGAGTGTGCTCATGGCTGCTATGGCTGCTGAGCTGCTGAGTGGAGC 3395
3229 CAGGAAGAGGCAAGGCTCTGA 3252
3396 CAGGAGGAGGCAAGGCTCTGA 3419

RESULT 7

US-09-600-776-5
; Sequence 5, Application US/09600776
; Patent No. 6326168
; GENERAL INFORMATION:
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: A novel potassium channel protein

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; FILE REFERENCE: Y9903-PCT
; CURRENT APPLICATION NUMBER: US/09/600,776
; CURRENT FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: JP P1998-011434
; PRIOR FILING DATE: 1998-01-23
; PRIOR APPLICATION NUMBER: JP P1998-346198
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 3064
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(3057)
US-09-600-776-5

Query Match      27.2%; Score 884.8; DB 4; Length 3064;
Best Local Similarity 65.5%; Pred. No. 3.1e-177;
Matches 1408; Conservative 0; Mismatches 622; Indels 120; Gaps 3;

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DB 4 ATGCGGCTCATGAAGGGGTTGCTGGCGCCCGCAAAACACCTTCTGACACCATCGGCACC 63
QY 61 CGTTTCAGCGGACGACACAGTAACTTCTGCTCGGCAACGCCAGGTGGCGGGCTTTC 120
DB 64 CGTTTTCAGGAACGACACAGCACTTCTGCTGGCCAAACGACACAGGGGACACCGGGCTTT 123
QY 121 CCGGTGCTCTAGTGTCTGTGAGCTCTGAGACCTCAACGGGCTTCTCCGGGCTGAGGTC 180
DB 124 CCCATGCTCTACTGCTCCGACGGCTTCTGCGAGCTCACAGGCTACGCTGCGACCGAGGTC 183
QY 181 ATGACGCGGGCTGCTGCTCTCTTCTTTATGGGCGACACACAGTGAAGTCTCTCCG 240
DB 184 ATGACGAAGACCTGCGAGCTCCGCTTCTCTACGCGCCAGAGACCAAGTGAAGCGCCCTG 243
QY 241 CAACAGATCGCAAGGCGCTTGGACGACCAAGGAGTTCAAGGCTGAGCTGATCTCTGTAC 300
DB 244 CAGCGCTGTCACAAAGCCCTGGAGGGCCACAGGAGCACCGGGCTGAATCTGCTTCTAC 303
QY 301 CGGAAGCGGGCTCCGCTTCTGCTGTCTCTGAGTGTGATACCCATAAAGATAGAAA 360
DB 304 CGCAAGGATGGCTCAGCGCTTTTGGTCTCTGACATGATGCCCCATCAAGATGAGATG 363
QY 361 GGGGAGTGGCTCTCTCTAGTCTCTCAAGAGCATC-----AGCGAAACCAAGAAC 414
DB 364 GGGGAGTCTGCTGCTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 423
QY 415 CGAGGGGGCCCGACAGATGGAAGGAGACAGGTGGTGGCGCGCGGATATGGCGCGGCA 474
DB 424 CTGGGCCCCCAAGGAGCGCGGGGACAGTAATACGAAACCTCCCTTGTGTAAGGGGA 483
QY 475 GATATCAAGGCTTCAATGCAACCGGCGGAGCGGGCGGTGCTCTACCACTGTTC 534
DB 484 GCCACCTGGAATTTTCGGTCTGCGCAGAGACGAGCGGCTACTGTCTTACACCGACTGACC 543
QY 535 GGGCACCTGCAAGACAGCCCAAGGGCAAGCACAGCTCAATAAGGGGTTGTTGGGAG 594
DB 544 GGGCACCTTGGCGCGCGGGCGAGGAGGATGAGGCCATTAATACGTTGTTGAGCCA 603
QY 595 AAACCAAACTTGCTCTAGTACAAAGTAGCGGCCATCGGAAGTCGCGCTTCTATCTGTTG 654
DB 604 AAGCCATCAGTCCCGAGTACAAAGTGGCTCCGTTGGGGGGTCTCGTCTCTCTCTCCTC 663
QY 655 CACTGTGGGCACTGAGAGCCACTGGGATGGCTTATCTGCTCGGCACACTCTATGTG 714
DB 664 CACTACAGGCTCTCCAAAGGCCATCTGGGAGGGCTTATCTCTTGGCCACTTCTACGTT 723
QY 715 GCTGTCACTGTGCTCTACAGCGTGTGTGAGCACACAGACGGGAGCCAGTGGCGCGCG 774
DB 724 GGGTCAACCGTCCCTTACATATGCTCTGTTTCTCGGGTGACATGACACCCCATCATCTCG 783
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QY 775 GGCCCGCCAGCGCTGTGTGACCTGCGCGTGGAGGTCTCTTCACTCTTCACTTGTGCTG 834
DB 784 CGACACACCTTGTGTGACGACATCGCGTGGAAATGCTCTTCACTCTAGATATCATCTG 843
QY 835 AATTTCCGTACCACTTGTGTCCAAAGTGGGCGAGGTGTTGTTGCCCCAAAGTCAATT 894
DB 844 AACTTCGCGACCACTTATGTGCCAGTCCGCGAGTAATCTCTGCTCTCGTTCCATT 903
QY 895 TGCCTCCACTAGCTCACCACTGGTTCTGCTGGATGTATCGACGGCTGCGCTTGTGAC 954
DB 904 GGCCTCCACTTACCTGCGCACCTGGTTCTTCACTGACCTTATGCTGCTGCGCTTGTGAC 963
QY 955 CTGCTACATGCCCTTCAAGGTCAACGTGTACTTTCGGGGGCCCATCTGCTGGAAGAGGTGCGC 1014
DB 964 CTGCTTTTACATCTTCAACATCACCGTGACCTGCTGTCACCTACTGGAAGACAGTGGCG 1023
QY 1015 CTGCTGCGCTGCTGCGCTGCTTCCGCGCTGGACCGGTACTCTGCGAGTACAGCGCGCTG 1074
DB 1024 CTGTTGCGCTGCTGCGCTGCTGCGAAGCTGGAGCGGTACTCTCAGTGCAGTGTGCTG 1083
QY 1075 GTGCTCACACTGCTCATGCGCGTGTGCGCTGCTGCGACACTGGTTCGCTCGCTCTGG 1134
DB 1084 GTGCTCACGCTGCTCATGCTGCTTTCGCTCTTGGCCACTGGATGGCTTGCATCTGG 1143
QY 1135 TTTTACATTTGGCCAGCGGAGATCGAGAGCAGCGAATCCGAGCTGCTGAGATTGGCTGG 1194
DB 1144 TATGTCTATCGGCGCGGAGATGGAGGCAATGACCCGCTGCTCTGGGACATTTGGCTGG 1203
QY 1195 CTGCGAGAGTGGCCGCGCTGCTGAGACTCTCTACTACTCTGTTGGGCGCGGAGCGCT 1254
DB 1204 TTGCATGAGTTGGGCAAGCTCTGGAGGTGCCCTATGTCAATGGCTC----- 1250
QY 1255 GGAGGGAACAGCTCCGCGCCAGAGTGAACAATGTCAGCAGCAGCAGCGAGGCCAACGGGACG 1314
DB 1251 ----- 1250
QY 1315 GGGCTGGAGCTGCTGGCGCGCGCTGCTGCGCAGCGCCTTACATCACTCTCTCTACTTC 1374
DB 1251 -----GTTGGCGCGCCCATCACGCGCGCAGCGCTTACATCGCGGCACTGTACTTC 1299
QY 1375 GCATCAGCAGCTTCAACGAGTGGCTTGGGCAACGTTGTCGCGCAACAGCGACACGGAG 1434
DB 1300 ACTCTAAGCAGCTTCAACGAGTGGCTTGGCAACGTTGTCGCGCAACAGCGGAG 1359
QY 1435 AAGATCTTCTCCATCTGACCTGCTCATCGCGCGCTGATGACAGCGGTGTTGGTGG 1494
DB 1360 AAGATCTTCTCCATCTGACGATGCTCATAGGCGCGCTGATGACCGCTGTTGTTGGG 1419
QY 1495 AAGGTGACGCGCCATCATCAGCGCATGTATCGCGCGCGCTTCTGTACCAAGCGCGACG 1554
DB 1420 AAGGTGACGCGCCATCATCAGCGCATGTATCTGCGCGCGCTCGCTTACCAAGCGCGCATG 1479
QY 1555 CGGACCTGGCGCATCTACATCGCATCCACCGTATCCCAAGCCCTCAGACGCGCATG 1614
DB 1480 AAGGACCTCAAGACTTCAATCGTGTGACCGCGCTGCGCGCGCTTCAAGCAGCGCATG 1539
QY 1615 CTGGAGTACTTTCAGGCGCACCTGGGCGGTGAACAATGGCATCGACACCAAGCGAGCTGCTG 1674
DB 1540 CTCGAATCTTCCAGACACGTTGGGCGGTCAACAGCGGATCGACGCGCAAGGATTACTG 1599
QY 1675 CAGAGCTCTCTGAGCGGTGGCGAGACATGCGCATGCACTGCAAGGAGGTCTGCTG 1734
DB 1600 CGTGAATCTCCACAGCAGCTGAGAGTGAATTTGCTATGCACTGTAATCGGAGATCTCTG 1659
QY 1735 CAGCTGCGCACTGTTTGGGCGCGCGCGGTGCTGCGGCACTGCTCTGCGCGCTG 1794
DB 1660 CAGCTGCGGTGTTTGGGCGCGCGCGGTGCTGCGGCGCTGCTGCGGCGCTATCGCTGCAATC 1719
QY 1795 CGGCGCGCGCTTCTGCAAGCGCGCGAGTACTCTCATCCACCAAGCGCGATGCTCTGCAAGGCC 1854
DB 1720 AAGACCTGTTCTGCGCTCCGCGCGAGTACTTGTGCGCGGTGGGATGCCCTGCGAGCA 1779
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1492 GGAAGCTGACGGCCATCATCCAGCGCATGTACGCCCGCGCTTTCTGTACCAACGCGC 1551
 1552 GGAATGTACAGCCATCATCCAGCGCATGTACTCCGACGCTCGCTTACCAACGCGC 1611
 1552 ACGGCGACCTGGGACATCATCCGATCCAGCCGATGTATCCCAAGCCCTCAAGACGCGC 1611
 1612 ATGAAGGATCTCAAGGACTTCAATCCGAGTGCATCGTCTGCCCGCCCACTCAAGACGCGC 1671
 1612 ATGCTGAGTACTTCCAGGCACTGGGCGGTGAACAATGGCATCCAGACCCAGAGCTG 1671
 1672 ATGCTGAGTACTTCCAGGCACTGATGGCCCGTCAAGCGGCATGATGCCAAGAGTTA 1731
 1672 CTGACAGGCTCCCTGACGAGCTGCGCGCAGACATCGCCATGACCTGCAACAAGAGGTC 1731
 1732 CTGCGTGAATCCCGGATGAGTGGAGCTGACATCGCCATGACCTGAATCGGAGATC 1791
 1732 CTGACGTCGCACTTTGAGGCGGCGAGCGCGGCTGCTGCGGCACTGTCTTGCC 1791
 1792 CTGACGTCGCTTTGTTGGAGCAAGCAGGGGCTGCTTCTGCGCCCTCTCCCTGCAC 1851
 1792 CTGCGGCGCCCTCTGACGCGCGGAGTACTCTCATCCCAAGCGCATGCCCTGCAG 1851
 1852 ATCAAGACCTATTTGTCTCTGAGGAGTTCTGCTAGCCGCTGGGATGCCCTGCAG 1911
 1852 GCCTCTACTTTGTCTCTGCTCCAGGAGGTGCTCAAGGTTGCGCACCGCTGCTGCC 1911
 1912 GCACACTACTATGCTGCTCTGCTCTTGGAGTGTCTGAGACCAACACGCTGCTGCC 1971
 1912 ATCTAGGAGGCGACCTGATCGCTGTGAGCTGCTGCCCGCGGAGCAG----- 1962
 1972 ATCTTTGGAAGGGGACTTGTATTTGGGCGCAGATCCCTGAGTTGGGCGAGGCGCTGG 2031
 1963 -----GTGGTAAAGGCCAATGCCGAGCTGAAGGGGCTGACGTACTGCTC 2007
 2032 GCAGGGCGAGGCTGCTGCTGAGACACGAGGCTGTGTGAAACATGACTTACTGCGC 2091
 2008 CTGACGTGCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2067
 2092 CTGACGAGCTGACGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2151
 2068 CGCGCTTACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2114
 2152 GCTGCTTACGGCTGCTGCTTACCCCGGACCTTAACCTTCAACCTGCG 2198

RESULT 9
 US-09-358-383C-9
 ; Sequence 9, Application US/09358383C
 ; Patent No. 6518398
 ; GENERAL INFORMATION:
 ; APPLICANT: Curtiss, Rory A.J.
 ; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
 ; FILE REFERENCE: MNI-055CP
 ; CURRENT APPLICATION NUMBER: US/09/358,383C
 ; CURRENT FILING DATE: 1999-07-21
 ; PRIOR APPLICATION NUMBER: US/09/119,855
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 9
 ; LENGTH: 870
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(870)
 US-09-358-383C-9
 Query Match 26.0%; Score 844.4; DB 4; Length 870;
 Best Local Similarity 99.9%; Pred. No. 7e-169;
 Matches 845; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCGCGCATGCGGGGCTCTGCGGCTCTAGAACACCTTCTGTGACACCATCGCTACG 60
 Db 1 ATGCGCGCATGCGGGGCTCTGCGGCTCTAGAACACCTTCTGTGACACCATCGCTACG 60
 QY 61 CGCTTCAGCGGACGACAGTAACTTCTGCTGGGCAACGCCAGCTGGCGGGCTCTTC 120
 Db 61 CGCTTCAGCGGACGACAGTAACTTCTGCTGGGCAACGCCAGCTGGCGGGCTCTTC 120
 QY 121 CCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCGGGCTGAGGTC 180
 Db 121 CCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCGGGCTGAGGTC 180
 QY 181 ATGACGCGGGCTGTGCTCTCTCTTATATGGGCGACACACAGTGTGCTGCTCCG 240
 Db 181 ATGACGCGGGCTGTGCTCTCTCTTATATGGGCGACACACAGTGTGCTGCTCCG 240
 QY 241 CAACAGATCCGCAAGGCCCTGGACGAGCAAGAGTCAAGGCTGAGCTGATCCGTATC 300
 Db 241 CAACAGATCCGCAAGGCCCTGGACGAGCAAGAGTCAAGGCTGAGCTGATCCGTATC 300
 QY 301 CGGAAGAGCGGGCTCCCGTTCTGCTGCTCTGATGATACCCATAAAGAAATGAGAAA 360
 Db 301 CGGAAGAGCGGGCTCCCGTTCTGCTGCTCTGATGATACCCATAAAGAAATGAGAAA 360
 QY 361 GGGAGGCTGCTCTCTCTCTCTCAAGGACATCAGCGAAACCAAGAACCGAGGG 420
 Db 361 GGGAGGCTGCTCTCTCTCTCTCAAGGACATCAGCGAAACCAAGAACCGAGGG 420
 QY 421 GCGCGCGACAGATGGAAGAGAGCAGGTGTGGCGCGCGGATATGCGCGGCGACCATCC 480
 Db 421 GCGCGCGACAGATGGAAGAGAGCAGGTGTGGCGCGCGGATATGCGCGGCGACCATCC 480
 QY 481 AAAGGCTTCAATGCCAACCGCGGCGAGCGCGGCTGCTCTACCACTGTCTCGGGCAC 540
 Db 481 AAAGGCTTCAATGCCAACCGCGGCGAGCGCGGCTGCTCTACCACTGTCTCGGGCAC 540
 QY 541 CTGCAAGAGCGCCCAAGGGCAAGCAAGCTCAATAAGGGGTGTGTTGGGAGAAACCA 600
 Db 541 CTGCAAGAGCGCCCAAGGGCAAGCAAGCTCAATAAGGGGTGTGTTGGGAGAAACCA 600
 QY 601 AACTTCCTCTGAGTACAAAGTAGCGGCATCCGGAAGTTCCTCTGTTGCACTGT 660
 Db 601 AACTTCCTCTGAGTACAAAGTAGCGGCATCCGGAAGTTCCTCTGTTGCACTGT 660
 QY 661 GGGGCACTGAGACCACTGGGATGCTTCTCTGCTGCGCACACTCTATGTGGCTGTC 720
 Db 661 GGGGCACTGAGACCACTGGGATGCTTCTCTGCTGCGCACACTCTATGTGGCTGTC 720
 QY 721 ACTGTCCCTTACAGCGTGTGTGAGCAGACGAGGAGCCAGTCCGCGCGCGCGCG 780
 Db 721 ACTGTCCCTTACAGCGTGTGTGAGCAGACGAGGAGCCAGTCCGCGCGCGCGCGCG 780
 QY 781 CCCAGGCTGTGACCTGCGCGGAGGCTCTTCTCATCTTGTGACATGTGCTGAATTC 840
 Db 781 CCCAGGCTGTGACCTGCGCGGAGGCTCTTCTCATCTTGTGACATGTGCTGAATTC 840
 QY 841 CGTACC 846
 Db 841 CGTACC 846
 RESULT 10
 US-09-358-383C-7
 ; Sequence 7, Application US/09358383C
 ; Patent No. 6518398
 ; GENERAL INFORMATION:
 ; APPLICANT: Curtiss, Rory A.J.
 ; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
 ; FILE REFERENCE: MNI-055CP
 ; CURRENT APPLICATION NUMBER: US/09/358,383C
 ; CURRENT FILING DATE: 1999-07-21
 ; PRIOR APPLICATION NUMBER: US/09/119,855
 ; PRIOR FILING DATE: 1998-07-21

; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1132
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (263)..(1132)
US-09-358-383C-7

Query Match 26.0%; Score 844.4; DB 4; Length 1132;
Best Local Similarity 99.9%; Pred. No. 7.6e-169;
Matches 845; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 ATGCGGCCATGCGGGCCCTCTGGCGCCTCAGAACACCTTCTGGACACCATCGCTACG 60
Db 263 ATGCGGCCATGCGGGCCCTCTGGCGCCTCAGAACACCTTCTGGACACCATCGCTACG 322
QY 61 CGCTTCGACGCGACGACAGTAATCTCGTGGGCAACGCCAGGTGGGGGCTCTTC 120
Db 323 CGCTTCGACGCGACGACAGTAATCTCGTGGGCAACGCCAGGTGGGGGCTCTTC 382
QY 121 CCGTGTCTACTGCTCTGTAGTGTCTGTGACCTCAGCGGCTTCTCCCGGCTGAGGTC 180
Db 383 CCGTGTCTACTGCTCTGTAGTGTCTGTGACCTCAGCGGCTTCTCCCGGCTGAGGTC 442
QY 181 ATGAGCGGGCTGTGCTGCTCTCTTTATGGCGACAGCATGAGTGTGCTCGG 240
Db 443 ATGAGCGGGCTGTGCTGCTCTCTTTATGGCGACAGCATGAGTGTGCTCGG 502
QY 241 CAACAGATCCGAGGCCCTGGAGGACAGAGTTCAGGCTGAGTGTGCTCTGATC 300
Db 503 CAACAGATCCGAGGCCCTGGAGGACAGAGTTCAGGCTGAGTGTGCTCTGATC 562
QY 301 CGGAAGAGCGGGCTCCCGTTCTGGTGTCTCTGGATGTGATACCCATAAAGATGAGAAA 360
Db 563 CGGAAGAGCGGGCTCCCGTTCTGGTGTCTCTGGATGTGATACCCATAAAGATGAGAAA 622
QY 361 GGGAGTGTGCTCTCTCTAGTCTCTACAGAGATCAGGAAACCAAGACCGAGG 420
Db 623 GGGAGTGTGCTCTCTCTAGTCTCTACAGAGATCAGGAAACCAAGACCGAGG 682
QY 421 GGGCCACAGATGGAAGGACAGAGTGTGGCGGCGGATGATGCGCGGACAGATCC 480
Db 683 GGGCCACAGATGGAAGGACAGAGTGTGGCGGCGGATGATGCGCGGACAGATCC 742
QY 481 AAAGGCTTCAATGCAACCGCGGCGGAGCGGCGGCTGTCTACCACTGTCCGGGCAC 540
Db 743 AAAGGCTTCAATGCAACCGCGGCGGAGCGGCGGCTGTCTACCACTGTCCGGGCAC 802
QY 541 CTGAGAGAGCGCCCAAGGCGAAGCAAGCTCAATAGGGGGTGTGGGAGAAACCA 600
Db 803 CTGAGAGAGCGCCCAAGGCGAAGCAAGCTCAATAGGGGGTGTGGGAGAAACCA 862
QY 601 AACTTGCTCAGTACAAAGTAGCCCATCCGGAAGTCGCCCTTCATCTGTTCACATGT 660
Db 863 AACTTGCTCAGTACAAAGTAGCCCATCCGGAAGTCGCCCTTCATCTGTTCACATGT 922
QY 661 GGGCACTGAGAGCACCTGCGGATGGCTTCACTCTGCTCGCCACACTCTATGTGGCTGC 720
Db 923 GGGCACTGAGAGCACCTGCGGATGGCTTCACTCTGCTCGCCACACTCTATGTGGCTGC 982
QY 721 ACTGTGCCCTACAGGTGTGTGAGCAGCAGCAGCGGAGCCAGTGGCGCCCGGGCCG 780
Db 983 ACTGTGCCCTACAGGTGTGTGAGCAGCAGCAGCGGAGCCAGTGGCGCCCGGGCCG 1042
QY 781 CCCAGCTGTGACCTGGCGGTGAGTCTCTTCACTCTGACATGTGCTGAATTC 840
Db 1043 CCCAGCTGTGACCTGGCGGTGAGTCTCTTCACTCTGACATGTGCTGAATTC 1102
QY 841 CGTACC 846
Db |||||
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Db 1103 CGTACC 1108

RESULT 11

US-09-358-383C-17
; Sequence 17, Application US/09358383C
; Patent No. 6518398
; GENERAL INFORMATION:
; APPLICANT: Curtis, RORY A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-055CP
; CURRENT APPLICATION NUMBER: US/09/358,383C
; CURRENT FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: USSN 09/119,855
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 3321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3321)
US-09-358-383C-17

Query Match 23.4%; Score 761.2; DB 4; Length 3321;

Best Local Similarity 62.2%; Pred. No. 3.4e-151;
Matches 1319; Conservative 0; Mismatches 708; Indels 93; Gaps 4;

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QY 1 ATGCGGCCATGCGGGCCCTCTGGCGCCTCAGAACACCTTCTGGACACCATCGCTACG 60
Db 1 ATGCGGTTATGAAGATTAATCTGGCGCCGCAAAACACCTTCTGGACACCATCGCCACC 60
QY 61 CGTTTCGACGCGACGACAGTAATCTCGTCTGGGCAACGCCAGTGGGGGCTCTTC 120
Db 61 CGTTTCGACGCGACGACAGTAATCTCATCTTGCCTTCCCAATGCCAGTGGCTAAGGGTTTC 120
QY 121 CCGTGTCTACTGCTCTGATGCTCTGAGCTCTGAGCTCTCCGGGCTTCTCCGGGCTGAGTC 180
Db 121 CCGATAGTCTACTGTTCCGATGGCTTCTGCGAGTGTCTGGATTGCTCCCACTGAAAGTC 180
QY 181 ATGAGCGGGCTGTGCTCTCTCTTTATGGGCGACACACAGTGTGCTCGCCG 240
Db 181 ATGAGAGAGTGTAGTCTCAAGTCTTATTTGGGGTGAACCAATGAGCACTGATG 240
QY 241 CAACAGATCCGAGGCCCTGGAGCGACACAAGAGTTCAGGCTGAGTGTCTGTAC 300
Db 241 CTTCAATAGAAAAGTCACTGGAGGAGAAAACAGAAATCAAGAGGAGAAATATGTTCTAC 300
QY 301 CGGAGAGCGGGCTCCCGTTCTGTGCTCTCTCAAGAGCATCAGCGAAACCAAGAACCCGAGGG 360
Db 301 AAGAAACCGGGTCTCCATTTTGTGCTCTACTGTGATTTGTTCCATAAGAAATGAAAA 360
QY 361 GGGAGTGTGCTCTCTTCTCTAGTCTCTCAAGAGCATCAGCGAAACCAAGAACCCGAGGG 420
Db 361 GGAGATGTAGTACTTTTCTGGCTCGTTCAAGATATACAGATA-CAAGAGTGAAGAT 419
QY 421 GGGCCGACAGATGGAAGAGGACAGGTGTGGCGCGCGATATGGCCGGGCAAGATCC 480
Db 420 TACTCCAGAGATAAAAAAGAGACAAAGTCAAGGAAAGATCAAGAGGAGGACCCCA- 476
QY 481 AAGGCTTCAATGCCAACCGCGCGGAGCGCGGCTGTCTTACCACTGTCCGGGCAC 540
Db 477 -----CTTTGACTCAGCCCGGAGACGGAGTCGAGAGTCTTTTATCATCTCTGGGCAC 531
QY 541 CTGAGAGCAGCCCAAGGGCAAGCACAAGCTCAATAAGGGGGTGTGGGAGAGAAACCA 600
Db 532 CTGCAAGAGAGAGAAAGAACAAATTAATAAATCAATGTTTGTAGATAAACCA 591
QY 601 AACTTGCTCAGTACAAAGTAGCGGCATCCGGAAGTCGCCCTTCATCTGTGTGCACTGT 660
Db 592 GCATTTCCGGAGTATAAAGTTTCTGATGCAAAAAAGTCCAAATTCATACTTCTGCAATTT 651
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Qy	661	GGGCACTGAGAGCCACTGGGATGGCTTCATCTCGCTCGCCACACTCTATATGGCGTCTC	720
Db	652	AGCACTTTTAAAGCTGGCTGGGACTGGCTATTATTTGTGGCAACGTTTATATGTTGCTGTG	711
Qy	721	ACTGTGCCCTACAGCTGTGTGTCAGCACAGCAGCGGAGCCAGTCGCCGCCGCCGCCG	780
Db	712	ACTGTACTTACAACGTTTGCTTTATTTGGCAATGACGACCTGTCCAACTCGGAGC---	768
Qy	781	CCCAGCGTCTGTGACCTGGCGTGGAGGTCTCTTTCATCTCTTGCATGTGCTGCAATTTTC	840
Db	769	ACAACCGTCACTGACATGTCAGTCGAGATCTCTTTTATATAGATAATATTTTAAATTTTC	828
Qy	841	CGTACACATTCGTGTCCAAGTCGGGCGCAGGTGGTGTGGCCCAAAAGTCCAATTGGCTTC	900
Db	829	CGAAACAATTTATGTGAGCAAGCTCTGGCCAAAGTTATCTTTGAAGCAAGATCAATTTGCATC	888
Qy	901	CACCTACGTCACCACTCGTCTCTCGATGTGATCGCAGCGCTGCCCTTTGACCTGCTA	960
Db	889	CACCTATGTCAAACTGTTTCATCATTTGATTTAATTCGCTGCCCTTTTGATCTTCTG	948
Qy	961	CATGCCCTCAAGGTCAACGTGTACTTCGGGCCCACTCTGTGAAGACGGTGCCTCTGCTG	1020
Db	949	TATGCTTTCAACGTCACAGTGGTGTCTCTCGTGCATCTTCTAAAGACAGTGCCTCTTG	1008
Qy	1021	CGCTGTCTGGCTGCTTCCGGGCTGGACCGGTACTCGCAGTACAGCGCGCTGGTGCCTG	1080
Db	1009	CGTCTTTTGGCTGTGCTGCAAAAGTTAGACGGCTATTTCCCAACACAGTACTATCGTCTG	1068
Qy	1081	ACACTGTCTATGGCCGTGTTTCGCCCTGCTCGCGCACTGGGTGCGCTCGCTCTGTTTTC	1140
Db	1069	ACTCTGCTCATGTCCATGTTTGGCACTCTCTTGCACACTGATGGCGGTATCTCTGTAGCTC	1128
Qy	1141	ATTGGCCAGCGGGAGATCGAGACAGCGAAATCCGAGCTGCTGAGATPGCTCGCTGCAG	1200
Db	1129	ATTGGAAAAATGGAGAGGGAAGACAACAGCCCTCTGAAGTGGGAAGTTGGTGGCTTCAT	1188
Qy	1201	GAGCTGGCCGCCCACTGGAGACTCCCTACTACTCTGTGGCGCGGAGCCAGCTGGAGGG	1260
Db	1189	GAGTTGGGAAGAGACTGGAACTCTCCATCATCTAT-----	1221
Qy	1261	AACAGCTCTCGGCCAGAGTGACAACTGCAGCAGCAGCAGCGACCGGCAACGGGCGTG	1320
Db	1222	-----GGCAAC	1227
Qy	1321	GAGCTGTGGCGGCCGTCTCGTCGGCAGCGCCTTACATCACTCCCTCTACTTTCGCACTC	1380
Db	1228	AATACCTTGGGGGGCCGTTCGATCCGAAGTGCCTTATATTCGCGCTCTGTACTTCACTGCTG	1287
Qy	1381	AGCAGCCTCACACGGTGGGCTTCGGCAACGTGTCCGCCAACACGGACCCGAGAGATC	1440
Db	1288	AGCAGCCTCACACGGTGGGTTTGGGAACGTCTCTCTAATACAGATGCAGAAAAATC	1347
Qy	1441	TTCTCCATCTGCACCATGCTCATCGCGCCCTGATGCACCGGTGGTGTGTTGGAAACGTG	1500
Db	1348	TTCTCCATCTGCACCATGCTGATTTGGTGGCTTGTATGCACGCTTGGTGTGGAAACGTG	1407
Qy	1501	ACGGCCATCATCCAGCGATGTACGCCCGCGCTTCTGTATCCACAGCCGCAACCGCGAC	1560
Db	1408	ACAGCAATCATACAGAGGATGTATCTCCAGATGGTTCCTCTATCACACTAGAACTAAGGAT	1467
Qy	1561	CTGGCGACTACATCCGATCCACCGTATCCCAAGCCCTCAAGCAGCGCATCTGGAG	1620
Db	1468	CTGAAGAATTCATCCGTGTCATCATCTTGGCCCCAACTTCAAGCAGAGGATGCTCGAA	1527
Qy	1621	TACTTCCAGGCCACTCGGGCGGTGAAACAAATGGCATCGACACCCAGCGAGCTGTGCAGAGC	1680
Db	1528	TATTTTCAAAACAACCTGCTCAGTCAAACAATGGATATGATTCAAATGAGCTTTTGAAGAC	1587
Qy	1681	CTCCCTGACGAGCTGGCGGACAGACATCGCCATGCACTGCAACGAGGAGTCTCTGCAGCTG	1740
Db	1588	TTTCCAGATGAACCTCGCTTCTTGACATCACTATGCACTTGAATGAACGAGAGATCTTACAGTTG	1647

QY	1741	CCACTGTTTGAGGGCGGCAGCGCGGTGCTGCGGGCACTGTCTCTGCGCCCTGCGGCC	1800
DB	1648	TCCCTTTTGAATGTGCACGCGGGGTGCTCAGGTCTCTGTCTTACACATCAAAACC	1707
QY	1801	GCCTTCTGCACGCGGGCGAGTACTCATCCACCAGGCGATGCCCTGCAAGGCCCTCTAC	1860
DB	1708	TCTTTCGTGCTCCGGGGAGTATCTGCTGCGTCAAGGGGATGTTTGCAGGCCATCTAC	1767
QY	1861	TTTGTCTGCTTGCTCCATGAGGAGTGTCTCAAGGGTGGCACCGTGTCTGCGCATCTTAGGG	1920
DB	1768	TTTGTATGCTCGGGCTCCATGGAAGTCTTAAAGACAGCATGTGTCTGGCTATTCTTGG	1827
QY	1921	AAGGGCACTGATCGGCTGTGAGTGCCTCCCGGGGGAGCAGTGGTAAAGGCCAATGCC	1980
DB	1828	AAAGGGATTTAATTGGAGCAAACTATCAATTAAGGACCAGATGATCAAGACCAATGCA	1887
QY	1981	GACGTGAAGGGCTGAGTACTGGTCTGCAGTGTCTGCAGCTGGCTGCCCTGCACGAC	2040
DB	1888	GATGTAAGGCTTTAACTTACTGTATCTCCAGTGTATCATCTCTCAAAGGACTCTTTGAA	1947
QY	2041	AGCCTTGCGCTGTACCCCGAGTTTGGCCCGCGCTTCAGTCTGTGCCCTCCGAGGGAGCTC	2100
DB	1948	GTGCTAGACCTTTACCAGATAATGCTCAAAATTCGTGGAAGACATTCAGCATGACCTC	2007
QY	2101	AGCTACAAACCTGGTGCTGG	2120
DB	2008	ACATACAAACCTCCAGAAAGG	2027

RESULT 12

US-09-358-383C-15
; Sequence 15, Application US/09358383C
; Patent No. 6518398

1 GENERAL INFORMATION: RORY A. J.
2 APPLICANT: Curtis,
3 TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
4 FILE REFERENCE: WNI-055CP
5 CURRENT APPLICATION NUMBER: US/09/358,383C
6 CURRENT FILING DATE: 1999-07-21
7 PRIORITY APPLICATION NUMBER: USSN 09/119,855
8 PRIOR FILING DATE: 1998-07-21
9 NUMBER OF SEQ ID NOS: 36
10 SOFTWARE: PatentIn Ver. 2.0

Query Match	23.4%	Score 761.2	DB 4	Length 5107
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Query Match
Best Local Similarity 62.2%; Pred. No. 3.8e-151; DB 4;
23.4%; SCORE 761.2; Mismatches 708;
Matches 1319: Conservative 0: Mismatches 708;

QY	1	ATGCGGCGCATGCGGGGCTCTGCGGCTCAGAAACCTTCCTCGAACACCATCGCTACG	60
Db	196	ATGCGGTTATGAAGGATTACTGCGCGCGAAAACAGCTTCCTCGAACACCATCGCCAC	255
QY	61	CGCTTCGACGGCAGCAGTAACCTTCGTGTGGGCAAGCCGACGTGCGGGGCTCTTC	120
Db	256	CGTTTGACGGAAACATAGCAACTTCATCTTGCCATGCCAGTGGCTAAGGTTTC	315
QY	121	CCGTTGGTCTACTGCTCTGATGGCTTCTGTGACCTCAAGGGCTTCTCCGGGCTGAGGTC	180
Db	316	CCCATAGTCTACTGTTCGGATGGCTTCTGCGAGCTTGCTGGAATTCGCCCGAATCGAAGTC	375
QY	181	ATGCAGCGGGGCTGTGCGCTGCTCTCTCTTTATGGGCAGACACCATGTCAGCTCGTCCGC	240

Db 376 ATGCAGAAAGTGTCTAGCTGCAAGTCTCTATTGCGGTTGAAACCAATGAGCAACTGATG 435
Qy 241 CAACAGATCCGACAGCCCTGGACGACGACAAAGAGTTCAAGGCTGAGCTGATCCTGTAC 300
Db 436 CTTCAATATAGAAAAGTCACTGGAGGAGAAAACAGAAATTCAAAGAGAAATATGTCTTAC 495
Qy 301 CGGAAGAGCGGCTCCCGTCTCTGCTGCTCTCTGATGTGATACCAATAGAAATGAGAAA 360
Db 496 AAAAAAAGCGGCTCCATTTGGTCTCTCTGATATGTTCCATTAAGAATGAAAA 555
Qy 361 GGGAGGTGGCTCTCTCTCTAGTCTCTCAAGGACATCAAGCAAAACCAAGAACCGAGG 420
Db 556 GGAGATGTAGTACTTTTCTGGCCTCGTTCAAGATATAACAGATA-CAAAAGTGAAGAT 614
Qy 421 GGGCCGACAGATGGAAGGACAGAGTGTGGCGCGGCCCGCCGATATGCGCGGCGACATCC 480
Db 615 TACTCCAGAGATAAAAAAGAGCAAAAGTCAAGGAAGATCAAGAGCAGGAGCCCA--- 671
Qy 481 AAAGGCTTCAATGCAACCGCGCGGAGCGCGCGCTGCTCTACCACTGTCCGGGCAC 540
Db 672 -----CTTTGACTCAGCCCGGAGCGGAGTCGACAGTCTTTTATCACAATCTCTGGGCAC 726
Qy 541 CTGCAGAAAGCCCAAGGCGCAAGCAAAAGTCAATAGGGGGTGTGTTGGGAGAAACCA 600
Db 727 CTGCAAAAGAGAGAAAAGAAACAAATGGAATAAATAACAATGTTTTGTAGATAAAACCA 786
Qy 601 AACTTGCTGAGTACAAAGTAGCGCCCATCGGAGTCGCGCTTCATCTCTGTCACCTGT 660
Db 787 GCAATTCGGAGATATAAGTTCTGATGCAAAAAGTCCAAATTCATACATCTCTGATTTT 846
Qy 661 GGGGCACTGAGAGCAACCTGGATGGCTTCATCTGCTGCGCACACACTATGTGGCTGTC 720
Db 847 AGCACTTTAAAGCTGGCTGGGACTGGCTTATTTGTTGGCAACGTTTATGTGCTGTG 906
Qy 721 ACTGTGCCCTACAGCGTGTGTGAGCACAGCAAGGAGCCGAGTCGCGCGCGCGGCGCG 780
Db 907 ACTGTACTTAAACAGTTGCTTTATTTGGCAATGACGACCTGTCCACAACTCGGAGC--- 963
Qy 781 CCCAGCTCTGTGACCTGGCGTGGAGTCTCTTCACTCTTGACATGTGCTGATTTTC 840
Db 964 ACACCGCTGAGTACATGTCAGTGGAGATCTCTTTATATAGATATTTTAAATTTTC 1023
Qy 841 CGTACCACATTCGTGTCAGAGTCGGGCCAGTGGTGTGTTGCCCAAGTCCATTTGCGCTC 900
Db 1024 CGAACAACTTATGTCAGCAAGTCTGGCCAGTATCTTTGAGCAAGATCAATTTGCATC 1083
Qy 901 CACTACGTCACCACTGGTCTCTCTGATGTGATCGCAGCGCTGCCCTTTGACCTGCTA 960
Db 1084 CACTATGTCAACACTGGTTCATCATTTGATTTAATCGCTGCGCTGCTTTGATCTTCTG 1143
Qy 961 CATGCTTCAGAGTCAACGTGTACTTTCGGGCGCCATCTGCTGAAGACGTTGGCGCTGCTG 1020
Db 1144 TATGCTTTCAACGTCACAGTGGTGTCTCTCGTGCATCTCTTAAAGACAGTGGCGCTTGT 1203
Qy 1021 CGCCTGTGCGCCTGCTTCCGCGGTGACCGGTACTCGCAGTACAGCGCGCTGGTGGTGTG 1080
Db 1204 CGTCTTTTGGCTGCTGCAAGATGACCGCTATTCGCAACACAGTACTATCGTCTGTG 1263
Qy 1081 ACATGCTCATGGCGGTGTCGCCCTGCTCGCGCACTGGGTGCGCTGCTGCTGTTTTTAC 1140
Db 1264 ACTCTGCTCATGTCCATGTTTGCATCTCTGACACTGCTGATGGCGGTGTATCTGGTACGTC 1323
Qy 1141 ATTGGCAGCGGAGATCGAGAGCGCAATCCGAGCTGCGCTGAGATTTGGCTGGCTGAG 1200
Db 1324 ATTGAAAAATGGAGAGGAGAGACAAACGCTTCTGAAAGTGGGAAGTTGGTTGGCTTCA 1383
Qy 1201 GAGCTGGCCCGGCTGAGACTCCCTACTACTCTGTTGGTGGCGGAGCCAGCTGGAGG 1260
Db 1384 GAGTTGGAAAGAGACTGGAATCTCCATACAT 1416
Qy 1261 AACAGCTCCGCGCAGAGTGAACAACCTGCAGCAGCAGCAGGAGCCCAACGGGACGGGCTG 1320
Db 1417 -----GGCAAC 1422

Qy 1321 GAGCTGCTGGCGCGCGTGGCTGCGCAGCGCCTACATCACTCCCTCTACTTGGCACTC 1380
Db 1423 AATACCTTTGGGGGCGCGTGCATCCGAAGTCCCTATATTGCGGCTCTCTACTTACGCTG 1482
Qy 1381 AGCAGCCTCACACAGCTGGGCTTCGGCAACGTTGCCCAACACGGAACACGAGAGATC 1440
Db 1483 AGCAGCCTCACACAGCTGGGTTTGGGAAACGTTCTGCTAATACAGATGCAAGAAAGATC 1542
Qy 1441 TTCTCCATCTGCACCATGCTCATCGGCGCCTGATGACGCGGTGGTGTGTTGGGAACGTC 1500
Db 1543 TTCTCCATCTGCACCATGCTGATTGGTGGCTTGTATGACGCGCTGGTGTGTTGGAAACGTC 1602
Qy 1501 ACGGCCATCATCCAGCGCATGTACGCGCGCTTCTGTACCAACAGCGCGCACCGCGCAC 1560
Db 1603 ACAGCAATCATACAGAGATGTACTTCAGATGGTCCCTCTATCACTAGAACTAAGAT 1662
Qy 1561 CTGGCGACTACATCCGCGCATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGCTGGAG 1620
Db 1663 CTGAAGATTTTCATCCGCTGTCATCACTTGGCCCCAACAACTCAAGCAGAGGATGCTCGAA 1722
Qy 1621 TACTTCAGGCCACCTGGGCGGTGAAACAATGGCATGCAACACCGAGCTGCTGAGAGC 1680
Db 1723 TATTTTCAACAACCTGGTCACTAGTCAACAATGGAATAGATTCAATGAGCTTTTGAAGAC 1782
Qy 1681 CTCCTGACGAGCTGCGCGCAGCATCGCCATGCACCTGCACAAAGGAGGCTCTGCAGCTG 1740
Db 1783 TTTCCAGATGAACCTGGTTCTGACATCACTATGCACTTGAACAAGAGATCTTACAGTTG 1842
Qy 1741 CCACTGTTTGAAGCGGCGCAGCGCGGCTGCTCGGGGCACTGTCTCTGGCCCTCGGGCCC 1800
Db 1843 TCCCTTTTGAATGTGCGCAGCGCGGCTGCTCAGTCTCTCTCTACACATCAAAACC 1902
Qy 1801 GCCTTCGACGCGCGGAGTACTCATTCACCAAGCGATGCCCTGACGCGCCTCTAC 1860
Db 1903 TCTTCTGTCTCGCGGGGAGTATCTGCTGCGTCAAGGGGATGCTTTGACGGCCATCTAC 1962
Qy 1861 TTTCTGCTCTGCTCCATGAGGTTGCTCAAGGTTGCAACCGTGTCTGCCATCTCAGG 1920
Db 1963 TTTGTATGCTCGGCTCCATGGAAGTCTTAAAGACAGATGCTGCTGCTGCTGCTGCTG 2022
Qy 1921 AAGCGCACCTGATCGGCTGTGAGCTGCCCGCGGAGCAGGTGTGTAAGGCCCAATGCC 1980
Db 2023 AAAGGGATTTAATTTGGAGCAATCTATCAATTAAGCAAGTGAATCAAGCAATGCA 2082
Qy 1981 GACGTGAAGGGCTGAGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
Db 2083 GATGTAAGGCTTTAACTACTGTGATCTCCAGTGTATCATCTCAAGGAGTCTCTTTGAA 2142
Qy 2041 AGCCTTGGCTGTACCGGAGTTTGGCGGCTTTCAGTCTGCTGCTGCTGCTGCTGCTGCTG 2100
Db 2143 GTGCTAGACCTTTTACCAGAAATATGCTCAANAATGCTGGAAGACATTCAGCATGACCTC 2202
Qy 2101 AGCTACAACTCGGTGCTGG 2120
Db 2203 ACATACAACCTCCGAGAAG 2222

RESULT 13

US-09-358-383C-6

; Sequence 6, Application US/09358383C

; Patent No. 6518398

; GENERAL INFORMATION:

; APPLICANT: Curtiss, Rory A.J.

; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR

; FILE REFERENCE: MNI-055CP

; CURRENT APPLICATION NUMBER: US/09/358,383C

; CURRENT FILING DATE: 1999-07-21

; PRIOR APPLICATION NUMBER: USSN 09/119,855

; PRIOR FILING DATE: 1998-07-21

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 6

US-09-358-383C-4

Query Match 17.6%; Score 572.8; DB 4; Length 2694;
 Best Local Similarity 61.8%; Pred. No. 1.5e-111;
 Matches 1034; Conservative 0; Mismatches 547; Indels 93; Gaps 4;

QY 1 ATGCGGCGCTATGCGGGGCTCTCGCGCTCAGAACACCTTCTCTGGACACCATCGCTACG 60
 DB 215 ATGCGGTTATGAAGGATTACTGGCGCGGAAACACCTTCTTGGACACCATCGCCACC 274

QY 61 CGCTTCGACGCGCACGCAAGTAACCTTGTGTGGGCAACGCCAGGTGGGGGCTTTC 120
 DB 275 CGTTTTCAGCGGAACACATAGCAACTTTCATCTTCCCAATGCCAGGTGGCTTAAGGGTTTC 334

QY 121 CCCGTGTCTACTGCTCTGTATGGCTTCTGTACCTCAGCGGCTTCTCCGGGCTGAGTTC 180
 DB 335 CCCATAGTCTACTGCTCGATGGCTTCTGTGAGTCTGTGATTTGCCCGAACTGAAATC 394

QY 181 ATGCGAGGGGCTGTGCTGCTCTCTCTTATGGGCGAGACACAGTAGTGTCTGTCGC 240
 DB 395 ATGCGAAGAGTTGTAGCTGCAAGTTCTTATTTGGGGTTGAAACCATGACCACTGATG 454

QY 241 CAACAGATCCGCAAGGCTCGACGAGCAACAGAGTTCAAGGCTGAGCTGATCTGATC 300
 DB 455 CTTCAATAGAAAGTCACTGGAGGAGAAACAGAAATTCAAAGGAGAAATTTATGTTCTAC 514

QY 301 CGGAAGAGCGGCTCCGCTTCTGTGTCTCTGTGATGTATACCATTAAGATGAGAA 360
 DB 515 AAGAAAAACGGGTCTCCATTTTGGTGCTCTGTGATTTTCCCATTAAGAAATGAAAA 574

QY 361 GGGGAGTGGCTCTCTCTTCTAGTCTCTCACAGGACATCAGCAAAACCAAGAACCGAGG 420
 DB 575 GGAGATGATGACTTTTCTGGCTCTGTTCAAGATTAACAGATA-CAAAAGTGAAGAT 633

QY 421 GGGCCGACAGATGGAAGAGACAGGTGGTGGCGGCGCCGATATGGCGGGCGACATCC 480
 DB 634 TACTCCAGAGATAAAAGAAAGCAAAAGTCAAGAGAGATCAAGAGCAGGAGCCCA- 690

QY 481 AAGGCTTCAATGCAACCGCGGGGAGCGCGGCGGTCTTACCACCTGTCGGGAC 540
 DB 691 -----CTTTGACTCAGCCGCGAGACGAGTCCGAGTCCCTTTATCAATCTCTGGGAC 745

QY 541 CTGCGAAGCAGCCCAAGGCAAGCACAGTCTCAATAGGGGGTGTGGGAGAGAAACA 600
 DB 746 CTGCAAGAGAGAAAGAAAGAAATGAATTAATTAACATGTTTGTAGATAAACCA 805

QY 601 AACTGCTGTAGTAAAGTAGCCGCCATCCGGAAGTCCGCCCTTCACTCTGTGACTGT 660
 DB 806 GCAITTCGGAGTATAAAGTTCTGTATGCAAAAAAGTCCAAATTCATACTTCTGCAITTT 865

QY 661 GGGGCACTGAGACCACTGGGATGGCTTCTATCTGCTCGCCACACTCTATGTGGCTGTC 720
 DB 866 AGCACTTTTAAAGTGGCTGGGACTGGCTTATTTTGTGGCAAGTTTATGTGCTGTG 925

QY 721 ACTGTGCCCTACAGCGTGTGTGAGCAGCAGCGGAGCCAGTCCGCCCGCGGCGCCG 780
 DB 926 ACTGTACTTACAGCTTGTGTTTATTTGGCAATGACGACCTGTCCACAACTCGGAC- 982

QY 781 CCCAGCGTCTGTGACCTGGCGGTGAGTCTCTTTCATCTTGAATGTGCTGAATTC 840
 DB 983 ACAACCGTCACTGACATTCGAGTGGAGATCTCTTTTATATAGATATTTTAAATTC 1042

QY 841 CGTACCAATTCGTCTCAAGTCCGGCGAGTGGTGTGGCCCAAGTCCATTTGCTC 900
 DB 1043 CGAACTTATGTGCAAGTCTGGCAAGTTATCTTTGAAGCAAGATCAATTTGCAATC 1102

QY 901 CACTACGTCACACCTGTTCTGTGATGTATCGCAGCGCTGCCCTTTGACCTGCTA 960
 DB 1103 CACTATGTCAACCTGTTTATCATTTATTCGCTGCCCTGCTGCTTTGATCTTCTG 1162

QY 961 CATGCTTTCAAGGTCAACGTGTACTTCGGGGCCCATCTGCTGAAGCGGTGGCGCTGCTG 1020
 DB 1163 TATGCTTTCAAGCTCACAGTGTGTCTCTCGTGATCTCTTAAAGACAGATGCGCCTCTG 1222

QY 1021 CGCTGTGCGCGCTTTCGCGCTGACCGGTACTCGAGTACAGCGCGTGTGCTG 1080
 DB 1223 CGTCTTTTGGTCTGCTGCGAAGTTAGACCGCTATTTCACACAGTACTATCGTCTG 1282

QY 1081 ACAGTCTCATGGCGTGTTCGCGCTCTCGCGACTGGGTGCGCTGCTGCTGTTTAC 1140
 DB 1283 ACTCTGCTCATGCTCATGTTTGCACCTCTTGCACACTGGATGGCTGTATCTGTGACGTC 1342

QY 1141 ATTGGCAGCGGAGATCGAGAGCAGCAATCCAGCTGCTGAGATGGCTGCTGCTGAG 1200
 DB 1343 ATTGGAAAAATGGAGAGGAGAACACAGCCCTTCTGAAGTGGGAAGTTGGTTGCTTCAT 1402

QY 1201 GAGTGGCGCGCCGACTGGAGTCTCTTACTTACTTCTGCTGGTGGCGCGGAGCGGAGG 1260
 DB 1403 GAGTTGGAAAGAGACTGGATCTTCCATCTA----- 1434

QY 1261 AACAGTCCCGCCAGAGTGAACACTGCAGCAGCAGCAGGAGCCAAACGGGACGGGCTG 1320
 DB 1435 -----TGGCAAC 1441

QY 1321 GAGTGTGGCGGCGCGTGTGCTGCGCAGCGCTTACATCAGCTCCCTCTACTTGCACATC 1380
 DB 1442 AATACTTGGGGGCGCGTGCATCCGAAGTGCCTATATTCGCGCTCTGTACTTCAACGCTG 1501

QY 1381 AGCAGCTTCAACAGCGTGGCTTCGCAACGCTGTCGCCAACACGACACCGCAAGATC 1440
 DB 1502 AGCAGCTTCAACAGCGTGGCTTGGGAACTCTCTGCTATACAGATGCAAGAAAGATC 1561

QY 1441 TTCTCCATCTGCACCATCTCATCGGCGCGCTGATGACGCGTGGTGTGGGAACTG 1500
 DB 1562 TTCTCCATCTGCACCATCTGATTTGGTGCCTTGTATGACGCGCTTGGTGTGGGAACTG 1621

QY 1501 AGGCAATCATCAGCGCATGACGCGCGCGCTTCTGTACACACGCGCACGCGGAC 1560
 DB 1622 ACAGCAATCATACAGAGATGTACTCCAGATGGTCCCTCTATCACTAGAACTAAGAT 1681

QY 1561 CTGCGCACTACATCCGCTCCGCTATCCCAAGCCCTCAAGCAGCGCATGCTGGAG 1620
 DB 1682 CTGAAGATTTTATCCGTGTCATCTTGGCCCAACACTCAAGCAGAGATGCTCGAA 1741

QY 1621 TACTTCCAGCGCACCTGGCGGTGAACAAATGGCATCGACACCGAGCTGCTG 1674
 DB 1742 TATTTTCAACAACCTGTGTAGTCAACAATGGAATAGATTCAAATGAGGTAATG 1795

RESULT 15
 US-09-358-383C-14
 ; Sequence 14, Application US/09358383C
 ; Patent No. 6518398
 ; GENERAL INFORMATION:
 ; APPLICANT: Curtis, Rory A.J.
 ; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
 ; FILE REFERENCE: NMI-055CP
 ; CURRENT APPLICATION NUMBER: US/09/358,383C
 ; PRIORITY FILING DATE: 1999-07-21
 ; PRIOR APPLICATION NUMBER: USN 09/119,855
 ; PRIOR FILING DATE: 1998-07-21
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 14
 ; LENGTH: 5955
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: (196)..(1770)
 ; NAME/KEY: intron
 ; LOCATION: (1771)..(2618)
 ; NAME/KEY: exon
 ; LOCATION: (2619)..(4364)
 ; OTHER INFORMATION: At position 5625, n=any nucleic acid
 US-09-358-383C-14

Query Match 17.6%; Score 572.8; DB 4; Length 5955;
Best Local Similarity 61.8%; Pred. No. 1.9e-111;
Matches 1034; Conservative 0; Mismatches 547; Indels 93; Gaps 4;

QY 1 ATGCGCGCATGCGGGCCCTCTGGCGCTCAGAACACCTTCTGAGACCATCGCTACG 60
DB 196 ATGCGCGTTATGAAGGATTTACTTGGCGCGCAAAACACCTTCTGAGACCATCGCCACC 255

QY 61 CGCTTCGAGCGGACGACAGTAACTTCTGCTCGGCAACGCGCAGGTGGCGGGCTCTTC 120
DB 256 CGTTTTGACGGAACACATAGCACTTCACTCTTGGCAATGCCAGGTGGCTAAGGGTTTC 315

QY 121 CCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCAGCGGCTTCTCCCGGGCTGAGGTC 180
DB 316 CCGATAGTCTACTGTTCCGATGCTTCTGCGAGCTTGTGATTTGCGCGAAGTGAAGTC 375

QY 181 ATGCGCGGGCTGTGCTGCTCTCTTCTTATATGGGCGAGACACAGTGAAGTCTGCGC 240
DB 376 ATGCGAAGAGTTGTAGCTGCAAGTTCTTATTTGGGGTTGAACCAATGAGCAACTGATG 435

QY 241 CAACAGATCCGCAAGGCTCTGAGCAGCACAAGAGTTCAAGGCTGAGCTGATCTCTGTAC 300
DB 436 CTTCAATAGAAAGTCACTGGAGGAGAAACAGAAATTAAGAGAAATATGTTCTAC 495

QY 301 CGGAAGAGCGGGCTCCGTTCTGCTGTCTCTGATGTGATACCCATAAGAAATAGAAA 360
DB 496 AAGAAAAACGGGCTCCATTTTGGTCTACTGGATATTGTTCCCATAAAGATGAAAA 555

QY 361 GGGAGGTGGCTCTCTCTAGTCTCTCAAGAGCATAGCGAAACCAAGAACCGAGGG 420
DB 556 GGAGATGTAGTACTTTTCTGGCTCTGTTCAAGATATTAACAGATA-CAAAAGTGAAGAT 614

QY 421 GGCCCCGACAGATGGAAGAGACAGGTGTGGCGCGCGATATGGCGGGGACCATCC 480
DB 615 TACTCCAGAGATAAAAGAGACAAAGTCAAGAGAGAGGACCCCA--- 671

QY 481 AAGGCTTCAATGCCAACCGGGCGGAGCGGGCGTGTCTTACCACTGTCTCGGGCAC 540
DB 672 -----CTTTGACTCAGCCCGGAGACGAGTCTGAGCAGTCTCTTATCAGATCTCTGGGCAC 726

QY 541 CTGCGAAGCGCCCAAGGGCAGCACAAGCTCAATAAGGGGTGTTGGGGAGAACCA 600
DB 727 CTGCAAGAGAGAAAGAACAAATTAAGAAATTAACAAATGTTTTGTAGATNAACCA 786

QY 601 AACTTGCCTGAGTACAAAGTAGCGGCATCCGGAAGTCTGCGCTTCTCTCTGTTGCACTGT 660
DB 787 GCATTTCCGGAGTATAAGTTTCTGATGCAAAAAGTCCMAATTCATCTTGCATTTT 846

QY 661 GGGGCACTGAGAGCCACCTGGGATGGCTTCACTGCTCGCCACACTCTATGTGGCTGTC 720
DB 847 AGCAGCTTTTAAAGCTGGCTGGGACTGGCTTATTTTGTGGCAACGTTTTATGTTGCTGTG 906

QY 721 ACTGTGCCCTACAGCTGTGTGTGAGCAGCAGCGGAGCCAGTGGCGCCCGGGCCCG 780
DB 907 ACTGTACCTTTACAACTTTGCTTTATTTGGCAATGACGACCTGTCCCAACTCGGAGC--- 963

QY 781 CCAGCGCTGTGACCTGGCGGTGGAGGTCCTCTTCACTGACATTTGCTGGAATTTTC 840
DB 964 ACAACCGTCAGTGACATTCAGTGGAGATCTTTTATATAGATATTTTAAATTTTC 1023

QY 841 CGTACCAATTCGTGTCGAAGTCGGGCGAGGTGGTGTGTCGCCCAAGTCCATTTGCGCTC 900
DB 1024 CGAACCAACTTATGTCAGCAAGTCTGGCCAAAGTTATCTTTGAAGCAAGATCAATTTGCATC 1083

QY 901 CACTAGTCAACACCTGTTCTGTGATGTCATCGCAGCGCTGCCCTTGAACCTGCTA 960
DB 1084 CACTATGTCAACACCTGGTTCACTATGATTTAATCGTGGCTGCTTTGATCTCTG 1143

QY 961 CATGCTTCAAGGTCACAGTGTACTTTGGGGGCCCATCTGTGAAAGCGGTGGCGCTGCTG 1020
DB 1144 TATGCTTTCAACGTCACAGTGGTGTCTCTGTCGATCTTCTTAAAGACAGTGGCGCTCTTG 1203

Search completed: September 1, 2004, 18:41:43
Job time : 177 secs

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DB 1204 CGTCTTTTGGCTGCTGTCGAGAAGTTAGACCGCTATTCCACACACAGTACTATCGTCTG 1263

QY 1081 ACAGTCTCATGGCGGTGTTCCGCTGCTGGGCACTGGGTGCGCTGCGTCTGCTGTTTAC 1140
DB 1264 ACTCTGCTCATGTCCTATGTTTGCACCTTGCACACTGATGGCGTGTATCTGGTACGTC 1323

QY 1141 ATTGGCCAGCGGAGATCGAGAGCAGGAATCGAGCTGCTGAGATTTGGCTGGCTGCGAG 1200
DB 1324 ATTGGAATAATGGAGAGGAGAACACAGCTTCTGAAGTGGAGTTGTTGGCTTCAT 1383

QY 1201 GAGTGGCGCGCGACTCGAGACTCCCTACTACTGCTGGGCGGAGGCGAGCTGGAGGG 1260
DB 1384 GAGTTGGGAAAGAGACTCGGAATCTCCATACTA----- 1415

QY 1261 AACAGCTCGCGCAGAGTGAACACTGACAGCAGCAGCGGCGCAACGGGACGGGGCTG 1320
DB 1416 -----TGGAAC 1422

QY 1321 GAGCTGCTGGGCGCGCTGCTGGCGAGCGCTACATCACCTCCCTCTACTTCGCACTC 1380
DB 1423 AATACCTTGGGGGCGCGCTGATCCGAGTGCCTATATTGCCGCTCTGTACTTCACGCTG 1482

QY 1381 AGCAGCTCACCAGCGTGGCTTTCGGCAACGTGTCGCGCAACACGAGACCCGAGAGATC 1440
DB 1483 AGCAGCTCACCAGCGTGGGTTTGGGAAACGTCTCTGCTAATAACAGATGCAGAAAAAGTC 1542

QY 1441 TTCTCCATCTGCACCATGCTCATCGCGCGCTGATGACGCGGTGCTGTTGGGAACGTG 1500
DB 1543 TTCTCCATCTGCACCATGCTGATTTGGTGCCTTATGACGCTTGGTGTGTTGGAACGTG 1602

QY 1501 AGGCGCATCATCCAGCGCATGTACGCGCGCTTCTGTATCCACAGCCGCGACCGCGAC 1560
DB 1603 ACAGCAATCATACAGAGGATGTACTCCAGATGCTCCCTCTATCAGTAACTAAGAT 1662

QY 1561 CTGCGGCACTACATCCGATCCACCGTATCCCAAGCCCTTAAAGCAGCGCATGCTGGAG 1620
DB 1663 CTGAAAGATTTTCATCGTGTCCATCACTTGGCCCAACAACTCAAGCAGAGGATGCTCGAA 1722

QY 1621 TACTTCCAGGCCACCTGGGCGGTGAACAATGGCATCGACACCCAGGCTGCTG 1674
DB 1723 TATTTTCAACCACTGGTGCAGTCAACAATGGAATAGATTCAATGAGGTAATG 1776

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 1, 2004, 14:38:36 ; Search time 8225 Seconds
(without alignments)
17136.966 Million cell updates/sec

Title: US-09-965-830-1_COPY_6_3257

Perfect score: 3252

Sequence: 1 atgcgcgcctgcggggcct.....aagaaggcacaggggtctga 3252

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rod.*

36: em_htg_mam.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	3252	100.0	3223	6	AR179189	AR179189 Sequence
2	3252	100.0	3610	9	AB022696	AB022696 Homo sapi
3	3250.4	100.0	3853	9	AB033108	AB033108 Homo sapi
4	3245.8	99.8	3249	6	AR217183	AR217183 Sequence
5	3244	99.8	3252	6	AX027893	AX027893 Sequence
6	3218	99.0	3857	6	AR212361	AR212361 Sequence
7	3156	97.0	3355	6	AR281263	AR281263 Sequence
8	3153	97.0	3249	6	AR281264	AR281264 Sequence
9	2664.8	81.9	3595	10	RN07627	AJ007627 Rattus no
10	2664.8	81.9	3715	6	AR179195	AR179195 Sequence
11	2664.8	81.9	3715	10	AB022697	AB022697 Rattus no
12	2660.8	81.8	3615	10	AF109143	AF109143 Mus muscu
13	2657	81.7	3285	10	AY380579	AY380579 Mus muscu
14	1055.4	32.5	1432	9	BC033141	BC033141 Homo sapi
15	884.8	27.2	3064	6	AR179192	AR179192 Sequence
16	884.8	27.2	3920	9	AB022698	AB022698 Homo sapi
17	869.8	26.7	3688	10	RN07628	AJ007628 Rattus no
18	869.8	26.7	3736	6	AR179196	AR179196 Sequence
19	869.8	26.7	3736	10	AB022699	AB022699 Rattus no
20	844.4	26.0	870	6	AR281268	AR281268 Sequence
21	844.4	26.0	1132	6	AR281267	AR281267 Sequence
22	803.2	24.7	3743	10	AF061957	AF061957 Rattus no
23	794.4	24.4	3742	6	BD231010	BD231010 Mammalian
24	761.2	23.4	3321	6	AR281271	AR281271 Sequence
25	761.2	23.4	5107	6	AR281270	AR281270 Sequence
26	761.2	23.4	5107	9	AY053503	AY053503 Homo sapi
27	601	18.5	161695	2	AC079849	AC079849 Homo sapi
28	601	18.5	186011	2	AC079461	AC079461 Homo sapi
29	601	18.5	188928	9	AC020612	AC020612 Homo sapi
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36	447.8	13.8	1099	10	RN07632	AJ007632 Rattus no
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ALIGNMENTS

RESULT 1
AR179189
LOCUS
DEFINITION Sequence 1 from patent US 6326168.
ACCESSION AR179189
VERSION AR179189.1 GI:20220744
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 3223)
AUTHORS Miyake,A., Mochizuki,S. and Yokoi,H.
TITLE Brain specific potassium channel protein
JOURNAL Patent: US 6326168-A 1 04-DEC-2001;
FEATURES Location/Qualifiers

linear PAT 20-APR-2002

Db 2046 AGCCTTGCGCTGACCCCGAGTTTGCCCGCGCTTCAGTGTGGCTCCGAGGGGAGCTC 2105
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AB022696
LOCUS Homo sapiens mRNA for BEC1, complete cds. 3610 bp mRNA linear PRI 31-AUG-1999
DEFINITION AB022696
ACCESSION AB022696
VERSION AB022696.1 GI:5804783
KEYWORDS BEC1; human BEC1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (sites)
REFERENCE Miyake,A., Mochizuki,S., Yokoi,H., Kohda,M. and Furuichi,K.
TITLE New ether-a-go-go K(+) channel family members localized in human telencephalon
J. Biol. Chem. 274 (35), 25018-25025 (1999)
JOURNAL 99386988
MEDLINE 10455180
PUBMED 2 (bases 1 to 3610)
REFERENCE Miyake,A., Mochizuki,S., Yokoi,H., Kohda,M. and Furuichi,K.
TITLE Direct Submission
SUBMITTED (21-JAN-1999) Akira Miyake, Yamanouchi Pharmaceutical Co.,Ltd., Molecular Medicine Laboratories; 21 Miyukioka, Tsukuba, Ibaraki 305-8585, Japan (E-mail:miyake@yamanouchi.co.jp, Tel:81-298-52-5111(ex.3324), Fax:81-298-52-5444)
FEATURES
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Query Match 100.0%; Score 3252; DB 9; Length 3610;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCCGCGCATCGGGGCGCTCTCGGCGCTCAGAACACCTCTCTCGGACACCATCGCTACG 60

Db	36	ATGCCGGCATCGGGGCTCTCTGGGCGCTCAGAACACCTTCTCGACACCATCGCTACG	95	Db	1116	ACACTGCTCATGGCCGTGTTGGCCCTGCTCGCGCACTGGGTGCGCTGCTGCTGTTTAC	1175
QY	61	CGCTTCGACGGCAGCAGTAACTTCGTCTGGGCAACGCCAGGTGGGGGCTCTTC	120	QY	1141	ATTGGCCAGCGGAGATCGAGAGCAGGAATCGAGCTGCCTGAGATTGGCTGGCTGCAG	1200
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QY	181	ATGACGGGGCTGTGCTGCTCTCTCTTATATGGGCGAGACACAGTAGCTGCTCCG	240	QY	1261	AACAGCTCCGGCCAGAGTGACAACTGACGAGCAGGAGCCAAACGGAGCGGGCTG	1320
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QY	241	CAACAGATCCGAAGGCTTGAAGAGCAAGAGGTTCAAGGCTGAGCTGATCTCTGTAC	300	QY	1321	GAGTCTCGGGGGCCGCTGCTGCGAGCGCTACATCACTCCCTCTACTTCGCACTC	1380
Db	276	CAACAGATCCGAAGGCTTGAAGAGCAAGAGGTTCAAGGCTGAGCTGATCTCTGTAC	335	Db	1356	GAGTCTCGGGGGCCGCTGCTGCGAGCGCTACATCACTCCCTCTACTTCGCACTC	1415
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QY	661	GGGGCACTGAGAGCCACTGGATGCTTATCTGCTGCCACACTATATGGGCTG	720	QY	1741	CGACTGTTGAGGGCGCAGCGCGCTGCTGGGCGACTGCTCTGCGCCCTGCGGCC	1800
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ORGANISM	Homo sapiens				
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AUTHORS	1 (sites)				
	Nagase,T., Ishikawa,K., Kikuno,R., Hirose,M., Nomura,N. and Ohara,O.				
TITLE	Prediction of the coding sequences of unidentified human genes. XV.				
	The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro				
JOURNAL	DNA Res. 6 (5), 337-345 (1999)				
	20039619				
MEDLINE	10574462				
	PUBMED				
REFERENCE	2. (bases 1 to 3853)				
	Ohara,O., Nagase,T. and Kikuno,R.				
AUTHORS	Direct Submission				
	Submitted (04-OCT-1999) Osamu Ohara, Kazusa DNA Research Institute,				
TITLE	Laboratory of DNA Technology; 1532-3 Yana, Kisarazu, Chiba				
	292-0812, Japan (E-mail:cdna@nfo.kazusa.or.jp, URL:http://www.kazusa.or.jp/huge/, Tel:+81-438-52-3913, Fax:+81-438-52-3914)				
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	CSDTGASSYCLQPPAGSVLSTWPHRPGPPLMAPWPGPPASQSPMPRATFWTS				
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Query Match	100.0%; Score 3250.4; DB 9; Length 3853;				
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Matches 3251; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db				Db	1401	ATTGGCAGCGGGAGATCGAGAGCAGCAATCGAGCTGCTGAGATTGGCTGGCTGCAG	1460
QY	61	CGCTTCGACGGCAACGACAGTAATCTTCGTGCTGGGCAACGCCAGGTGCGGGGCTCTTC	120	QY	1201	GAGCTGGCGCGCGACTGGAGACTCCCTACTACTCTGGTGGCGGAGGCGAGCTGGAGGG	1260
Db				Db	1461	GAGCTGGCGCGCGACTGGAGACTCCCTACTACTCTGGTGGCGGAGGCGAGCTGGAGGG	1520
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Db				Db	1521	AACAGCTCCGGCCAGAGTGACAACTGACAGCAGCAGCGAGCGCAACCGGAGCGGGCTG	1580
QY	381	CCGCTGGTCTACTGCTCTGATGCTTCTGTGACTCAACGGGCTTCTCCGGGCTGAGGTC	440	QY	1321	GAGCTGCTGGCGGCGCGCTGCTGGCAGCGGCTACATCACCCTCTACTTTCGCACATC	1380
QY	181	ATGCACGGGGCTGTCCTCTCTTCTTATGCGGCCAGACACCAAGTGAAGTCTGTCGCG	240	Db	1581	GAGCTGCTGGCGGCGCGCTGCTGGCAGCGGCTACATCACCCTCTACTTTCGCACATC	1640
Db				QY	1381	AGCAGCTCACCAGCGTGGGCTTTCGGCAACGTGTCGCGCAACACGACACCGGAGAGATC	1440
QY	441	ATGCACGGGGCTGTCCTCTCTTCTTATGCGGCCAGACACCAAGTGAAGTCTGTCGCG	500	Db	1641	AGCAGCTCACCAGCGTGGGCTTTCGGCAACGTGTCGCGCAACACGACACCGGAGAGATC	1700
QY	241	CAACAGATCCGCAAGGCCCTGAGCAGAGCAACAGGAGTTCAGGCTGAGCTGATCTGTATC	300	QY	1441	TTCTCCATCTGCAACCACTCATGCGCGGCTGATGCAACGGGTGCTGTTTGGGAAAGCTG	1500
Db				Db	1701	TTCTCCATCTGCAACCACTCATGCGCGGCTGATGCAACGGGTGCTGTTTGGGAAAGCTG	1760
QY	501	CAACAGATCCGCAAGGCCCTGAGCAGAGCAACAGGAGTTCAGGCTGAGCTGATCTGTATC	560	QY	1501	AGGGCCATCATCCAGCGCATGTACGCCCGCGCTTCTGTACCAAGCGCGACCGCGCAC	1560
QY	301	CGGAAGAGCGGGCTCCCGTTCCTGCTGCTCTCTGATGTATACCCATAAAGATGAGAAA	360	Db	1761	AGGGCCATCATCCAGCGCATGTACGCCCGCGCTTCTGTACCAAGCGCGACCGCGCAC	1820
Db				QY	1561	CTGCGGAGTACATCCGCGATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGCTGGAG	1620
QY	561	CGGAAGAGCGGGCTCCCGTTCCTGCTGCTCTCTGATGTATACCCATAAAGATGAGAAA	620	Db	1821	CTGCGGAGTACATCCGCGATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGCTGGAG	1680
QY	361	GGGAGGCTGCTCTCTTCTAGTCTCTCAACAGGACATCAGCGAAACCAAGAACCGAGGG	420	QY	1621	TACTTCCAGGCACTTGGGCGGTGAACAATGGCATCGACACCGAGCTGCTGCAGAGC	1680
Db				Db	1881	TACTTCCAGGCACTTGGGCGGTGAACAATGGCATCGACACCGAGCTGCTGCAGAGC	1940
QY	621	GGGAGGCTGCTCTCTTCTAGTCTCTCAACAGGACATCAGCGAAACCAAGAACCGAGGG	680	QY	1681	CTCCCTGACGAGTGGCGCAGACATCGCATCGCATCCCAAGCCCTCAAGCAGCGCATGCTGGAG	1740
QY	421	GGGCGCGACATGGAAGAGACAGGTGCTGGCGCGCGGATGATGGCGGGGACGATCC	480	Db	1941	CTCCCTGACGAGTGGCGCAGACATCGCATCGCATCCCAAGCCCTCAAGCAGCGCATGCTGGAG	1800
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QY	481	AAAGGCTTCAATCCCAACCGCGCGGAGCGCGCGTGTCTTACCACTGTCCGCGCAC	540	QY	1801	GCCTTCTGCAACGCCGGCGAGTACCTCATCCCAAGGCGATGCTGCAAGGCCCTCTAC	1860
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QY	661	GGGGCACTGAGACCACTGGGATGCTTCATCTGCTGCGCACACTCTATGTGGCTGTC	720	Db	2301	AGCTTGGCTGTACCCCGAGTGTGCGCGGCTTTCAGTGTGCTGCGGCTCCGAGGGAGCTC	2360
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QY	921	GGGGCACTGAGACCACTGGGATGCTTCATCTGCTGCGCACACTCTATGTGGCTGTC	980	Db	2361	AGCTAACAACCTGGTGTGCGGGAGGCTGTGAGAGTGGACACAGCTCCCTGAGCGGC	2420
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RESULT 4
AR217183

LOCUS AR217183 3249 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 2 from patent US 6413741.

ACCESSION AR217183

VERSION AR217183.1 GI:23316610

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 3249)

AUTHORS Jegla, T.J. and Wickenden, A.

TITLE Human elk a voltage-gated potassium channel subunit

JOURNAL Patent: US 6413741-A 2 02-JUL-2002;

FEATURES Location/Qualifiers

source 1..3249

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Query Match 99.8%; Score 3245.8; DB 6; Length 3249;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3247; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 ATGCGGCCCATGCGGGGCTCTCTGGCGCCTCAGAACACCTTCTTGGACACCATCGCTACG 60

Qy 61 CGCTTCACGGCAGCAGTAATCTTCTGCTGGGCAACGCCAGGTGGGGGCTCTTC 120

Db 61 CGCTTCACGGCAGCAGTAATCTTCTGCTGGGCAACGCCAGGTGGGGGCTCTTC 120

Qy 121 CCGGTGCTTACTGCTCTGATGGCTTCTGTGACCTCAGCGGCTTCTCCCGGGCTGAGGTC 180

Db 121 CCGGTGCTTACTGCTCTGATGGCTTCTGTGACCTCAGCGGCTTCTCCCGGGCTGAGGTC 180

Qy 181 ATGACGCGGGGCTGTGCTCTCTCTTTATGGGCCAGACACAGTGTGCTCGC 240

Db 181 ATGACGCGGGGCTGTGCTCTCTCTTTATGGGCCAGACACAGTGTGCTCGC 240

Qy 241 CAACAGATCCGCAAGGCCCTGGACGAGCAAGAGTTCAGGCTGAGCTGATCTGTAC 300

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Qy	1081	ACACTGCTCATGCGCGCTGTTGCGCCCTGCTCGCGCACTGGGTGCGCTGCTGTTTAC	1140
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Qy	1261	AACAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGCGAGGCCAACCGGACGGGGCTG	1320
Db	1261	AACAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGCGAGGCCAACCGGACGGGGCTG	1320
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Db	1321	GAGCTGCTGGGCGGCCGCTGCTGCGCAGCGCTACATCACCTCCCTACTTCGCACTC	1380
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Db	1381	AGCAGCTCACAGCTGGGCTTCGGCAAGCTGTCCGCCAAGCTGTCCGCCAACCGAGAGATC	1440
Qy	1441	TTCTCCATCTGACCATGCTCATCGCGGCCCTGATGCAAGCGGTGGTGTGTTGGGAACGTG	1500
Db	1441	TTCTCCATCTGACCATGCTCATCGCGGCCCTGATGCAAGCGGTGGTGTGTTGGGAACGTG	1500
Qy	1501	ACGGCCATCATCAGCGCATGTAAGCCCGCGCTTTCTGTACCAAGCCGACGCGCGAC	1560
Db	1501	ACGGCCATCATCAGCGCATGTAAGCCCGCGCTTTCTGTACCAAGCCGACGCGCGAC	1560
Qy	1561	CTGCGGACTCATCCGATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGCTGGAG	1620
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DEFINITION Sequence 1 from Patent EP1002863.
ACCESSION AX027893
VERSION AX027893.1 GI:10188725
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Avenet, P. and Renard, S.
TITLE A potassium channel member of the erg family
JOURNAL Patent: EP 1002863-A 1 24-MAY-2000;
SANOFI SYNTHELABO (FR)
FEATURES
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ORIGIN

Query Match 99.8%; Score 3244; DB 6; Length 3252;
Best Local Similarity 99.8%; Pred. No. 0;
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DEFINITION Sequence 19 from patent US 6399761.

ACCESSION AR212361

VERSION AR212361.1 GI:21515915

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 3857)

AUTHORS Muller,A.P., Hu,P., Curran,M.Edward., Rutter,M. and Jiang-Yang,W.

TITLE Nucleic acid encoding human potassium channel K+ novl protein

JOURNAL Patent: US 6399761-A 19 04-JUN-2002;

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DEFINITION Sequence 3 from patent US 6518398.
ACCESSION AR281264
VERSION AR281264.1 GI:29716864
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 3249)
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 Rattus.
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 Identification of three rat potassium channel genes homologous to
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 Unpublished
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 England, B.
 Direct Submission
 Submitted (03-JUL-1998) England B., Zentrum fuer Molekulare
 Neurobiologie Hamburg, Institut fuer Neurale Signalverarbeitung,
 Martinistrasse, D-20246 Hamburg, GERMANY
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 QY 661 GGGGCACTGAGAGCACCCTGGGATGGCTTCTCTCTCGCACACTCTATGTGGCTGTC 720
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QY 3169 CCCACAGCCTGGAGATGGTCTATTATGGCTGCATGGCTCTGGCACAGTCCAGTGGACC 3228

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RESULT 10

AR179195

LOCUS AR179195 3715 bp DNA linear PAT 20-APR-2002

DEFINITION Sequence 9 from patent US 6326168.

ACCESSION AR179195

VERSION AR179195.1 GI:20220750

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 3715)

AUTHORS Miyake,A., Mochizuki,S. and Yokoi,H.

TITLE Brain specific potassium channel protein

JOURNAL Patent: US 6326168-A 9 04-DEC-2001;

FEATURES

Location/Qualifiers

1..3715

/organism="unknown"

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ORIGIN

Query Match 81.9%; Score 2664.8; DB 6; Length 3715;

Best Local Similarity 89.0%; Pred. No. 0;

Matches 2905; Conservative 0; Mismatches 347; Indels 12; Gaps 2;

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QY 361 GGGAGGTGGCT 420

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QY	1732	CTGCAGCTGCCACTGTTTGAAGCGCGCAGCCGCGCTCTGCGGGGACATGTCTCTCGGCC	1791
Db	1896	CTGCAGCTGCCATTTGTTGAGGACAGACCCGTGGCTGCTGCGGGGACATGTCTCTCGGCC	1955
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QY	2512	AAGTTCTCTTTCCGCTGGGCGAGTCTGGGCCCGGAATGTAGCAGCAGCCCTCCGCTGGA	2571
Db	2676	AAGTTCTCTTTCCGGGTGGGTCAGTCTGGGCCGGAATGTAGCAGCAGCCCTCCGAGGA	2735
QY	2572	CCAGAGAGCGGCTGTCTACTGTTTCCCATGTTGGGCCCGACGAGGCAAGGAACACAGACACA	2631
Db	2736	ACAGAGAGTGGCTGTCTCATCTGTCCCTTTGGTGCCAGTGAAGGCAAGAACACAGACACA	2795
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QY	3169	CCC	CA	CA	CA	CT	GG	AG	AT	GG	T	AT	GG	CT	3229
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QY	3229	CAG	GA	GA	AG	GC	CA	CA	GG	GG	CT	CT	GA		3252
Db	3396	CAG	GA	GA	AG	GC	CA	CA	GG	GG	CT	CT	GA		3419

RESULT 11

AB022697

LOCUS

AB022697

DEFINITION

Rattus norvegicus mRNA for BEC1, complete cds.

ACCESSION

AB022697

VERSION

AB022697.1

KEYWORDS

GI:5804785

SOURCE

J. Biol. Chem. 274 (35), 25018-25025 (1999)

ORGANISM

Rattus norvegicus (Norway rat)

REFERENCE

1

Miyake, A., Mochizuki, S., Yokoi, H., Kohda, M. and Furuichi, K.

Submitted (21-JAN-1999)

Direct Submission

Co., Ltd., Molecular Medicine Laboratories; 21 Miyukigaoka, Tsukuba, Ibaraki 305-8585, Japan (E-mail: miyake@yamanouchi.co.jp, Tel: 81-298-52-5111 (ex. 3124), Fax: 81-298-52-5444)

Location/Qualifiers

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CDS

3715 bp

linear

31-AUG-1999

[illegible]

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VERSION BC033141.1 GI:21620039
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1432)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DRP
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saedi, Jacqueline
Schein, Duane Smalius, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 43 Row: c Column: 13
This clone was selected for full length sequencing because it
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ACCESSION AR179192
VERSION AR179192.1 GI:20220747
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SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 3064)
AUTHORS Miyake,A., Mochizuki,S. and Yokoi,H.
TITLE Brain specific potassium channel protein
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ORIGIN

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001as.*
5: Geneseq2001bs.*
6: Geneseq2002s.*
7: Geneseq2003as.*
8: Geneseq2003bs.*
9: Geneseq2003cs.*
10: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	3252	100.0	3252	9 ADC47039	ADC47039 BECl pota
2	3252	100.0	3323	2 AAX84910	Aax84910 Human bra
3	3250.4	100.0	3829	3 AAZ87712	Aaz87712 Human ESK
4	3245.8	99.8	3249	3 AAZ50119	Aaz50119 Human Elk
5	3244	99.8	3252	2 AAX14893	Aax14893 DNA encod
6	3218	99.0	3857	2 AAZ11906	Aaz11906 Human pot
7	3156	97.0	3355	3 AAZ50452	Aaz50452 Monkey po
8	3156	97.0	3355	7 ACA61728	ACA61728 Monkey ER
9	3156	97.0	3355	9 ADB66794	ADB66794 cDNA enco
10	3153	97.0	3249	7 ACA61729	ACA61729 Monkey ER
11	2664.8	81.9	3715	2 AAX84919	Aax84919 Rat brain
12	2664.8	81.9	3715	9 ADB58253	ADB58253 Toxicity-
13	884.8	27.2	3064	2 AAX84911	Aax84911 Human bra
14	869.8	26.7	3736	2 AAX84918	Aax84918 Rat brain
15	869.8	26.7	3736	9 ADB53481	ADB53481 Primary r
16	844.4	26.0	870	7 ACA61733	ACA61733 Human ERG
17	844.4	26.0	1132	3 AAZ50454	Aaz50454 Human pot
18	844.4	26.0	1132	7 ACA61732	ACA61732 Human ERG
19	844.4	26.0	1132	9 ADB66798	ADB66798 Partial c
20	794.4	24.4	3742	3 AAZ93334	Aaz93334 Rat elk1
21	761.2	23.4	3321	7 ACA61736	ACA61736 Human ERG
22	761.2	23.4	5107	3 AAZ50455	Aaz50455 Human pot
23	761.2	23.4	5107	7 ACA61735	ACA61735 Human ERG

24	761.2	23.4	5107	9	ADB66803	ADB66803	cDNA	encod	
25	601	18.5	10579	4	AAX70045	Aak70045	Human	imm	
26	601	18.5	10579	5	ABA20014	Abaz20014	Human	ner	
27	601	18.5	28995	4	AAX70046	Aak70046	Human	imm	
c	28	601	18.5	28995	4	AAX79967	Aak79967	Human	imm
c	29	601	18.5	28995	4	AAX85213	Aak85213	Human	imm
30	601	18.5	28995	5	ABA20015	Abaz20015	Human	ner	
31	572.8	17.6	1626	7	ACA61731	Acac61731	Human	ERG	
32	572.8	17.6	2694	9	ADB66796	Acab66796	Partial c		
33	572.8	17.6	5955	7	ACA61734	Acac61734	Human	ERG	
34	572.8	17.6	5955	9	ADB66802	Acab66802	Human	ERG	
35	572.4	17.6	2694	3	AAX50453	Aaz50453	Human	POT	
36	571.2	17.6	2694	7	ACA61730	Acac61730	Human	ERG	
37	561.2	17.3	20974	5	AAS92595	Acas92595	DNA	encod	
38	384	11.8	464	3	AAX93335	Aaz93335	Rat	elk2	
39	365.6	11.2	2877	8	ADB68013	Adb68013	Human	529	
40	365.6	11.2	3164	7	ABZ58129	Abz58129	Human	POT	
41	365.6	11.2	3164	8	ADB68011	Adb68011	Human	529	
42	364.2	11.2	4112	4	ABL08835	Ab108835	Drosophil		
43	364	11.2	3135	7	ABX12009	Abx12009	Transport		
44	362.4	11.1	2746	6	ABK88234	Abk88234	Human	erg	
45	362.4	11.1	2877	6	AAL44675	Aal44675	Human	tra	

ALIGNMENTS

RESULT 1
ID ADC47039 standard; DNA; 3252 Bp.
XX AC ADC47039;
XX DT 18-DEC-2003 (first entry)
XX DE BECl potassium channel inhibitor encoding DNA #SEQ ID 1.
XX KW BECl potassium channel inhibitor; nontropic; neuroprotective;
KW brain-specific eag-like channel 1; dementia; learning disability;
KW inhibitor; gene; ds.
XX OS Homo sapiens.
XX PH Key Location/Qualifiers
FT CDS 1..3252
FT /tag= a
FT /product= "BECl potassium channel inhibitor"
XX PN WO2003066099-A1.
XX FD 14-AUG-2003.
XX 03-FEB-2003; 2003WO-JP001065.
XX 05-FEB-2002; 2002JP-00028844.
XX (YAMA) YAMANOUCHI PHARM CO LTD.
XX Kubota H, Suzuki T, Miura M, Nakai E, Yaihiro K, Miyake A;
XX Mochizuki S, Nakatou K;
XX WPI; 2003-697418/66.
XX P-PSDB; ADC47040.
XX Antidementia agents comprise new and known brain-specific eag-like
XX channel 1 (BECl) potassium channel inhibitors.
XX Disclosure; Page 75-83; 95pp; Japanese.
XX The invention relates to an antidementia agent that comprises a brain-
XX specific eag-like channel 1 (BECl) potassium channel inhibitor. Agents of
XX the invention are used as BECl potassium channel inhibitors for treating
XX and preventing dementia and learning disabilities. The current sequence

Db 2041 AGCCTTGCGCTGTACCCCGAGTTTGCCCGCGCTTCAGTGTGGCTCCGAGGGGAGCTC 2100
QY 2101 AGCTAACACCTCGGTGCTGGGGAGGCTCTGCAGAGGTGACACACAGCTCCCTGAGCGC 2160
Db 2101 AGCTAACACCTCGGTGCTGGGGAGGCTCTGCAGAGGTGACACACAGCTCCCTGAGCGC 2160
QY 2161 GACAAATACCTTTATGTCCACGCTGGAGGAGAGGAGACAGATGGGAGCAGAGGCCCCACG 2220
Db 2161 GACAAATACCTTTATGTCCACGCTGGAGGAGAGGAGACAGATGGGAGCAGAGGCCCCACG 2220
QY 2221 GTCTCCCGAGCCCGAGCTGATGAGCGCTCCAGCCCTCTGCTGCTGCCCTGGCTGCACTCC 2280
Db 2221 GTCTCCCGAGCCCGAGCTGATGAGCGCTCCAGCCCTCTGCTGCTGCCCTGGCTGCACTCC 2280
QY 2281 TCATCTCAGCTGCCAAGCTGTATCCACGCTCGAACACAGACCCCGGCTCTGTAGT 2340
Db 2281 TCATCTCAGCTGCCAAGCTGTATCCACGCTCGAACACAGACCCCGGCTCTGTAGT 2340
QY 2341 GGCAGAGGAGGCCAGGCGAGGGGCTTTGAAGGCTGAGGCTGGCCCTCTCTCTCC 2400
Db 2341 GGCAGAGGAGGCCAGGCGAGGGGCTTTGAAGGCTGAGGCTGGCCCTCTCTCTCC 2400
QY 2401 CCAGGGCCCTAGAGGGGCTACGGCTGCCCCCATGCCATGGAATGTGCCCCAGATCTG 2460
Db 2401 CCAGGGCCCTAGAGGGGCTACGGCTGCCCCCATGCCATGGAATGTGCCCCAGATCTG 2460
QY 2461 AGCCCCAGGCTAGTAGTGGCATTTGAAGCGCTGTGGCTGGACAGCCCAAGTTCT 2520
Db 2461 AGCCCCAGGCTAGTAGTGGCATTTGAAGCGCTGTGGCTGGACAGCCCAAGTTCT 2520
QY 2521 TTCGCGTGGCCAGTGTGGCCCGGAATGTAGCAGCAGCCCTCCCTGGACCAGAGAGC 2580
Db 2521 TTCGCGTGGCCAGTGTGGCCCGGAATGTAGCAGCAGCCCTCCCTGGACCAGAGAGC 2580
QY 2581 GGCCTGCTCACTGTTCCTCCATGGGCCAGCAGGAGCAAGAACACACACTGAGCAAG 2640
Db 2581 GGCCTGCTCACTGTTCCTCCATGGGCCAGCAGGCAAGAAACACACACTGAGCAAG 2640
QY 2641 CTTGGCAGGGCGGTGACAGAGCTGTGACAGAGGTGTGACAGATGCGGAGAGGAGCTGCAG 2700
Db 2641 CTTGGCAGGGCGGTGACAGAGCTGTGACAGAGGTGTGACAGATGCGGAGAGGAGCTGCAG 2700
QY 2701 TCATTTGCCAGGCTGTGACAGTGTCTCTGGCGCCCAACAGGAGGGTCCGCTGCCCTCG 2760
Db 2701 TCATTTGCCAGGCTGTGACAGTGTCTCTGGCGCCCAACAGGAGGGTCCGCTGCCCTCG 2760
QY 2761 GCATCGGAGAGGGCGCTGCCAGCCAGCAGCTCCGGCTTTCGACGCTCTGTGTGTG 2820
Db 2761 GCATCGGAGAGGGCGCTGCCAGCCAGCAGCTCCGGCTTTCGACGCTCTGTGTGTG 2820
QY 2821 GACACTGGGGATCTCTACTGCTGCAGCCCCCAGCTGGCTCTGTTCAGTGGGACT 2880
Db 2821 GACACTGGGGATCTCTACTGCTGCAGCCCCCAGCTGGCTCTGTTCAGTGGGACT 2880
QY 2881 TGGCCCCACCTCTGTCGGGGCTCTCTCCCTCATGGCACCTGGCCCTGGGGTCCCCCA 2940
Db 2881 TGGCCCCACCTCTGTCGGGGCTCTCTCCCTCATGGCACCTGGCCCTGGGGTCCCCCA 2940
QY 2941 GCGTCTCAGAGCTCCCTGCTGAGCCAGCAGCTTTCGAGCCTCCACTCAGACTCA 3000
Db 2941 GCGTCTCAGAGCTCCCTGCTGAGCCAGCAGCTTTCGAGCCTCCACTCAGACTCA 3000
QY 3001 GAGCCCCCTGCTCAGGAGACCTCTGTCTGAGCCAGCAGCCCTGCTCCCTCCCTCCT 3060
Db 3001 GAGCCCCCTGCTCAGGAGACCTCTGTCTGAGCCAGCAGCCCTGCTCCCTCCCTCCT 3060
QY 3061 TCTGAGGAAGGGGTAGGACTGGGCCCGCAGAGCCTGTGTAGCCAGGCTGAGGCTACCAAGC 3120
Db 3061 TCTGAGGAAGGGGTAGGACTGGGCCCGCAGAGCCTGTGTAGCCAGGCTGAGGCTACCAAGC 3120
QY 3121 ACTGGAGAGCCCCACACAGGCTCAGGGGGCTGTGCTTCCCTGGACCCCCACAGCTG 3180
Db 3121 ACTGGAGAGCCCCACACAGGCTCAGGGGGCTGTGCTTCCCTGGACCCCCACAGCTG 3180

QY 3181 GAGATGGTCTTATTGGCTGCCATGGCTTGCCACAGTCCAGTGGACCCAGGAAGAGC 3240
Db 3181 GAGATGGTCTTATTGGCTGCCATGGCTTGCCACAGTCCAGTGGACCCAGGAAGAGC 3240
QY 3241 ACAGGGGCTCTGA 3252
Db 3241 ACAGGGGCTCTGA 3252

RESULT 2
AAx84910

ID AAx84910 standard; DNA; 3323 BP.

XX AAx84910;

XX 28-SEP-1999 (first entry)

XX Human brain specific potassium channel protein coding sequence.

XX Brain specific potassium channel; human; central nervous system disorder;
dementia; cerebral ischaemic sclerosis; therapy; ss.

XX Homo sapiens.

FH Key Location/Qualifiers

FT CDS 6..3257
FT /*tag= a

XX WO9937677-A1.

XX 29-JUL-1999.

XX 20-JAN-1999; 99WO-JP000190.

XX 23-JAN-1998; 98JP-00011434.

PR 04-DEC-1998; 98JP-00346198.

XX (YAMA) YAMANOUCHI PHARM CO LTD.

XX Miyake A, Mochizuki S, Yokoi H;

XX WPI; 1999-458683/38.

P-PSDB; AAY22426.

PT Potassium channel protein expressed specifically in brain tissue and
method for its production.

PS Claim 6; Page 33-39; 63pp; English.

CC This sequence encodes the potassium channel protein of the invention,
that is expressed specifically in brain tissue. The protein is used to
treat and investigate disorders of the central nervous system such as
dementia and cerebral ischaemic sclerosis

SQ Sequence 3323 BP; 577 A; 1121 C; 1018 G; 607 T; 0 U; 0 Other;

Query Match 100.0%; Score 3252; DB 2; Length 3323;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCGGCGCATGCGGGGCTCTGGCGCTCTGAGACCTCTCTGGACACCATCGCTACG 60

Db 6 ATGCGGCGCATGCGGGGCTCTGGCGCTCTGAGACCTCTCTGGACACCATCGCTACG 65

QY 61 CGCTTCACCGCGCAGCAGTAACTTCGTGCTGGCAACGCCACAGGTGGGGGCTCTTC 120

Db 66 CGCTTCACCGCGCAGCAGTAACTTCGTGCTGGCAACGCCACAGGTGGGGGCTCTTC 125

QY 121 CCCGTGCTTACTGCTCTGATGGCTTCTGTGACCTCAAGGCTTCTCCCGGCTGAGGTC 180

Db 126 CCCGTGCTTACTGCTCTGATGGCTTCTGTGACCTCAAGGCTTCTCCCGGCTGAGGTC 185

QY 181 ATGCAGCGGGGTGTGCTGCTCTTCTTTATGGCCAGACACAGTAGTGAGCTCGTCCGC 240
 Db 186 ATGCAGCGGGGTGTGCTGCTCTTCTTTATGGCCAGACACAGTAGTGAGCTCGTCCGC 245
 QY 241 CAACAGATCCGCAAGGCCCTGACAGAGCAAGAGATTCAAGGCTGAGCTGATCTGTATC 300
 Db 246 CAACAGATCCGCAAGGCCCTGACAGAGCAAGAGATTCAAGGCTGAGCTGATCTGTATC 305
 QY 301 CGGAGAGCGGGCTCCGCTCTGCTGCTCTCTGATGTATACCAATAAGATGAGAAA 360
 Db 306 CGGAGAGCGGGCTCCGCTCTGCTGCTCTCTGATGTATACCAATAAGATGAGAAA 365
 QY 361 GGGGAGGTGGCTCTCTTCTTAGTCTCTCAAGAGACATCAGCGAAACCAAGACCGAGGG 420
 Db 366 GGGGAGGTGGCTCTCTTCTTAGTCTCTCAAGAGACATCAGCGAAACCAAGACCGAGGG 425
 QY 421 GGGCCCGACAGATGGAAGGAGAGACAGGTGTGGCCGGCCGATATGGCCGGGACAGATCC 480
 Db 426 GGGCCCGACAGATGGAAGGAGAGACAGGTGTGGCCGGCCGATATGGCCGGGACAGATCC 485
 QY 481 AAGAGCTTCAATGCAACCGCGCGGAGCGCGCGTGTCTTACCACTGTCTCGGGCAC 540
 Db 486 AAGAGCTTCAATGCAACCGCGCGGAGCGCGCGTGTCTTACCACTGTCTCGGGCAC 545
 QY 541 CTGCAGAGCAGCCCAAGGGCAAGCAAGCTCAATAAGGGGGTGTGTTGGGGAAGAACCA 600
 Db 546 CTGCAGAGCAGCCCAAGGGCAAGCAAGCTCAATAAGGGGGTGTGTTGGGGAAGAACCA 605
 QY 601 AACTTGGCTGAGTACAAAGTAGCGGCATCGGGAAGTCGCCCTTATCTCTGTGCACTGT 660
 Db 606 AACTTGGCTGAGTACAAAGTAGCGGCATCGGGAAGTCGCCCTTATCTCTGTGCACTGT 665
 QY 661 GGGGCACTGAGAGCACCTGGATGGCTTCACTCTGCTCGCCACACTCTATGTGGCTGTC 720
 Db 666 GGGGCACTGAGAGCACCTGGATGGCTTCACTCTGCTCGCCACACTCTATGTGGCTGTC 725
 QY 721 ACTGTGCCCTACAGCGTGTGTGAGACAGCAGCGAGGCCAGTGGCCCGCGGGCCCG 780
 Db 726 ACTGTGCCCTACAGCGTGTGTGAGACAGCAGCGAGGCCAGTGGCCCGCGGGCCCG 785
 QY 781 CCAGCGTCTGTGACCTGGCGGTGGAGGTCTCTTCACTCTGACATGTGCTGAATTC 840
 Db 786 CCAGCGTCTGTGACCTGGCGGTGGAGGTCTCTTCACTCTGACATGTGCTGAATTC 845
 QY 841 CGTACACATTCGTGTCTCAAGTCCGGCCAGGTGTGTTGCCCCAAAGTCAATTTGCCCTC 900
 Db 846 CGTACACATTCGTGTCTCAAGTCCGGCCAGGTGTGTTGCCCCAAAGTCAATTTGCCCTC 905
 QY 901 CACTACGTCAACCTGCTGCTGATGTGATGATGATGATGATGATGATGATGATGATGATG 960
 Db 906 CACTACGTCAACCTGCTGCTGATGTGATGATGATGATGATGATGATGATGATGATGATG 965
 QY 961 CATGCCCTCAAGTCAAGTGTATCTTGGGGCCATCTGCTGAGACGCTGCGCTGCTG 1020
 Db 966 CATGCCCTCAAGTCAAGTGTATCTTGGGGCCATCTGCTGAGACGCTGCGCTGCTG 1025
 QY 1021 CGCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
 Db 1026 CGCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1085
 QY 1081 ACATGCTCATGCGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
 Db 1086 ACATGCTCATGCGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1145
 QY 1141 ATTGGCCAGCGGAGATCGAGAGCAGCAATCCGAGCTGCTGAGATTTGGCTGCTGCTGAG 1200
 Db 1146 ATTGGCCAGCGGAGATCGAGAGCAGCAATCCGAGCTGCTGAGATTTGGCTGCTGCTGAG 1205
 QY 1201 GAGCTGGCCCGCCGACTGGAGACTCCCTACTACTGCTGGGCGGAGGCCAGCTGGAGGG 1260
 Db 1206 GAGCTGGCCCGCCGACTGGAGACTCCCTACTACTGCTGGGCGGAGGCCAGCTGGAGGG 1265
 QY 1261 AACAGCTCGGCCAGAGTGACAACTGACAGCAGCAGCAGGAGGCCAACCGGACGGGGCTG 1320

Db 1266 AACAGCTCGGCCAGAGTGACAACTGACAGCAGCAGCAGGAGCCAAACGGGACGGGGCTG 1325
 QY 1321 GAGCTGCTGGGGGGCCGCTGCTGCTGCGAGCGCCTACATCACTTCTCTTCTTCTGCACTC 1380
 Db 1326 GAGCTGCTGGGGGGCCGCTGCTGCGAGCGCCTACATCACTTCTCTTCTTCTGCACTC 1385
 QY 1381 AGCAGCTCACAGCGTGGCTTGGCAACAGTGTGCGCAACACACGAGACACCGAGAATC 1440
 Db 1386 AGCAGCTCACAGCGTGGCTTGGCAACAGTGTGCGCAACACACGAGACACCGAGAATC 1445
 QY 1441 TTCTCCATCTGACCATGCTCATCGCGCCCTGATGACAGCGTGTGTTTGGGAACGTG 1500
 Db 1446 TTCTCCATCTGACCATGCTCATCGCGCCCTGATGACAGCGTGTGTTTGGGAACGTG 1505
 QY 1501 ACGGCCCATCATCAGCGCATGTACGCCCGCGCTTCTGTACACAGCGCACCGCGCAC 1560
 Db 1506 ACGGCCCATCATCAGCGCATGTACGCCCGCGCTTCTGTACACAGCGCACCGCGCAC 1565
 QY 1561 CTGCGGCACTACATCCGATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGCTGGAG 1620
 Db 1566 CTGCGGCACTACATCCGATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGCTGGAG 1625
 QY 1621 TACTTCCNGCCACCTGGGGGTGAACAATGGCATCGACACACCGAGCTGTGCGAGGC 1680
 Db 1626 TACTTCCAGGCCACCTGGGGGTGAACAATGGCATCGACACACCGAGCTGTGCGAGGC 1685
 QY 1681 CTCCTTGACGAGTGGCGCAGACATCGCCATGCATCTGCAAGAGAGTCTTGCAGCTG 1740
 Db 1686 CTCCTTGACGAGTGGCGCAGACATCGCCATGCATCTGCAAGAGAGTCTTGCAGCTG 1745
 QY 1741 CCACTGTTTGAAGCGGCGAGCGGCTGCTGCGGGCACTGTCTTGGGCCCTGCGGCC 1800
 Db 1746 CCACTGTTTGAAGCGGCGAGCGGCTGCTGCGGGCACTGTCTTGGGCCCTGCGGCC 1805
 QY 1801 GCCTTGTGACGCGCGGCGAGTACTCATCCACCAAGCGCATGCCCTGCAAGGCCCTCTAC 1860
 Db 1806 GCCTTGTGACGCGCGGCGAGTACTCATCCACCAAGCGCATGCCCTGCAAGGCCCTCTAC 1865
 QY 1861 TTTGTCTGCTCTGCTCTCATGAGAGTGTCAAAGGTGGCAACCGTGTCTGCGCATCTTAGG 1920
 Db 1866 TTTGTCTGCTCTGCTCTCATGAGAGTGTCAAAGGTGGCAACCGTGTCTGCGCATCTTAGG 1925
 QY 1921 AAGGGCACTGATCGCTGAGTGTGCGCGGCGGAGCAGGTGTAAAGGCCAAGTCC 1980
 Db 1926 AAGGGCACTGATCGCTGAGTGTGCGCGGCGGAGCAGGTGTAAAGGCCAAGTCC 1985
 QY 1981 GAGGTGAAGGCGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
 Db 1986 GAGGTGAAGGCGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2045
 QY 2041 AGCCTTGGCTGTACCCCGAGTTTGGCCCGCTTCAAGTGTGCTGCTGCTGCTGCTGCTGCTG 2100
 Db 2046 AGCCTTGGCTGTACCCCGAGTTTGGCCCGCTTCAAGTGTGCTGCTGCTGCTGCTGCTGCTG 2105
 QY 2101 AGCTACAACTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160
 Db 2106 AGCTACAACTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2165
 QY 2161 GACAAATACCTTATGTCTCCAGCTGAGAGAGAGAGACAGATGGGAGAGAGAGAGAGAG 2220
 Db 2166 GACAAATACCTTATGTCTCCAGCTGAGAGAGAGAGAGACAGATGGGAGAGAGAGAGAG 2225
 QY 2221 GTCTCCCCAGCCAGCTGATGAGCCCTTCAAGCCCTTGTGCTGCTGCTGCTGCTGCTGCTG 2280
 Db 2226 GTCTCCCCAGCCAGCTGATGAGCCCTTCAAGCCCTTGTGCTGCTGCTGCTGCTGCTGCTG 2285
 QY 2281 TCATCTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2340
 Db 2286 TCATCTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2345
 QY 2341 GGCAGAGGAGCGCAGGCGAGGGGCTTTTGAAGGCTGAGGCTGGGCGCTTCTGCTGCC 2400

Db 2346 GGCAGAGGAGGCGCAGGCGAGGCGGCTTTGAAGCTGAGGCTGGCCCTCTGTCTCCC 2405
Qy 2401 CCACGGGCGCTAGAGGGGCTACGGCTGCCCCCCTCCATGCAATGAGTGGCCCGCAGACTG 2460
Db 2406 CCACGGGCGCTAGAGGGGCTACGGCTGCCCCCCTCCATGCAATGAGTGGCCCGCAGACTG 2465
Qy 2461 AGCCCGAGGCTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2520
Db 2466 AGCCCGAGGCTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2525
Qy 2521 TTCCGGTGGGCGCAGTCTGCGCCCGGATGTAGCAGCAGGCGCCCTCCCTGACACAGAGC 2580
Db 2526 TTCCGGTGGGCGCAGTCTGCGCCCGGATGTAGCAGCAGGCGCCCTCCCTGACACAGAGC 2585
Qy 2581 GGCTGCTCACTGTTCCCATGGGCCCGCAGCGGCAAGGAAACACAGACACACTGGACAAG 2640
Db 2586 GGCTGCTCACTGTTCCCATGGGCCCGCAGCGGCAAGGAAACACAGACACACTGGACAAG 2645
Qy 2641 CTTCCGACGGCTGACAGAGCTGTGAGAGAGGCTGTCAGATGCGGGAAGGACTGCAG 2700
Db 2646 CTTCCGACGGCTGACAGAGCTGTGAGAGAGGCTGTCAGATGCGGGAAGGACTGCAG 2705
Qy 2701 TCACCTTCGCGAGGCTGTGAGAGCTGTGAGAGAGGCTGTCAGATGCGGGAAGGACTGCAG 2760
Db 2706 TCACCTTCGCGAGGCTGTGAGAGCTGTGAGAGAGGCTGTCAGATGCGGGAAGGACTGCAG 2765
Qy 2761 GCATCGGAGAGGGGCGCTGCCAGCAGCAGCCTCCCGGCTCTGAGAGCTCTGTGTGTG 2820
Db 2766 GCATCGGAGAGGGGCGCTGCCAGCAGCAGCCTCCCGGCTCTGAGAGCTCTGTGTGTG 2825
Qy 2821 GACACTGGGCGATCTCTCTGCTGCTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2880
Db 2826 GACACTGGGCGATCTCTCTGCTGCTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2885
Qy 2881 TGGCCCGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2940
Db 2886 TGGCCCGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2945
Qy 2941 GGTCTCAGAGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3000
Db 2946 GGTCTCAGAGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3005
Qy 3001 GAGCCCGCTGCTGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3060
Db 3006 GAGCCCGCTGCTGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3065
Qy 3061 TCTGAGGAAGGGCTAGGACTGGGCGCGCAGAGCCTGTGAGCCAGCAGCCCTGCTGCTGCTG 3120
Db 3066 TCTGAGGAAGGGCTAGGACTGGGCGCGCAGAGCCTGTGAGCCAGCAGCCCTGCTGCTGCTG 3125
Qy 3121 ACTGAGAGCCCGCAGAGGCTGAGGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3180
Db 3126 ACTGAGAGCCCGCAGAGGCTGAGGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3185
Qy 3181 GAGATGGTCTATTTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3240
Db 3186 GAGATGGTCTATTTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3245
Qy 3241 ACAGGGGTCTGA 3252
Db 3246 ACAGGGGTCTGA 3257

RESULT 3
AAZ87712
ID AAZ87712 standard; DNA; 3829 BP.
XX
AC AAZ87712;
XX
DT 19-MAY-2000 (first entry)
XX
DE Human ESK1 (hESK1) protein encoding DNA.
XX

ESK1: eag similar K⁺ channel; potassium channel associated disorder; neurological; Alzheimer's disease; anxiety; panic; autism; hyperactivity; obsessive-compulsive disorder; schizophrenia; Huntington's disease; epilepsy; cardiovascular; musculoskeletal; proliferative; cancer; ESK channel blocker; nootropic; neuroprotective; antidepressant; tranquilizer; neuroleptic; antiparkinsonian; cardiac; cytostatic; anticonvulsant; ds.

Homo sapiens.

Key Location/Qualifiers
CDS 254..3496
/*tag= a
/product= "ESK1 protein"

W0200009534-A1.

24-FEB-2000.

13-AUG-1999; 99WO-US018556.

14-AUG-1998; 98US-0096570P.

(ELAN-) ELAN PHARM INC.

Forsayeth JR, Zhao BB;

WPI; 2000-224270/19.

P-PSDB; AAY77738.

Novel eag similar potassium channel polypeptide useful for treating various neurological, cardiovascular, musculoskeletal and proliferative disorders.

Claim 8; Fig 1A-E; 52pp; English.

This DNA encodes a eag similar K⁺ channel (ESK) polypeptide (hESK1). The hESK1 protein can be expressed by standard recombinant methodology. The ESK polypeptide, polynucleotides and antibodies are useful for treating and diagnosing various potassium channel associated disorders such as neurological disorders, e.g. Alzheimer's disease, depression, anxiety, panic, obsessive-compulsive disorders, attention deficit, epilepsy; hyperactivity disorders, autism, schizophrenia, Huntington's disease and Parkinson's disease, cardiovascular disorders, musculoskeletal disorders and proliferative disorders such as cancer. The ESK polynucleotide is also useful for synthesis of ESK and gene mapping. The polypeptide can be used in an assay to identify molecules such as synthetic drugs, antibodies, peptides or other molecules which have an effect on the activity of the ESK channel

Sequence 3829 BP; 650 A; 1302 C; 1202 G; 675 T; 0 U; 0 Other;

Query Match 100.0%; Score 3250.4; DB 3; Length 3829;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3251; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGCCGCGCATGCGGGCGCTCTGGCGCCTCAGAACACCTTCTCTGACACCATCGCTACG 60
Db 245 ATGCCGCGCATGCGGGCGCTCTGGCGCCTCAGAACACCTTCTCTGACACCATCGCTACG 304
Qy 61 CGCTTCACCGCAGCAGCAGTAACTTCTGCTGGGCAACGCCAGGTGGCGGGCTCTTC 120
Db 305 CGCTTCACCGCAGCAGCAGTAACTTCTGCTGGGCAACGCCAGGTGGCGGGCTCTTC 364
Qy 121 CCGTGTGCTACTGCTCTGATGGCTTCTGTGACCTACCGGCTTCTCCCGGCTGAGGTC 180
Db 365 CCGTGTGCTACTGCTCTGATGGCTTCTGTGACCTACCGGCTTCTCCCGGCTGAGGTC 424
Qy 181 ATGACGCGGGCTGTGCTGCTCTCTTATGGGCGACACACAGTGTGCTGCTCCG 240
Db 425 ATGACGCGGGCTGTGCTGCTCTCTTATGGGCGACACACAGTGTGCTGCTCCG 484
Qy 241 CAACAGATCGCAAGGCCCTGGAGGACCAAGGATTTCAAGGTGAGTGTGCTGTATC 300

Db	485	CAACAGATCCGAAAGCCCTGGACGAGCAACAGGATTCAGGCTGAGTCTCTGTAC	544	1565	GAGCTGTGGGGCGCCGCTGCTGGCAGCGCTACATCACCTCCCTCTACTTCGCACCTC	1624
Qy	301	CGGAAGAGCGGGCTCCCGTTCTTGGTGTCTCTGGATGTATACCCATTAAGAAATGAGAAA	360	1381	AGCAGCCTCACAGCGTGGGCTTCGGCAACAGTGTCCGCAACACGAGACACCGAAGATC	1440
Db	545	CGGAAGAGCGGGCTCCCGTTCTTGGTGTCTCTGGATGTATACCCATTAAGAAATGAGAAA	604	1625	AGCAGCCTCACAGCGTGGGCTTCGGCAACAGTGTCCGCAACACGAGACACCGAAGATC	1684
Qy	361	GGGGAGGTGGCTCTCTCTAGTCTCTCAAGGACATCAGCGAAACCAAGAACCCAGAGG	420	1441	TTCTCCATCTGACCAATGCTCATCGGCGCCCTGATGCAACGCGTGTGTGTTGGAACTG	1500
Db	605	GGGGAGGTGGCTCTCTCTAGTCTCTCAAGGACATCAGCGAAACCAAGAACCCAGAGG	664	1685	TTCTCCATCTGACCAATGCTCATCGGCGCCCTGATGCAACGCGTGTGTGTTGGAACTG	1744
Qy	421	GGCCCCGACAGATGGAAGAGACAGTGTGGCGCGCGATATGGCGGGGACGATCC	480	1501	AGGGCCATCATCAGCGCATGTACGCGCGCGCTTCTGTACCAACGCGCACCGCGAC	1560
Db	665	GGCCCCGACAGATGGAAGAGACAGTGTGGCGCGCGATATGGCGGGGACGATCC	724	1745	AGGGCCATCATCAGCGCATGTACGCGCGCGCTTCTGTACCAACGCGCACCGCGAC	1804
Qy	481	AAAGGCTTCAATGCCAAACCGCGCGGAGCGCGCGGTGTCTTACACCTGTCCGGGCAC	540	1561	CTGCGGACTACATCCGCAATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGCTGGAG	1620
Db	725	AAAGGCTTCAATGCCAAACCGCGCGGAGCGCGCGGTGTCTTACACCTGTCCGGGCAC	784	1805	CTGCGGACTACATCCGCAATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGCTGGAG	1864
Qy	541	CTCGAAGCAGCGCCAAAGGCAAGCAAGCTCAATAAGGGGTGTTTGGGAGAAACCA	600	1621	TACTTCCAGGCCACCTGGGGGTGAACATGGCATCGACACCAACCGAGCTGTGCAAGC	1680
Db	785	CTCGAAGCAGCGCCAAAGGCAAGCAAGCTCAATAAGGGGTGTTTGGGAGAAACCA	844	1865	TACTTCCAGGCCACCTGGGGGTGAACATGGCATCGACACCAACCGAGCTGTGCAAGC	1924
Qy	601	AACCTGCTCAGTACAAAGTAGCGCCATCCGGAAGTGCCTTCATCTGTTGCACTGT	660	1681	CTCCCTGACAGCTGCGCGCAGACATCGCCATGCACTGCAACAGGAGTCTCTGAGCTG	1740
Db	845	AACCTGCTCAGTACAAAGTAGCGCCATCCGGAAGTGCCTTCATCTGTTGCACTGT	904	1925	CTCCCTGACAGCTGCGCGCAGACATCGCCATGCACTGCAACAGGAGTCTCTGAGCTG	1984
Qy	661	GGGGCACTGAGAGCACCTGGATGGTTCATCTGCTCGGCACACTCTATGGGCTGTC	720	1741	CCACTGTTTGGAGCGCGCAGCGCGCTGCTGGGGCACTGTCTCTGCGCCCTGCGGCC	1800
Db	905	GGGGCACTGAGAGCACCTGGATGGTTCATCTGCTCGGCACACTCTATGGGCTGTC	964	1985	CCACTGTTTGGAGCGCGCAGCGCGCTGCTGGGGCACTGTCTCTGCGCCCTGCGGCC	2044
Qy	721	ACTGTGCCCTACAGCGTGTGTGAGCAGACAGGAGCCAGTGGCGCGCGCGCGCG	780	1801	GCCTTCTGACGCGCGGCGAGTACCTCATCCCAAGCGCATGCCCTGCAAGGCCCTCTAC	1860
Db	965	ACTGTGCCCTACAGCGTGTGTGAGCAGACAGGAGCCAGTGGCGCGCGCGCGCG	1024	2045	GCCTTCTGACGCGCGGCGAGTACCTCATCCCAAGCGCATGCCCTGCAAGGCCCTCTAC	2104
Qy	781	CCAGCGCTCTGACCTGGCGGTGGAGTCTCTTTCATCTCTGATGCTGCAATTC	840	1861	TTTGTCTGCTCTGCTCCATGGAGTCTCAAGGGTGGCCACCTGCTCGCCATCTAGGG	1920
Db	1025	CCAGCGCTCTGACCTGGCGGTGGAGTCTCTTTCATCTCTGATGCTGCAATTC	1084	2105	TTTGTCTGCTCTGCTCCATGGAGTCTCAAGGGTGGCCACCTGCTCGCCATCTAGGG	2164
Qy	841	CGTACCAATTCGTGTCAAGTGGGCGCAGTGGTGTGGTGGTGGTGGTGGTGGTGG	900	1921	AAGGGCACTGATGCTGCTGAGTGTGCTGCGCGCGGAGAGTGTAAAGGCCAATGCC	1980
Db	1085	CGTACCAATTCGTGTCAAGTGGGCGCAGTGGTGTGGTGGTGGTGGTGGTGGTGG	1144	2165	AAGGGCACTGATGCTGCTGAGTGTGCTGCGCGCGGAGAGTGTAAAGGCCAATGCC	2224
Qy	901	CACCTAGTCAACCTGCTTCTGCTGATGTCATCGCAGCGCTGCCCTTGGCTGCTA	960	1981	GACGTGAAGGGCTGAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2040
Db	1145	CACCTAGTCAACCTGCTTCTGCTGATGTCATCGCAGCGCTGCCCTTGGCTGCTA	1204	2225	GACGTGAAGGGCTGAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2284
Qy	961	CATGCTTCAAGGTCAACGTGTACTTTGGGGGCCATCTGCTGAAGACGGTGGCTGCTG	1020	2041	AGCCTTGGCTGTATACCCCGAGTTTGGCGCGCTTCACTGCTGCTGCTGCTGCTGCTG	2100
Db	1205	CATGCTTCAAGGTCAACGTGTACTTTGGGGGCCATCTGCTGAAGACGGTGGCTGCTG	1264	2285	AGCCTTGGCTGTATACCCCGAGTTTGGCGCGCTTCACTGCTGCTGCTGCTGCTGCTG	2344
Qy	1021	CGCTGTGCGCTGCTTCCGCGGTGACCGGTACTCGAGTACAGCGCGTGGTGGTGG	1080	2101	AGCTACAACTGGGTGTGCGGGGAGGCTCTGAGAGTGGACACCGCTGCTGAGCGGC	2160
Db	1265	CGCTGTGCGCTGCTTCCGCGGTGACCGGTACTCGAGTACAGCGCGTGGTGGTGG	1324	2345	AGCTACAACTGGGTGTGCGGGGAGGCTCTGAGAGTGGACACCGCTGCTGAGCGGC	2404
Qy	1081	ACACTGCTCATGGCGGTGTTCCCTGCTGCGGCACTGGGTGCTGCTGCTGCTGCTTAC	1140	2161	GACAAATACCTTATGTCCACCGTGGAGAGAGAGACAGATGGGGAGCAGGGCCCCACG	2220
Db	1325	ACACTGCTCATGGCGGTGTTCCCTGCTGCGGCACTGGGTGCTGCTGCTGCTGCTTAC	1384	2405	GACAAATACCTTATGTCCACCGTGGAGAGAGAGACAGATGGGGAGCAGGGCCCCACG	2464
Qy	1141	ATTGGCCAGCGGAGATCGAGAGCAGCAATCCGAGTGCCTGAGATTGGCTGGCTGGAG	1200	2221	GTCTCCCGAGCGCCAGCTGATGAGCCCTCCAGCCCGCTGCTGCTGCTGCTGCTGCTG	2280
Db	1385	ATTGGCCAGCGGAGATCGAGAGCAGCAATCCGAGTGCCTGAGATTGGCTGGCTGGAG	1444	2465	GTCTCCCGAGCGCCAGCTGATGAGCCCTCCAGCCCGCTGCTGCTGCTGCTGCTGCTG	2524
Qy	1201	GAGCTGGCGCGGCTGAGACTCCCTACTACTGCTGGCGCGGAGCCAGCTGAGGG	1260	2281	TCATCTCAGCTGCGCAAGCTGTATCCCACTGCGAAGCAGCAGCCCGGCTGCTTAGGT	2340
Db	1445	GAGCTGGCGCGGCTGAGACTCCCTACTACTGCTGGCGCGGAGCCAGCTGAGGG	1504	2525	TCATCTCAGCTGCGCAAGCTGTATCCCACTGCGAAGCAGCAGCCCGGCTGCTTAGGT	2584
Qy	1261	AAAGCTCCGCGCAGAGTGAACACTGACAGCAGCAGCAGCAGCAGCAGCAGCAGC	1320	2341	GGCAGAGGAGGCGCAGGCGAGGCGGCTTGAAGGCTGAGGCTGAGGCTGCTGCTGCTG	2400
Db	1505	AAAGCTCCGCGCAGAGTGAACACTGACAGCAGCAGCAGCAGCAGCAGCAGCAGC	1564	2585	GGCAGAGGAGGCGCAGGCGAGGCGGCTTGAAGGCTGAGGCTGAGGCTGCTGCTGCTG	2644
Qy	1321	GAGCTGCTGGCGCGCGCTGCTGCGCAGCGCTTACATCTCTCTCTCTCTCTCTCTCT	1380	2401	CCACGGCGCCTTAGAGGGGCTACGGCTGCGCCCGCTGCGCTGCGCTGCGCTGCGCTG	2460
				2645	CCACGGCGCCTTAGAGGGGCTACGGCTGCGCCCGCTGCGCTGCGCTGCGCTGCGCTG	2704

QY 2461 AGCCCGAGGCTAGTAGATGGATTGAAGCGGTGGCTCGAACAGCCCAAGTTCTCT 2520
Db |||||
QY 2705 AGCCCGAGGCTAGTAGATGGATTGAAGCGGTGGCTCGAACAGCCCAAGTTCTCT 2764
Db |||||
QY 2521 TTCGGCGTGGCGAGCTCTGGCCGGAATAGCAGCAGCCCTCCCTCGACACAGAGC 2580
Db |||||
QY 2765 TTCGGCGTGGCGAGCTCTGGCCGGAATAGCAGCAGCCCTCCCTCGACACAGAGC 2824
Db |||||
QY 2581 GGCCTGCTCACTGTTCCCATGGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2640
Db |||||
QY 2825 GGCCTGCTCACTGTTCCCATGGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2884
Db |||||
QY 2641 CTTGCGCAGGCGGTGACAGAGCTGTGACAGAGGCTGTGACAGATGGCGAAGGACTGCGAG 2700
Db |||||
QY 2885 CTTGCGCAGGCGGTGACAGAGCTGTGACAGAGGCTGTGACAGATGGCGAAGGACTGCGAG 2944
Db |||||
QY 2701 TCACCTGCGCAGGCTGTGAGCTTGTCTGCGGCCCGCCACACAGGAGGAGGTCGCTCGCTCGG 2760
Db |||||
QY 2945 TCACCTGCGCAGGCTGTGAGCTTGTCTGCGGCCCGCCACACAGGAGGAGGTCGCTCGCTCGG 3004
Db |||||
QY 2761 GCATCGGAGAGGAGGCGGCGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2820
Db |||||
QY 3005 GCATCGGAGAGGAGGCGGCGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 3064
Db |||||
QY 2821 GACACTGGGGCATCTCTCTACTGCTGACAGCCCGCCAGCTGGCTCTGTCTTGAAGTGGGACT 2880
Db |||||
QY 3065 GACACTGGGGCATCTCTCTACTGCTGACAGCCCGCCAGCTGGCTCTGTCTTGAAGTGGGACT 3124
Db |||||
QY 2891 TGGCCCGCACCCTGCTGCTGGGGGCTCTCTCTGATGCAACCTGCGCTGGGGTCCCCCA 2940
Db |||||
QY 3125 TGGCCCGCACCCTGCTGCTGGGGGCTCTCTCTGATGCAACCTGCGCTGGGGTCCCCCA 3184
Db |||||
QY 2941 GCGTCTCAGAGCTCCCTCGCTCGAGCCAGCAGCTTCTGACCTTCCACCTCAGACTCA 3000
Db |||||
QY 3185 GCGTCTCAGAGCTCCCTCGCTCGAGCCAGCAGCTTCTGACCTTCCACCTCAGACTCA 3244
Db |||||
QY 3001 GAGCCCTGCTCAGGAGACCTCTGCTGAGCCCGCCAGCAGCTGTGAGCAGGCTGAGGCTACCA 3120
Db |||||
QY 3245 GAGCCCTGCTCAGGAGACCTCTGCTGAGCCCGCCAGCAGCTGTGAGCAGGCTGAGGCTACCA 3304
Db |||||
QY 3061 TCTGAGGAGGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3200
Db |||||
QY 3305 TCTGAGGAGGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3364
Db |||||
QY 3121 ACTGAGAGCCCGCCAGGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3180
Db |||||
QY 3365 ACTGAGAGCCCGCCAGGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3424
Db |||||
QY 3181 GAGATGCTGCTTATTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3240
Db |||||
QY 3425 GAGATGCTGCTTATTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3484
Db |||||
QY 3241 ACAGGGGCTGCA 3252
Db |||||
QY 3485 ACAGGGGCTGCA 3496
Db |||||

RESULT 4

AAZ50119
ID AAZ50119 standard; cDNA; 3249 BP.
XX AC AAZ50119;
XX AC AAZ50119;

04-MAY-2000 (first entry)

Human Elk voltage gated potassium channel monomer encoding cDNA.

Voltage gated potassium channel subunit; VGPs; elk; human; stroke;
Kv superfamily; Bag family; ether a go-go; Elk subfamily; modulator;
chromosome 12q13; resting potential; cell excitability; seizure; CNS;
migraine; psychotic; anticonvulsant; ion flux disorder; detection;
gene therapy; antimigraine; cerebroprotective; neuroprotective;

KW antipsychotic; ss.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT mat_peptide 1..3249
FT /tag= a
FT /product= "Human Elk polypeptide"
FT /note= "Alpha subunit of voltage gated potassium channel
monomer"
FT /transl_except= (pos:2893..2895, aa:Ala)
XX
PN W0200001819-A1.
XX
XX 13-JAN-2000.
PD
XX
PF 30-JUN-1999; 99WO-US014944.
XX
PR 01-JUL-1998; 98US-0091469P.
PR 21-JAN-1999; 99US-0116621P.
XX
XX (ICAG-) ICAGEN INC.
XX
XX Jegla TJ, Wickenden A;
XX
XX WPI: 2000-182114/16.
DR P-PSDB; AAY44778.
XX
PT Novel polynucleotides and polypeptides of human ELK, a voltage-gated
potassium channel subunit useful for treating ELK miss-expression and to
screen for inhibitors and activators of such channels.
XX
XX
PS Claim 4; Page 62-64; 79pp; English.

The present sequence is the cDNA encoding human ELK (hElk) polypeptide
monomer, comprising an alpha subunit of the voltage-gated potassium
channel (VGPs). It is a member of the Kv (Voltage gated potassium)
superfamily, Bag (ether a go-go) family and Elk subfamily of potassium
channel monomers. hElk gene is mapped to chromosome 12q13. It is isolated
from brain and maintains the resting potential and controls excitability
of the cell. It has antimigraine, cerebroprotective, antipsychotic, can be
used to screen for modulators of VGPs, that are useful for treating
abnormal ion flux disorders, CNS disorders such as migraines, hearing and
vision problems, seizures, psychotic disorders and to prevent strokes. It
can be used as a marker for diagnosis of diseases linked to this gene and
also as reporter molecule in detection systems. The polynucleotide is
useful for gene therapy, to rectify ELK expression

Sequence 3249 BP; 562 A; 1097 C; 1000 G; 590 T; 0 U; 0 Other;
Query Match 99.8%; Score 3245.8; DB 3; Length 3249;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3247; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGCGCGCATGCGGGGCTCTCTGGCGCTCAGAACCTTCTTGGACACCATCGCTACG 60
Db |||||
QY 1 ATGCGCGCATGCGGGGCTCTCTGGCGCTCAGAACCTTCTTGGACACCATCGCTACG 60
Db |||||
QY 61 CGCTTCGACGGCAGCAGTAACTTGTGTGTGGCAACGCCAGGTGGCGGGCTCTTC 120
Db |||||
QY 61 CGCTTCGACGGCAGCAGTAACTTGTGTGTGGCAACGCCAGGTGGCGGGCTCTTC 120
Db |||||
QY 121 CCCGTGTTACTCTCTCTGTGGCTTCTGTGACCTCAGCGGCTTCTCCCGGGCTGAGTC 180
Db |||||
QY 181 ATGCGCGGGCTGTGCTGCTCTCTCTTATATGGCCAGACACAGTGTGCTGCTGCTG 240
Db |||||
QY 181 ATGCGCGGGCTGTGCTGCTCTCTCTTATATGGCCAGACACAGTGTGCTGCTGCTG 240
Db |||||
QY 241 CAACAGATCCGACGAGGCTTGGAGGAGCAAGAGGTTCAAGCTGAGCTGATCTGCTGATC 300
Db |||||

Db 241 CAACAGATCCGCAAGGCCCTTGACGAGCACAAGGAGTTCAAGGCTGAGCTGATCCTGTAT 300
 Qy 301 CGGAAGAGGGGCTCCGCTTCTGCTGCTCTGATGTGATACCCATAAAGATGAGAAA 360
 Db 301 CGGAAGAGGGGCTCCGCTTCTGCTGCTCTGATGTGATACCCATAAAGATGAGAAA 360
 Qy 361 GGGAGGTGGCTCTCTTCTTAGTCTCTCAAGAGACATCAGCGAAACCAAGAACCGAGGG 420
 Db 361 GGGAGGTGGCTCTCTTCTTAGTCTCTCAAGAGACATCAGCGAAACCAAGAACCGAGGG 420
 Qy 421 GGGCCGACAGATGGAAGAGACAGAGTGGTGGCGGCGCGATATGGCGGGCAGCATCC 480
 Db 421 GGGCCGACAGATGGAAGAGACAGAGTGGTGGCGGCGCGATATGGCGGGCAGCATCC 480
 Qy 481 AAAGGCTTCAATGCCAAACCGGCGGAGCGGGCGGCTGCTTACACACCTGTCCGGGCAC 540
 Db 481 AAAGGCTTCAATGCCAAACCGGCGGAGCGGGCGGCTGCTTACACACCTGTCCGGGCAC 540
 Qy 541 CTGCAAGAGCAGCCCAAGGGCAAGCAAGCTCAATAAGGGGTGTTTGGGGAGAAACCA 600
 Db 541 CTGCAAGAGCAGCCCAAGGGCAAGCAAGCTCAATAAGGGGTGTTTGGGGAGAAACCA 600
 Qy 601 AACTTGCCTAGTACAAAGTAGCGGCATCGGAGTCCGCTTCACTCTGTTGCACTGT 660
 Db 601 AACTTGCCTAGTACAAAGTAGCGGCATCGGAGTCCGCTTCACTCTGTTGCACTGT 660
 Qy 661 GGGGCACTGAGAGCCACTGGGATGGCTTCACTCTGCTCGCCACACTCTATGTGGCTGTC 720
 Db 661 GGGGCACTGAGAGCCACTGGGATGGCTTCACTCTGCTCGCCACACTCTATGTGGCTGTC 720
 Qy 721 ACTGTGCCCTPACAGCGTGTGTGAGCAGCAGCGGAGCCAGTGCAGCGCGGCGGCGCG 780
 Db 721 ACTGTGCCCTPACAGCGTGTGTGAGCAGCAGCGGAGCCAGTGCAGCGCGGCGGCGCG 780
 Qy 781 CCCAGGCTCTGACCTGGGCGTGGAGGTCTTTCATCTTGTGATGTTGCTGAAATTC 840
 Db 781 CCCAGGCTCTGACCTGGGCGTGGAGGTCTTTCATCTTGTGATGTTGCTGAAATTC 840
 Qy 841 CGTACCACTTCGTGTCAAAGTGGGCGAGTGGTGTGTTGCCCAAGTCCATTGCTC 900
 Db 841 CGTACCACTTCGTGTCAAAGTGGGCGAGTGGTGTGTTGCCCAAGTCCATTGCTC 900
 Qy 901 CACTACGTACCACTGCTTCTGCTGATGTATCGAGCGTGCCTTTGACTGCTA 960
 Db 901 CACTACGTACCACTGCTTCTGCTGATGTATCGAGCGTGCCTTTGACTGCTA 960
 Qy 961 CATGCTTCAAGTCAAGTGTACTTGGGGCCCATCTGTGAGAGCGTGGCGCTGCTG 1020
 Db 961 CATGCTTCAAGTCAAGTGTACTTGGGGCCCATCTGTGAGAGCGTGGCGCTGCTG 1020
 Qy 1021 CGCCTGCTGGCCTGCTTCCGCGCTGGACCGGTACTCGCAGTACAGCGCGTGGTGTG 1080
 Db 1021 CGCCTGCTGGCCTGCTTCCGCGCTGGACCGGTACTCGCAGTACAGCGCGTGGTGTG 1080
 Qy 1081 ACATGCTCATGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1140
 Db 1081 ACATGCTCATGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1140
 Qy 1141 ATTGGCCAGCGGAGATCGAGCAGCGAATCCGAGCTGCTGAGATTGGCTGGCTGCAG 1200
 Db 1141 ATTGGCCAGCGGAGATCGAGCAGCGAATCCGAGCTGCTGAGATTGGCTGGCTGCAG 1200
 Qy 1201 GAGCTGGCCCGGAGTGGAGTCCCTTACTTACTTGGTGGCGGAGCCAGCTGGAGGG 1260
 Db 1201 GAGCTGGCCCGGAGTGGAGTCCCTTACTTACTTGGTGGCGGAGCCAGCTGGAGGG 1260
 Qy 1261 AACAGCTCGGCGAGTGAACATGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1320
 Db 1261 AACAGCTCGGCGAGTGAACATGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1320
 Qy 1321 GAGCTGTGGGCGGCGCTGCTGCGAGCGCTTACATCACTCCCTCTACTTGGCACTC 1380
 Db 1321 GAGCTGTGGGCGGCGCTGCTGCGAGCGCTTACATCACTCCCTCTACTTGGCACTC 1380

Qy 1381 AGCAGCCTCACCAGCGTGGGCTTTCGCAACAGTGTTCGCGCAACACGACACCGAGAGATC 1440
 Db 1381 AGCAGCCTCACCAGTGTGGGCTTTCGCAACAGTGTTCGCGCAACACGACACCGAGAGATC 1440
 Qy 1441 TTCTCCATCTGCACCATGCTCATCGGCGCTGATGACGCGTGTGTGTTTGGAAAGCTG 1500
 Db 1441 TTCTCCATCTGCACCATGCTCATCGGCGCTGATGACGCGTGTGTGTTTGGAAAGCTG 1500
 Qy 1501 ACGGCCATCATCAGCGCATGTACGCGCGCTTCTTGTACACAGCGCACCGCGCAC 1560
 Db 1501 ACGGCCATCATCAGCGCATGTACGCGCGCTTCTTGTACACAGCGCACCGCGCAC 1560
 Qy 1561 CTGCGGCACTAATCCGATCCACCGTATCCCAAGCGCTTCAAGCAGCGCATGCTGGAG 1620
 Db 1561 CTGCGGCACTAATCCGATCCACCGTATCCCAAGCGCTTCAAGCAGCGCATGCTGGAG 1620
 Qy 1621 TACTTCCAGGCCACCTGGGCGGTGAACATGGCATCGACACCGAGCTGTGTCAGAGC 1680
 Db 1621 TACTTCCAGGCCACCTGGGCGGTGAACATGGCATCGACACCGAGCTGTGTCAGAGC 1680
 Qy 1681 CTCCTGACGAGCTGCGCGCAGACATCGCCATGCACTGCAAGGAGTCTTGCAGCTG 1740
 Db 1681 CTCCTGACGAGCTGCGCGCAGACATCGCCATGCACTGCAAGGAGTCTTGCAGCTG 1740
 Qy 1741 CCACTGTTTGGGCGGCGAGCGCGCTGCTTGGGCACTGCTTGGGCGCTTGGGCGCC 1800
 Db 1741 CCACTGTTTGGGCGGCGAGCGCGCTGCTTGGGCACTGCTTGGGCGCTTGGGCGCC 1800
 Qy 1801 GCCTTGTGACGCGCGGCGAGTACCTCATCCCAAGCGCATGCTGTCAGGCGCTCTAC 1860
 Db 1801 GCCTTGTGACGCGCGGCGAGTACCTCATCCCAAGCGCATGCTGTCAGGCGCTCTAC 1860
 Qy 1861 TTTGTCTGCTCTGGCTCATGAGGTGCTCAAGGTTGGCAACGCTGTCGCATCCTAGGG 1920
 Db 1861 TTTGTCTGCTCTGGCTCATGAGGTGCTCAAGGTTGGCAACGCTGTCGCATCCTAGGG 1920
 Qy 1921 AAGGGCACTGATCGGCTGAGTCCCGGGGGAGCAGTGGTAAAGGCCAATGCC 1980
 Db 1921 AAGGGCACTGATCGGCTGAGTCCCGGGGGAGCAGTGGTAAAGGCCAATGCC 1980
 Qy 1981 GAGTGAAGGCGCTGAGCTGCTGCTGAGTGTGTCAGTGGCTGGCTGTCAGCGAC 2040
 Db 1981 GAGTGAAGGCGCTGAGCTGCTGCTGAGTGTGTCAGTGGCTGGCTGTCAGCGAC 2040
 Qy 2041 AGCCTTGGCTGTACCCCGAGTTTGGCCCGGCTTCACTGCTGGCTCCGAGGGAGCTC 2100
 Db 2041 AGCCTTGGCTGTACCCCGAGTTTGGCCCGGCTTCACTGCTGGCTCCGAGGGAGCTC 2100
 Qy 2101 AGCTAACCTTATGTCCAGCTGAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2160
 Db 2101 AGCTAACCTTATGTCCAGCTGAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2160
 Qy 2161 GACAAATACCTTATGTCCAGCTGAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2220
 Db 2161 GACAAATACCTTATGTCCAGCTGAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2220
 Qy 2221 GTCTCCCGAGCCCGAGCTGATGAGCCCTTCCAGCGCTTGTGCTGCTGGTGGTGGTGG 2280
 Db 2221 GTCTCCCGAGCCCGAGCTGATGAGCCCTTCCAGCGCTTGTGCTGCTGGTGGTGGTGG 2280
 Qy 2281 TCATCTCAGCTGCAAGCTGCTATCCCGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2340
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 Qy 2341 GGCAGAGGGGCGGCGAGCGGCGAGGGCTTTGAAGCTGAGGCTGAGGCTGGCCCTCTGCTCC 2400
 Db 2341 GGCAGAGGGGCGGCGAGCGGCGAGGGCTTTGAAGCTGAGGCTGAGGCTGGCCCTCTGCTCC 2400
 Qy 2401 CCAAGGGGCGCTAGAGGGGCTACGGTGGCCCGCTGCGATGCGATGTCGCTGGTGGTGGTGG 2460
 Db 2401 CCAAGGGGCGCTAGAGGGGCTACGGTGGCCCGCTGCGATGCGATGTCGCTGGTGGTGGTGG 2460

QY	481	AAAGGCTTCAATGCCAACCGGGCGGAGCGGGCGGTGCTTACCACTGTCCGGGCAC	540	QY	1561	CTGGCGGACTACATCGCATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGCTGGAG	1620
DB	481	AAAGGCTTCAATGCCAACCGGGCGGAGCGGGCGGTGCTTACCACTGTCCGGGCAC	540	DB	1561	CTGGCGGACTACATCGCATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGCTGGAG	1620
QY	541	CTGCAGAGCAGCCCAAGGGCAAGCAACAAGCTCAATTAAGGGGGTGTGGGGAGAACA	600	QY	1621	TACTTCCAGGCCACCTGGGCGGTGAACATGGCATCGACACCAACCGAGTGTGCGAGC	1680
DB	541	CTGCAGAGCAGCCCAAGGGCAAGCAACAAGCTCAATTAAGGGGGTGTGGGGAGAACA	600	DB	1621	TACTTCCAGGCCACCTGGGCGGTGAACATGGCATCGACACCAACCGAGTGTGCGAGC	1680
QY	601	AATTCGCTGAGTACAAAGTAGCGGCATCCGGAAGTCGCCCTTCATCTGTGTGCACTGT	660	QY	1681	CTCCCTGACGAGCTGGCGCAGACATCGCATGCACTGCAAGAGGTCTGCGAGCTG	1740
DB	601	AATTCGCTGAGTACAAAGTAGCGGCATCCGGAAGTCGCCCTTCATCTGTGTGCACTGT	660	DB	1681	CTCCCTGACGAGCTGGCGCAGACATCGCATGCACTGCAAGAGGTCTGCGAGCTG	1740
QY	661	GGGGCACTGAGACCACTGGGATGGCTTCACTGCTCGCCACACTCTATGTGGGTGTC	720	QY	1741	CCACTGTTTGAAGCGCGCAGCGCGGTGCTTGGGGCACTGTCTCTGGGCCCTGCGGCC	1800
DB	661	GGGGCACTGAGACCACTGGGATGGCTTCACTGCTCGCCACACTCTATGTGGGTGTC	720	DB	1741	CCACTGTTTGAAGCGCGCAGCGCGGTGCTTGGGGCACTGTCTCTGGGCCCTGCGGCC	1800
QY	721	ACTGTGCCCTPACAGCGTGTGTGAGACACAGCAGCGGAGGCCAGTGGCGCGCGGCCG	780	QY	1801	GCCTTCTGACGCGCGCGGAGTACCTCATCCACAAGGGGATGCCCTGCAAGGCCCTTAC	1860
DB	721	ACTGTGCCCTPACAGCGTGTGTGAGACACAGCAGCGGAGGCCAGTGGCGCGCGGCCG	780	DB	1801	GCCTTCTGACGCGCGCGGAGTACCTCATCCACAAGGGGATGCCCTGCAAGGCCCTTAC	1860
QY	781	CCAGCGTCTGTGACCTGGCGGTGGAGTCTCTTCACTCTGACATTGCTGAATTC	840	QY	1861	TGTGTCTGTCTGTGCTCCATGAGGTGCTCAAGGTGGCACCGTGTGCGCATCTTAGGG	1920
DB	781	CCAGCGTCTGTGACCTGGCGGTGGAGTCTCTTCACTCTGACATTGCTGAATTC	840	DB	1861	TGTGTCTGTCTGTGCTCCATGAGGTGCTCAAGGTGGCACCGTGTGCGCATCTTAGGG	1920
QY	841	CGTACCACTTCTGTCCAAAGTCGGGCGAGGTGTGTTCGCCAAAGTCCATTTGCCCTC	900	QY	1921	AAGGGCGACCTGATCGCTGTGAGCTGCCCGCGGAGCAGGTGTGTAAAGGCCAATGCC	1980
DB	841	CGTACCACTTCTGTCCAAAGTCGGGCGAGGTGTGTTCGCCAAAGTCCATTTGCCCTC	900	DB	1921	AAGGGCGACCTGATCGCTGTGAGCTGCCCGCGGAGCAGGTGTGTAAAGGCCAATGCC	1980
QY	901	CACCTACCTACCACTGCTGCTGATGTGATGTCATGCGAGGCTGCGCTTACCTGCTA	960	QY	1981	GAGCTGAAGGGGCTGAGTACTGCTGCTCGATGCTGAGCTGGCTGGCTGCGCAGCAG	2040
DB	901	CACCTACCTACCACTGCTGCTGATGTGATGTCATGCGAGGCTGCGCTTACCTGCTA	960	DB	1981	GAGCTGAAGGGGCTGAGTACTGCTGCTCGATGCTGAGCTGGCTGGCTGCGCAGCAG	2040
QY	961	CATGCTTCAAGTCAAGTGTACTTCGGGGCCCATCTGTGAAGAGCTGCGCTGCTG	1020	QY	2041	AGCTTTCGCTGTACCCCGAGTTTGGCCCGGCTTCACTGCTGCGCTCCCGAGGGAGCTC	2100
DB	961	CATGCTTCAAGTCAAGTGTACTTCGGGGCCCATCTGTGAAGAGCTGCGCTGCTG	1020	DB	2041	AGCTTTCGCTGTACCCCGAGTTTGGCCCGGCTTCACTGCTGCGCTCCCGAGGGAGCTC	2100
QY	1021	CGCTGCTGCGCTTCCCGGCTGAGACCGGTACTCGCAGTACAGCGCGTGGTGTG	1080	QY	2101	AGCTTACAACTGGTGTGCGGGAGGCTCTGCAAGGTGGACACACAGCTCCCTGAGCGGC	2160
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DB	1141	ATTGGCCAGCGGGAGATCGAGCAGCGAATCCGAGCTGCTGAGATTGGCTGGCTGAG	1200	DB	2221	GTCTCCCGAGCCCGAGCTGATGAGCCCTCCAGCCCTGCTGCTCCCTGGCTGCACTCC	2280
QY	1201	GAGCTGGCCCGGACTGGAGACTCCCTACTACCTGTGGGCGGAGGCCAGCTGGAGG	1260	QY	2281	TCATCCTCAGCTGCCAAGCTGCTATCCCAAGTGGAGCAGCAGCCCGGCTCGTCTAGGT	2340
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 Db 3241 ACAGGGGCTGA 3252

RESULT 6
 ID AAZ11906
 XX AAZ11906 standard; cDNA; 3857 BP.
 XX
 AC AAZ11906;
 XX
 DT 30-NOV-1999 (first entry)
 XX
 DE Human potassium channel K-Hnov14 cDNA.
 XX
 KW Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;
 KW cardiovascular disorder; CNS disorder; renal disorder; ds.
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 OS Homo sapiens.
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 FH Key Location/Qualifiers
 FT CDS 249..3497
 FT /*tag= a
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 FT variation replace(3168,T)
 FT /*tag= b
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 PD 02-SEP-1999.
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 PF 22-FEB-1999; 99WO-US003826.
 XX
 PR 25-FEB-1998; 98US-0076687P.

PR 07-AUG-1998; 98US-0095836P.
 PR 19-JAN-1999; 99US-0116448P.
 XX
 PA (AXYS-) AXYS PHARM INC.
 XX
 PI Miller AP, Curran ME, Hu P, Rutter M, Wang J;
 XX
 DR WPI; 1999-527591/44.
 DR P-PSDB; AAY34128.
 XX
 PT New nucleic acids encoding mammalian K-Hnov potassium channel proteins,
 PT useful for the diagnosis and treatment of episodic ataxia with myokymia,
 PT cardiac arrhythmia, epilepsy and Bartter's syndrome.
 XX
 PS Claim 4; Page 72-76; 112pp; English.
 XX
 CC This sequence represents human potassium channel K-Hnov14 cDNA. K-Hnov
 CC proteins have a high degree of homology to known potassium channels and
 CC may be alpha subunits, which form the functional channel, or accessory
 CC subunits that act to modulate the channel activity. K-Hnov14 is a 6
 CC transmembrane domain, voltage gated potassium channel. The gene's
 CC chromosomal location is 12q14, determined via PCR chromosomal
 CC localisation using primers AAZ11928 and AAZ11929. K-Hnov cDNAs were
 CC isolated by extension of expressed sequence tags (ESTs) which were
 CC related but not identical to known human potassium channels. Potential
 CC polymorphisms detected as sequence variants between multiple independent
 CC clones. Potassium channels have critical roles in various cell types and
 CC biochemical pathways. Defective potassium channels are known to cause
 CC four human diseases: episodic ataxia with myokymia; cardiac arrhythmia
 CC (long QT syndrome); epilepsy; and Bartter's syndrome. As potassium
 CC channels are critical components of virtually all cells, it is likely
 CC that abnormal potassium channels are also implicated in certain renal,
 CC cardiovascular and central nervous system (CNS) disorders. Nucleotides
 CC encoding K-Hnov proteins may be used for identifying homologous or
 CC related proteins and the DNA sequences encoding them. They may be used to
 CC produce recombinants that modulate the expression and function of the
 CC K-Hnov protein and in studying the biochemical pathways associated with
 CC it. They may also be used for the recombinant production of K-Hnov
 CC protein in fermentation cultures. Additionally, such nucleotides may be
 CC used in gene therapy protocols for the treatment of diseases associated
 CC with abnormal potassium channels
 XX
 SQ Sequence 3857 BP; 677 A; 1301 C; 1201 G; 678 T; 0 U; 0 Other;

Query Match 99.0%; Score 3218; DB 2; Length 3857;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 3244; Conservative 0; Mismatches 5; Indels 3; Gaps 2;
 QY 1 ATGCGCGCATGCGGGGCTCTGGCGCTCAGACACCTTCTTGGACACCATCGCTACG 60
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 Db 309 GCCTTCGACGGCAGCAGTAACCTTGTGTGGCAACGCC--AGTGGCGGGCTCTT- 365
 QY 121 CCGGTGTCTACTGCTCTGATGGCTTCTGTGACCTCAGGGCTTCTCCGGGCTGAGTC 180
 Db 366 CCGGTGTCTACTGCTCTGATGGCTTCTGTGACCTCAGGGCTTCTCCGGGCTGAGTC 425
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Qy	421	GGCCCGACAGATGAGAGAGACAGTGTGTGGCGCGCGGATATAGCGCGGACGATCC	480	1501	ACGGCCATCATCCAGCGCATGTAAGCCCGCCGCTTTCTGTATCCACAGCGCAGCGCGAC	1560
Db	666	GGCCCGACAGATGAGAGAGACAGTGTGTGGCGCGCGGATATAGCGCGGACGATCC	725	1746	ACGGCCATCATCCAGCGCATGTAAGCCCGCCGCTTTCTGTATCCACAGCGCAGCGCGAC	1805
Qy	481	AAAGGCTTCAATGCCAAACCGGCGGAGCGCGCGCTGTCTTACCACCTGTCCGCGGCAC	540	1561	CTGGCGGACTACATCCGATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGTCTGGAG	1620
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Qy	661	GGGGCACTGAGACCACTGGGATGGCTTCACTCTGCTCGCCACACTCTATGTGGCTGTC	720	1741	CCACTGTTTGAAGGCGCGCAGCGCGCTGCTGCGGGCACTGTCTCTGGCCCTGCGGCC	1800
Db	906	GGGGCACTGAGAGCCACTGGGATGGCTTCACTCTGCTCGCCACACTCTATGTGGCTGTC	965	1986	CCAATGTTTGAAGGCGCGCAGCGCGCTGCTGCGGGCACTGTCTCTGGCCCTGCGGCC	2045
Qy	721	ACTGTGCCCTACAGCGTGTGTGAGCAGACGAGAGCCGAGTGGCGCCCGCGGCCG	780	1801	GCCTTCTGCACGCGCGCGGAGTACTCTCATCCAAAGGCGATGCCCTGAGGCCCTCTAC	1860
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Qy	781	CCAGCGCTGTGACCTGGCGGTGGAGTCTCTTCACTCTGACATGCTGCTGAATTC	840	1861	TTTGTCTGCTCTGGCTCCATGAGGCTCTCAAGGTTGGACCCGTCTCGGCATCTCTAGG	1920
Db	1026	CCAGCGCTGTGACCTGGCGGTGGAGTCTCTTCACTCTGACATGCTGCTGAATTC	1085	2106	TTTGTCTGCTCTGGCTCCATGAGGCTCTCAAGGTTGGACCCGTCTCGGCATCTCTAGG	2165
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Db	1086	CGTACCACTTCTGCTGCTCAAGTCCGCGCAGTGTGTGTTGCCCAAGTCCATTTGCCCTC	1145	2166	AAGGGCGACTGATCGGCTGTGAGCTGCCCGCGGAGCAGGTGTAAAGGCCAATGCC	2225
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Qy	961	CATGCTTCAAGTCAAGTGTACTTCGGGCGCCATCTGCTGAAGAGGTGGCGCTCTG	1020	2041	AGCTTTCGCTGTACCCCGAGTTCGCCCCGGCTTCACTGCTGGCTCCGAGGGGAGCTC	2100
Db	1206	CATGCTTCAAGTCAAGTGTACTTCGGGCGCCATCTGCTGAAGAGGTGGCGCTCTG	1265	2286	AGCTTTCGCTGTACCCCGAGTTCGCCCCGGCTTCACTGCTGGCTCCGAGGGGAGCTC	2345
Qy	1021	CGCTGCTGCGCTGCTTCGCGCGCTGGAACGGTACTCGAGTACAGCGCGCTGGTCTG	1080	2101	AGCTTAACACTGGTGTGGGGAGGCTCTGAGAGGTGGACACAGTCCCTGAGCGGC	2160
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Qy	1141	ATTGGCCAGCGGAGATCGAGACAGCAATCCGAGCTGCTGAGATTGGCTGGCTGCAG	1200	2221	GTCTCCCGAGCCCGAGTGTAGAGCCCTCCAGCCCCCTGTCTGCTCCCTGGCTGACCTCC	2280
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Qy	1201	GAGCTGGCCCGCACTGGAGTCTCCCTACTACTGCTGGCGCCGAGGCGCAGCTGGAGG	1260	2281	TCATCTCAGTGTCCAAAGTGTCTATCCCAAGTGAACAGACACCCCGCTCTGCTTAGGT	2340
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Db 3486 ACAGGGGTCTGA 3497

RESULT 7
ID AAZ50452
XX AAZ50452 standard; cDNA; 3355 BP.
AC AAZ50452;
XX
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DT 18-MAY-2000 (first entry)
XX
DE Monkey potassium channel molecule ERG-LP1 cDNA.
XX
KW Monkey; potassium channel molecule; ERG-like protein 1; ERG-LP1;
KW neuroprotective; antiParkinsonian; anticonvulsant; antidepressant;
KW neuroleptic; nootropic; treatment; CNS disorder; central nervous system;
KW potassium channel mediated disorder; epilepsy; Alzheimer's disease;
KW Parkinson's; multiple sclerosis; depression; schizophrenia; amnesia; ss.
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WO200005346-A1.

03-FEB-2000.

21-JUL-1999; 99WO-US016752.

21-JUL-1998; 98US-00119855.

(MILL-) MILLENNIUM PHARM INC.

Curtis RAJ;

WPI; 2000-182682/16.

P-PSDB; AAY44904.

Novel gene encoding potassium channel molecule useful in treating central nervous system disorders such as Alzheimer's disease, multiple sclerosis, and schizophrenia.

Claim 2; Fig 1; 144pp; English.

The present sequence is a cDNA encoding ERG-like protein 1 (ERG-LP1) which is a member of ERG potassium channel family. This sequence is from a full length clone jlkba25d10 which was derived from monkey hippocampal library. ERG-LP1 is expressed exclusively in the brain. Highest expression is found in cortical regions, hippocampus, caudate and amygdala. The protein functions as a potassium channel modulator and has neuroprotective, antiParkinsonian, anticonvulsant, antidepressant, neuroleptic and nootropic activities. The present sequence is useful for treating several potassium channel mediated disorders (CNS disorders) such as Alzheimer's disease, Parkinson's disease, multiple sclerosis, epilepsy, depression, schizophrenic disorders and amnesia

Sequence 3355 BP; 580 A; 1128 C; 1041 G; 606 T; 0 U; 0 Other;

Query Match 97.0%; Score 3156; DB 3; Length 3355;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 3192; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

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Db 164 CGCTTCGACGCGCAGCAGTAACTTCTGTGTGGGCAACGCCAGGTGGCGGGCTCTTC 223
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764 GGGGCGCTGAGGCGCCACCTGGGATGGCTTCACTCTGCTCGCCACACTCTATGTGGCTGTC 823
721 ACTGTGCCCCACAGCGTGTGTGAGCAGCAGCAGCGGAGCCAGTGC CGCGCGCGCGCGCG 780
824 ACCGTGCCCTACAGCGTGTGTGAGCAGCAGCAGCGGAGCCAGTGC CGCGCGCGCGCGCA 883
781 CCCAGGCTGTGTGACCTGGCGGTGAGGTCCTCTTCACTTGCATTTGACATTTGCTGAATTC 840
884 CCCAGGCTGTGTGACCTGGCGGTGAGGTCCTCTTCACTTGCATTTGCTGAATTC 943
841 CGTACCACATTCGTGTCCAAAGTCGGGCGAGGTGGTGTTCGCCCCAAAGTCCATTTGCCTC 900
944 CGTACCACATTCGTGTCCAAAGTCGGGCGAGGTGGTGTTCGCCCCAAAGTCCATTTGCCTC 1003
901 CACTAGCTCACACCTGGTTCCTGCTGGATGTATCGCAGCGGTGCCCTTTGACCTGCTA 960
1004 CACTAGCTCACACCTGGTTCCTGCTGGATGTATCGCAGCGGTGCCCTTTGACCTGCTG 1063
961 CATGCTTCAAGGTCACCTGGTTCCTGCTGGATGTATCGCAGCGGTGCCCTTTGACCTGCTG 1020
1064 CATGCTTCAAGGTCACCTGGTTCCTGCTGGATGTATCGCAGCGGTGCCCTTTGACCTGCTG 1123
1021 CGCTGCTGCGCTGCTTCCGGGCTGGACCGGCTACTCGCAGTACAGCGCGCTGGTGTGCTG 1080
1124 CGCTGCTGCGCTGCTTCCGGGCTGGACCGGCTACTCGCAGTACAGCGCGCTGGTGTGCTG 1183
1081 ACATGCTCATGCGCGTGTTCGCGCTGCTCGCGCACTGGGTGCGCTGCTGCTGCTTTTAC 1140
1184 ACATGCTCATGCGCGTGTTCGCGCTGCTCGCGCACTGGGTGCGCTGCTGCTGCTTTTAC 1243
1141 ATTGGCAGCGGAGATCGAGAGCGGAATCCGAGCTGCTGAGATTGCTGCTGCTGCTGCTGCTG 1200
1244 ATTGGTACGCGGAGATCGAGAGCGGAATCCGAGCTGCTGAGATTGCTGCTGCTGCTGCTGCTG 1303
1201 GAGCTGGCGCGGACTGGAGACTCCCTACTACTGCTGGGCGCGGAGCCAGCTGGAGGG 1260
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1261 AACAGCTCCGGCCAGAGTGACAACTGAGCAGCAGCAGCAGGAGCCAGCGGAGCGGCTG 1320
1364 AACAGCTCTGGCCAGAGTGACAACTGAGCAGCAGCAGCAGGAGCCAGCGGAGCGGCTG 1423
1321 GAGCTGTGGCGCGGCGCTGCTGCGAGCGGCTTACATCACTTCTTCTACTTCTGCACTC 1380
1424 GAGCTGTGAGCGCGCGCTGCTGCGAGCGGCTTACATCACTTCTTCTACTTCTGCACTC 1483
1381 AGCAGCTCACACGCTGGGCTTCGGCAACGCTGTCCGCCAACACGAGCAGCAGGAGATC 1440
1484 AGCAGCTCACACGCTGGGCTTCGGCAACGCTGTCCGCCAACACGAGCAGCAGGAGATC 1543
1441 TTCTCCATCTGCACCATGCTCATCGCGCCCTGATGACGCGGTGGTGTTCGGGAGCGT 1500
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1904 GCCTTCTGCAACCGCGGCGAGTACTCTATCCACCAAGCGGATGCTCTGAGGCGCTCTAC 1963
1861 TTTGTCTGCTCTGGCTCCATGAGAGGTGCTCAAGGCTGGCAACCGTCTGCGCATCTTAGGG 1920
1964 TTTGTCTGCTCTGGCTCCATGAGAGGTGCTCAAGGCTGGCAACCGTCTGCGCATCTTAGGG 2023
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2024 AAGGCTGAGCTGATCGGCTGTGAGTGCCTGCGGCGAGGAGCAGGTGCTAAAGGCGCAATGCC 2083
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2084 GATGTGAAGGGGCTGAGCTACTGCTCTGCACTGTCTGAGTGGCTGCGCTGCAAGAC 2143
2041 AGCCTTTCGCTGTACCCCGAGTTTGGCCCGGCTTCAAGTGGGCTCCGAGGGGAGCTC 2100
2144 AGCCTTTCGCTGTACCCCGAGTTTGGCCCGGCTTCAAGTGGGCTCCGAGGGGAGCTC 2203
2101 AGCTACAACTGGGTGCTGGGAGGCTCTGAGAGGTGACACAGCTCCCTGAGGGGC 2160
2204 AGCTACAACTGGGTGCTGGGAGGCTCTGAGAGGTGACACAGCTCCCTGAGGGGC 2263
2161 GACAAATACCTTATGTCCACGCTGGAGGAGAGAGACAGATGGGAGCAGGGCCCCACA 2220
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2324 GTCTCCCGAGCCCGAGTGAAGCCCTCAGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2383
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2341 GGCAGAGGAGGCGCAGCAGGCGCTTGAAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 2400
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2401 CCAAGGCGCTGAGAGGCGCTGAGGCTGCGCCCGCTGCTGAGTGAAGTGTGCGGCGAGCTG 2460
2504 CCAAGGCGCTGAGAGGCGCTGAGGCTGCGCCCGCTGCTGAGTGAAGTGTGCGGCGAGCTG 2563
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2564 AGCCCGAGGCTGAGTGAAGGCGCTGAGGCTGCGGAGCTGAGGCTGAGGCTGAGGCTGAGGCTG 2623
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2624 TTCCGCGATGGGCGAGTGTGCGCCCGGAAATGTAGCAGCAGCGGCTGCTGAGCAGGAGT 2683
2581 GGCCTGCTCACTGTTCCCGATGGGCGCGCAGGAGGAGGACAGACACAGCTGAGCAGAG 2640
2684 GGCCTGCTCACTGTTCCCGATGGGCGCGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2743
2641 CTTGCGGAGGCGGTGACAGAGCTGTGAGAGCGAGTGTGTCAGATGCGGAGGAGGAGGAGGAGG 2700


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Db 2744 CTTTCGCGAGCGGTGATGGAGCTGTGAGAAAGGTGCTCAGATCGGGAAGACTACAG 2803
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Db 2804 TCACCTTCGCGAGGCTGTGAGCTTGTCTGGCGCCCCATAGGAGGTCCTGCGCTCGG 2863
Qy 2761 GCATCGGAGAGGGGCGGTGCGCCAGCAGCAGCTCCGGGCTTCTGAGGCTCTGTGTGTG 2820
Db 2864 GCCTCAGGAGAGGGGCGCATGCCAGCCAGCAGCTCGGGCTTCTGAGGCTCTGTGTGTG 2923
Qy 2821 GACACTGGGGCATCTCTCTACTGCTGAGCGAGCCCGCCAGCTGCTGTCTGTGAGTGGGACT 2880
Db 2924 GACACTGGGGCATCTCTCTACTGCTGAGCGAGCCCGCCAGCTGCTGTCTGTGAGTGGGACT 2983
Qy 2881 TGGCCCCACCTTCGCGGGGCTCTCCCTCATGCGACCTGCGCCCTGGGGTCCCCCA 2940
Db 2984 TGGCCCCACCTTCGCGGGGCTCTCCCTCATGCGACCTGCGCCCTGGGGTCCCCCA 3043
Qy 2941 GCGTCTCAGAGCTCCCGCTCGAGCCAGCAGCTTCTGACCTCCACCTTCAGACTCA 3000
Db 3044 GCATCTCAGAGCTCCCGCTCGAGCCAGCAGCTTCTGACCTCCACCTTCAGACTCA 3103
Qy 3001 GAGCCCCCTGCTCAGGAGACTCTGCTCTGAGCCAGCAGCCCTGCTCCTCTCTCT 3060
Db 3104 GAGCCCCCTGCTCAGGAGACTCTGCTCTGAGCCAGCAGCCCTGCTCCTCTCTCT 3163
Qy 3061 TCTGAGGAGGGGCTAGGACTGGGCGCCGAGAGCTGTGAGCCAGCTGTGAGGCTACGAGC 3120
Db 3164 TCTGAGGAGGGGCTAGGACTGGGCGCCGAGAGCTGTGAGCCAGCTGTGAGGCTACGAGC 3223
Qy 3121 ACTGAGAGCCCGCCACAGGCTGAGGGGCTGCGGCTTGGCCCTGGGACCCCGAGGCTG 3180
Db 3224 ACTGAGAGCCCGCCAGGCTGAGGGGCTGCGGCTTGGCCCTGGGACCCCGAGGCTG 3283
Qy 3181 GAGATGGTCTATTGGCTGCATGGCTCTGGCAGCTCCAGTGGACCCAGGAGGAGGCG 3240
Db 3284 GAGATGGTCTATTGGCTGCACGGCTCTGGCAGCTCCAGTGGACCCAGGAGGAGGCG 3343
Qy 3241 ACAGGGGTCTGA 3252
Db 3344 ACAGGGGTCTGA 3355

RESULT 8
ACA61728
ID ACA61728 standard; cDNA; 3355 BP.
XX
XX ACA61728;
XX
XX 19-AUG-2003 (first entry)
XX
XX Monkey ERG-like protein 1 (ERG-LP1) cDNA.
XX
XX Monkey; ERG-like protein 1; ERG-LP1; gene; ss; ERG potassium channel;
XX neuronal cell; muscle cell; potassium channel associated disorder; pain;
XX neurodegenerative disorder; psychiatric disorder; learning disorder;
XX memory disorder; obesity; cardiac disorder; gastrointestinal disorder.
XX
XX Macaca sp.
XX
XX Key Location/Qualifiers
XX CDS 104..3355
XX FT /*tag=a
XX FT /product= "Monkey ERG-LP1"
XX
XX US6518398-B1.
XX
XX 11-FEB-2003.
XX
XX 21-JUL-1999; 99US-00358383.
XX
XX 21-JUL-1998; 98US-00119855.
XX
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(MILL-) MILLENNIUM PHARM INC.

Curtis RAJ;

WPI; 2003-455687/43.

P-PSDB; ABU61670.

New human ERG-like protein (ERG-LP2) potassium channel polypeptide and nucleic acid, useful for treating or diagnosing e.g. Alzheimer's disease, schizophrenia, obesity, restenosis, myocardial infarction, Crohn's disease, pain.

Example 1; Fig 1; 116pp; English.

The invention relates to an isolated human ERG-like protein (ERG-LP2) of the ERG potassium channel family and the nucleic acid encoding it. The ERG-LP2 polypeptide or nucleic acid is useful for modulating potassium channel mediated activity in a cell, such as a neuronal cell or a muscle cell. The ERG-LP2 polypeptide or nucleic acid is particularly useful for treating potassium channel associated disorders, e.g. neurodegenerative disorders (e.g. Alzheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis, psychiatric disorders (e.g. depression, schizophrenia, Korsakoff's psychosis, mania, anxiety or phobias), learning or memory disorders (e.g. amnesia or age-related memory loss), obesity, cardiac disorders (e.g. arteriosclerosis, ischaemic reperfusion injury, restenosis, congestive heart failure, angina, hypertension, myocardial infarction, coronary artery disease or arrhythmia), gastrointestinal disorders (e.g. atresia, hiatal hernia, peptic ulcers, gastritis, stomach tumours, Crohn's disease or ischaemic bowel disease) or pain (e.g. joint pain, tooth pain or headaches). This sequence represents cDNA encoding the monkey ERG-like protein 1 (ERG-LP1)

Sequence 3355 BP; 580 A; 1128 C; 1041 G; 606 T; 0 U; 0 Other;

Query Match

Best Local Similarity 97.0%; Score 3156; DB 7; Length 3355;

Matches 3192; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

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Qy 1 ATGCGCGCATGCGGGGCTCTCGCGCTCAGAACCTTCCTGACACCATCCCTACG 60
Db 104 ATGCGCGCATGCGGGGCTCTCGCGCCGAGAACCTTCCTGGACACCATCGTAGC 163
Qy 61 CGCTTGACGGCAGCAGTAACCTTGTGTGGGCAACCCAGGTGGCGGGCTCTTC 120
Db 164 CGCTTCGACGGCAGCAGTAACCTTGTGTGGGCAACCCAGGTGGCGGGCTCTTC 223
Qy 121 CCCGTGTTACTCTCTGTGAGGCTTGTGACCTCAGGGCTTCCCGGGCTGAGTC 180
Db 224 CCCGTGTTACTCTCTGTGAGGCTTGTGACCTCAGGGCTTCCCGGGCTGAGTC 283
Qy 181 ATGCGCGGGGCTGTGCTGCTCTCTTTATGGGCGAGACACAGTAGCTCGTCGC 240
Db 284 ATGCGCGGGGCTGTGCTGCTCTCTTTATGGGCGAGACACAGTAGCTCGTCGC 343
Qy 241 CAACAGATCCGAAAGGCCCTTGAGCAGACAAAGAGTTCAAGCTGAGCTGATCTGTAC 300
Db 344 CAACAGATCCGAAAGGCCCTTGAGCAGACAAAGAGTTCAAGCTGAGCTGATCTGTAC 403
Qy 301 CGGAAGAGCGGGTCCCGTTCTGTGTCTCTGTGATGATACCATTAAGAATGAGAA 360
Db 404 CGGAAGAGCGGGTCCCGTTCTGTGTCTCTGTGATGATACCATTAAGAATGAGAA 463
Qy 361 GGGAGGTGGCTCTCTTCTTAGTCTCTCAAGAGACATCAGCGAAACCAAGAACCGAGGG 420
Db 464 GGGAGGTGGCTCTCTTCTTAGTCTCTCAAGAGACATCAGTGAACCAAGAACCGAGGG 523
Qy 421 GGCCCCCAGAGTGAAGGAGACAGGTGGTGGCGGCCGATATGCGCGGACGATCC 480
Db 524 GGCCCTGACAGTGAAGGAGACAGGTAGTGGCGGCCGATATGCGCGGACGATCC 583
Qy 481 AAAGGCTTCAATGCCAACCGCGGAGCGGGCGGTGCTCTACACCTGTTCGGGAC 540
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 Db 644 CTGCAGAACAGCCCAAGGGCAGCAGCTCAATAAGGGGGTGTTCGGGAGAAACCA 703
 QY 601 AACTTGCCTGAGTACAAAGTAGCCGCATCCGGAAGTCGCCCTTCATCTCTGTTGCACTGT 660
 Db 704 AACTTGCCTGAGTACAAAGTAGCTGCATCCGGAAGTCGCCCTTCATCTCTGTTGCACTGT 763
 QY 661 GGGGCACTGAGAGCCCACTGGGATGGCTTCATCTCTGCTGCGCACACTATATGTGGCTGTC 720
 Db 764 GGGGCGCTGAGGCGCACCTGGATGGCTTCATCTCTGCTGCGCACACTATATGTGGCTGTC 823
 QY 721 ACTGTGCCCTACAGCGTGTGTGACACAGCAGGGAGCCAGTCGCGCGCGCGCCG 780
 Db 824 ACCGTGCCCTACAGCGTGTGTGACACAGCAGGGAGCCAGTCGCGCGCGCGCCCA 883
 QY 781 CCAGCGTCTGTGACCTGCGCGTGGAGTCTCTTTCATCTCTGACATTTGTGTGAATTTTC 840
 Db 884 CCAGCGTCTGTGACCTGCGCGTGGAGTCTCTTTCATCTCTGACATTTGTGTGAATTTTC 943
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 Db 1004 CACTAGCTACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1063
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 Db 1184 ACATGCTCATGCGCGTGTTCGCCCTGCTGCGCAGTGGTTCGCTGCTGCTGCTGCTGCTTAC 1243
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 Db 1424 GAGCTGCTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1483
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Db 1664 CTGCGGACTACATCGGATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGCTGGAG 1723
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 QY 1861 TTTGTCTGCTTGGCTCCATGGAGTGTCCAAAGGTGGCACCGTGTCCGCATCTTAGGG 1920
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 Db 2744 CTTTCGGAGGCGGTGATGAGTGTGAGAGCAGTGTGCTGAGATGCGGGAAGGAGTGGAG 2803

QY 2701 TCACCTTCGACGGCTGTGTGACGCTTGTCTGTGGCGCCCAACAGGAGGGTCCGTGCGCTCGG 2760
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 QY 2804 TCACCTTCGACGGCTGTGTGACGCTTGTCTGTGGCAACCCATAGGAGGGTCCATGCGCTCGG 2863
 DB |||||
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 DB |||||
 QY 3104 GAGCCCTCTGCTCAGGAGACTCTGCTGTGAGCCCGCAGCGCTGAGCTGAGGCTACACAGC 3163
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 DB |||||
 QY 3164 TCTGAGGAGGGGCTTAGGACTGGGCGCCGACAGCGCTGTGAGCCAGGCTGAGGCTACACAGC 3223
 DB |||||
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 DB |||||
 QY 3224 ACTGAGAGCCCGCCACAGGGTCTAGGGGCTGTGGCTTGGCGCTTGGGACCCCGCAGCGCTG 3283
 DB |||||
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 QY 3284 GAGATGTGTCTATTGGCTGCGCATGGCTCTGCGCAGTCCAGTCCAGCGGAGAGGCG 3343
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 DB |||||
 QY 3344 ACAGGGGTCTGA 3355

RESULT 9
 ADB66794
 ID ADB66794 standard; cDNA; 3355 BP.
 XX
 AC ADB66794;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE cDNA encoding monkey ERG-like protein 1 (ERG-LP1).
 XX
 KW Monkey; ERG potassium channel like protein; ERG-LP1; tumour; cytostatic;
 KW gene; ss.
 XX
 OS Macaca sp.
 XX
 FH Key Location/Qualifiers
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 FT /*tag= a
 FT /product= "ERG-LP1"
 FT /note= "The coding region given as SEQ ID No:3 is
 specifically claimed in Claim 2"
 XX
 PN US2003104429-A1.
 XX
 PD 05-JUN-2003.
 XX
 PF 27-JUN-2002; 2002US-00185867.
 XX
 PR 21-JUL-1998; 98US-00119855.
 PR 21-JUL-1999; 99US-00358383.
 XX

(CURT/) CURTIS R A J.
 Curtis RAJ;
 WPI; 2003-687835/65.
 P-PSDB; ADB66795.
 New isolated nucleic acid, useful for producing a polypeptide and
 preparing a composition for diagnosing or treating diseases e.g., a
 tumor.
 Claim 2; Fig 1; 122pp; English.
 The present invention relates to novel ERG potassium channel like
 proteins, designated ERG-LPs, and the polynucleotide sequences encoding
 them. Also disclosed are: a host cell containing the polynucleotide, an
 antibody that selectively binds to the polypeptide, a method for
 producing the polypeptide, a method for detecting the presence of the
 polypeptide or the nucleic acid in a sample, a method for identifying a
 compound that binds to the polypeptide, a method for modulating the
 activity of the polypeptide, a method for identifying a compound that
 modulates the activity of the polypeptide, and a kit. The polynucleotide
 sequences are useful for producing the ERG-LP polypeptides. The ERG-LP
 polynucleotide and polypeptide sequences are useful for preparing a
 composition for diagnosing or treating diseases e.g. tumours. The present
 sequence encodes monkey ERG-LP1.
 Sequence 3355 BP; 580 A; 1128 C; 1041 G; 606 T; 0 U; 0 Other;
 Query Match 97.0%; Score 3156; DB 9; Length 3355;
 Best Local Similarity 98.2%; Pred. No. 0;
 Matches 3192; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
 QY 1 ATGCCGGCATGCGGGGCTCTCTGGCGCGCAGAACCTTCTCTGGACACCATCGCTACG 60
 DB |||||
 QY 104 ATGCCGGCATGCGGGGCTCTCTGGCGCGCAGAACCTTCTCTGGACACCATCGCTACG 163
 DB |||||
 QY 61 CGCTTCGACGGCAGCGACAGTAACCTTGTGTGGCAAGCCCGAGGTGGCGGGGCTCTTC 120
 DB |||||
 QY 164 CGCTTCGACGGCAGCGACAGTAACCTTGTGTGGCAAGCCCGAGGTGGCGGGGCTCTTC 223
 DB |||||
 QY 121 CCCGTGCTTACTGCTCTGTATGGGCTTCTGTGACCTCACGGGCTTCTCCCGGGCTGAGTTC 180
 DB |||||
 QY 224 CCCGTGCTTACTGCTCTGTATGGGCTTCTGTGACCTCACGGGCTTCTCCCGGGCTGAGTTC 283
 DB |||||
 QY 181 ATGACGGGGGCTGTGCTGCTCTCTCTTTATGGGCAGACACAGTGTGCTTCGCGC 240
 DB |||||
 QY 284 ATGACGGGGGCTGTGCTGCTCTCTCTTTATGGGCAGACACAGTGTGCTTCGCGC 343
 DB |||||
 QY 241 CAACAGATCCGCAAGGCCCTGGACGACACAGGATTCAGGGCTGAGTGTATCTGTAC 300
 DB |||||
 QY 344 CAACAGATCCGCAAGGCCCTGGACGACACAGGATTCAGGGCTGAGTGTATCTGTAC 403
 DB |||||
 QY 301 CGGAAGAGCGGGCTCCCGTTCTGTGTGTCTCTGTATGTATACCATTAAGAAATGAGAAA 360
 DB |||||
 QY 404 CGGAAGAGCGGGCTCCCGTTCTGTGTGTCTCTGTATGTATACCATTAAGAAATGAGAAA 463
 DB |||||
 QY 361 GGGAGGTGTGCTCTCTTCTTCTAGTCTCTCAAGGACATCAGCGAAACCAAGAACCGAGGG 420
 DB |||||
 QY 464 GGGAGGTGTGCTCTCTTCTTCTAGTCTCTCAAGGACATCAGTGAACCAAGAACCGAGGG 523
 DB |||||
 QY 421 GGCCCCACAGATGGAGGAGACAGGTGTGGCGCGCGCATGTATGCCGGGCGACGATCC 480
 DB |||||
 QY 524 GGCCCCACAGATGGAGGAGACAGGTGTGGCGCGCGCATGTATGCCGGGCGACGATCC 583
 DB |||||
 QY 481 AAAGGCTTCAATGCCAACCGCGCGGAGCGCGCTGTCTTACCACTGTCCGGGCAC 540
 DB |||||
 QY 584 AAAGGCTTCAATGCCAACCGCGCGGAGCGCGCTGTCTTACCACTGTTCGGGGAC 643
 DB |||||
 QY 541 CTGCAGAGCAGCCCCAAGGGCAAGCAAGCTCAATAAGGGGGTGTGTTGGGGAGAAACCA 600
 DB |||||
 QY 644 CTGCAGAGCAGCCCCAAGGGCAAGCAAGCTCAATAAGGGGGTGTGTTGGGGAGAAACCA 703
 DB |||||

Qy	601	AACCTTGCTGAGTACAAAGTAGCCGACATCCGGAAGTCGCCCTTCATCTCTGTGCACTGT	660	1784	CTCCCTGAGAGCTGCGCGCAGACATCGCATGTGCACCTGCAACAAGAGGTCTCTGCAGCTG	1843	
Db	704	AACCTTGCTGAGTACAAAGTAGCTGCATCCGGAAGTCGCCCTTCATCTCTGTGCACTGT	763	Qy	1741	CAACTGTTTGTAGCGGCCAGCCGCGCTGCTCGCGGCACTGTCTCTGCGCCCTTGCGGCCC	1800
Qy	661	GGGGCACTGAGAGCCACCTGGAGATGCTTCATCTGCTCGCCACACTCTATGTGGGTGTC	720	Db	1844	CGCTGTTTGTAGCGGCCAGCCGCGCTGCTCGCGGCACTGTCTCTGCGCCCTTGCGGCCC	1903
Db	764	GGGGCGCTGAGGCCACCTGGAGATGCTTCATCTGCTCGCCACACTCTATGTGGGTGTC	823	Qy	1801	GCCTTTGCAACCGCGGGCGAGTACTCATCAACCAAGGCGATGCTCTGACGGCCCTCTAC	1860
Qy	721	ACTGTGCCCTACAGCGTGTGTGACACAGCAGCGGAGCCAGTGCAGCGCCGCGCCG	780	Db	1904	GCCTTTGCAACCGCGGGCGAGTACTCATCAACCAAGGCGATGCTCTGACGGCCCTCTAC	1963
Db	824	ACCGTCCCTACAGCGTGTGTGACACAGCAGCGGAGCCAGTGCAGCGCCGCGCCCA	883	Qy	1861	TTTGTCTGCTCTGGCTTCATGAGAGTGTCAAGGTGGCCACCTGCTCGCATCTCTAGGG	1920
Qy	781	CCAGCGCTGTGACCTGGCCGCTGGAGTCTCTTCATCTGCTGACATGTGCTGAATTC	840	Db	1964	TTTGTCTGCTCTGGCTTCATGAGAGTGTCAAGGTGGCCACCTGCTCGCATCTCTAGGG	2023
Db	884	CCAGCGCTGTGACCTGGCTGTGGAGTCTCTTCATCTGACATGTGCTGAATTC	943	Qy	1921	AAGGGGACCTGATCGGCTGTGAGCTGCCCGCGCGGAGCAGGTGTGTAAGGCAATGCC	1980
Qy	841	CGTACCAATTCGTGTCCAAAGTCGGGCGAGGTGGTGTGTCGCCCAAGTCCATTTGCCTC	900	Db	2024	AAGGGTGAACCTGATCGGCTGTGAGCTGCCCGGAGGAGCAGGTGTGTAAGGCAACGCC	2083
Db	944	CGTACCAATTCGTGTCCAAAGTCGGGCGAGGTGGTGTGTCGCCCAAGTCCATTTGCCTC	1003	Qy	1981	GAGCTGAAGGGGCTGACGTACTGCTGCTGCACTGTCTGAGCTGGCTGGCTGCAAGC	2040
Qy	901	CACTAGTCACACACTGGTTCCTGCTGGATGTCTATCGCAGCGCTGCCCTTTGACCTGCTA	960	Db	2084	GATGTGAAGGGGCTGACGTACTGCTGCTGCACTGTCTGAGCTGGCTGGCTGCAAGC	2143
Db	1004	CACTAGTCACACACTGGTTCCTGCTGGATGTCTATCGCAGCGCTGCCCTTTGACCTGCTG	1063	Qy	2041	AGCCTTGGCTGTACCCCGAGTTTGGCCCGGCTTCAGCCGCTGGCTTCCGAGGGAGCTC	2100
Qy	961	CATGCTTCAAGGTCAACGTGTACTTTCGGGGCCCATCTGCTGAAGACGCTGCGCTGCTG	1020	Db	2144	AGCCTTGGCTGTACCCCGAGTTTGGCCCGGCTTCAGCCGCTGGCTTCCGAGGGAGCTC	2203
Db	1064	CATGCTTCAAGGTCAACGTGTACTTTCGGGGCCCATCTGCTGAAGACGCTGCGCTGCTG	1123	Qy	2101	AGCTACAACCTGGGTGCTCGGGGAGGCTCTGCAAGAGTGGACACCAAGTCCCTGAGCGC	2160
Qy	1021	CGCTGTGGCTGCTTCCGGGCTGGACCGGTACTCGCAGTACAGCGCGCTGGTGTGCTG	1080	Db	2204	AGCTACAACCTGGGTGCTGGGGAGGCTCTGCAAGAGTGGACACCAAGTCCCTGAGCGC	2263
Db	1124	CGCTGTGGCTGCTTCCGGGCTGGACCGGTACTCGCAGTACAGCGCGCTGGTGTGCTG	1183	Qy	2161	GACAATACCTTATGTCCACGCTGAGAGAGAGAGACAGATGGGAGCAGGCCCCACA	2220
Qy	1081	ACACTGCTCATGCGGTGTTCCGCTGCTCGCGCACTGGGTGCTGCTGCTGCTGCTTAC	1140	Db	2264	GACAATACCTTATGTCCACGCTGAGAGAGAGAGACAGATGGGAGCAGGCCCCACA	2323
Db	1184	ACACTGCTCATGCGGTGTTCCGCTGCTCGCGCACTGGGTGCTGCTGCTGCTGCTTAC	1243	Qy	2221	GTCTCCCGCAGCCAGCTGATGAGCCCTCCAGCCCTGCTGCTGCTGCTGCTGCTGCTGCT	2280
Qy	1141	ATTGGCCAGCGGAGATCGAGAGCAGCGAATCCGAGCTGCTGAGATGCTGCTGCTGCTG	1200	Db	2324	GTCTCCCGCAGCCAGCTGATGAGCCCTCCAGCCCTGCTGCTGCTGCTGCTGCTGCTGCT	2383
Db	1244	ATTGGTCAGCGGAGATCGAGAGCAGCGAATCCGAGCTGCTGAGATGCTGCTGCTGCTG	1303	Qy	2281	TCATCTCTGAGTCCCAAGTGTCTATCCCACTGCAACAGCAGCCCGCGCTCGTCTAGGT	2340
Qy	1201	GAGTGTGCCCGCGACTGGAGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1260	Db	2384	TCATCTCTGAGTCCCAAGTGTCTATCCCACTGCAACAGCAGCCCGCGCTCGTCTAGGT	2443
Db	1304	GAGTGTGCCCGCGACTGGAGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1363	Qy	2341	GGCAGAGGAGGCCAGGCGGCTTTGAAAGCTGAGGCTGAGGCTGCGCCCTCTGCTGCTG	2400
Qy	1261	AACAGCTCCGCGCAGAGTGAACCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	1320	Db	2444	GGCAGAGGAGGCCAGGCGGCTTTGAAAGCTGAGGCTGAGGCTGCGCCCTCTGCTGCTG	2503
Db	1364	AACAGCTCCGCGCAGAGTGAACCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	1423	Qy	2401	CCACGGGCTTACGAGGCTTACGCTGCCCGCCATGCAATGCAATGCAATGCAATGCAATG	2460
Qy	1321	GAGTGTGGGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1380	Db	2504	CCACGGGCTTACGAGGCTTACGCTGCCCGCCATGCAATGCAATGCAATGCAATGCAATG	2563
Db	1424	GAGTGTGGGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1483	Qy	2461	AGCCCCAGGCTAGTAGATGGCATTTGAAAGCGGCTGTGGCTCGGACCAAGCCCAAGTTCT	2520
Qy	1381	AGAGCCTACAGCGTGGGCTTCGGCAACGTGTCCGCAACAGCAGCAGCAGCAGCAGC	1440	Db	2564	AGCCCCAGGCTAGTAGATGGCATTTGAAAGCGGCTGTGGCTCGGACCAAGCCCAAGTTCT	2623
Db	1484	AGAGCCTACAGCGTGGGCTTCGGCAACGTGTCCGCAACAGCAGCAGCAGCAGCAGC	1543	Qy	2521	TTCCGCTGGGCGAGTCTGGCCCGGAAATGAGCAGCAGCCCTCCCTCGACCAAGAGC	2580
Qy	1441	TTCTTCCATCTGACCATGCTCATCGCGCCCTGATGCAAGCGGTGGTGTGGGAAAGTG	1500	Db	2624	TTCCGCTGGGCGAGTCTGGCCCGGAAATGAGCAGCAGCCCTCCCTCGACCAAGAGC	2683
Db	1544	TTCTTCCATCTGACCATGCTCATCGCGCCCTGATGCAAGCGGTGGTGTGGGAAAGTG	1603	Qy	2581	GGCTGTGCTACTGTTCCCATGAGCCCGCAGCGAGGCAAGGAACACAGACACTGCAAG	2640
Qy	1501	ACGCCATCATCCAGCGCATGTACGCCCGCGCTTTCTGTATCCACAGCCGCAAGCGGAC	1560	Db	2684	GGCTGTGCTACTGTTCCCATGAGCCCGCAGCGAGGCAAGGAACACAGACACTGCAAG	2743
Db	1604	ACGCCATCATCCAGCGCATGTACGCCCGCGCTTTCTGTATCCACAGCCGCAAGCGGAC	1663	Qy	2641	CTTCGGCAGGCGGTGACAGAGCTGTACAGCAGGTGCTGAGATGCGGGAGGAGCTGAG	2700
Qy	1561	CTGGGACATCATCCAGCATCCAGGTATCCCGAGCCCTTCAGCAGCGCATCTGGAG	1620	Db	2744	CTTCGGCAGGCGGTGATGAGCTGTAGAACAGGTGCTGAGATGCGGGAGGAGCTACAG	2803
Db	1664	CTGGGACATCATCCAGCATCCAGGTATCCCGAGCCCTTCAGCAGCGCATCTGGAG	1723	Qy	2701	TCATTTCCAGGCTGTGAGCTGTGCTGCGGCCCGCAGAGGAGGTTCCTGCGCCCTCGG	2760
Qy	1621	TACTTTCCAGGCTGTGAGGCGGTGAACAAATGGCATCGACACCAAGAGCTGCTGAGAGC	1680	Db	2804	TCATTTCCAGGCTGTGAGCTGTGCTGCGGCCCGCAGAGGAGGTTCCTGCGCCCTCGG	2863
Db	1724	TACTTTCCAGGCTGTGAGGCGGTGAACAAATGGCATCGACACCAAGAGCTGCTGAGAGC	1783	Qy	2761	GCATCGGAGAGGCGGCTGCCCGCAGCAGCTCCGGGCTTCTGACGCTCTGCTGTGTG	2820
Qy	1681	CTCCCTGACGAGCTGCGCGCAGACATCGCCATGCACTGTGCAAAAGAGGTCTCTGAGCTG	1740				

Db 2761 GCCTCAGGAGAGGGGCGATGCCAGCAGCAGCCTCCGGGCTTCTGCAGCCTCTGTGTG 2820
QY 2821 GACACTGGGGCATCTCTACTCTGCTGCAGCCCGCAGCTGGCTGTCTTGTAGTGGGACT 2880
Db 2821 GACACTGGGGCATCTCTACTCTGCTGCAGCCCGCAGCTGGCTGTCTTGTAGTGGGACT 2880
QY 2881 TGGCCCCACCCCTGCTCGGGGCTCTCTCCCTCATGGCACCCCTGGGCTGCCCCCA 2940
Db 2881 TGGCCCCACCCCTGCTCGGGGCTCTCTCCCTCATGGCACCCCTGGGCTGCCCCCA 2940
QY 2941 GCCTCTCAGAGTCCCTTGGGCTCGAGCCACAGCTTCTGACCTCCACCTCAGACTCA 3000
Db 2941 GCATCTCAGAGTCCCTTGGGCTCGAGCCACAGCTTCTGACCTCCACCTCAGACTCA 3000
QY 3001 GAGCCCTCTGCTCAGAGACTCTCTCTGAGCCCGCAGCACCCCTGCCCTCCCTCTCTCT 3060
Db 3001 GAGCCCTCTGCTCAGAGACTCTCTCTGAGCCCGCAGCACCCCTGCCCTCCCTCTCTCT 3060
QY 3061 TCTGAGGAGGGCTAGGACTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 3120
Db 3061 TCTGAGGAGGGCTAGGACTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 3120
QY 3121 ACTGAGAGCCGCCACCCAGGGCTCAGGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 3180
Db 3121 ACTGAGAGCCGCCACCCAGGGCTCAGGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 3180
QY 3181 GAGATGGTCTTATTGGCTGCGCATGGCTCTGGCACAGTCCAGTGGACCCAGGAAGGCG 3240
Db 3181 GAGATGGTCTTATTGGCTGCGCACGGCTCTGGCACAGTCCAGTGGACCCAGGAAGGCG 3240
QY 3241 ACAGGGGTC 3249
Db 3241 ACAGGGGTC 3249

RESULT 11

AAx84919
ID AAX84919 standard; DNA; 3715 BP.

AC AAX84919;

DT 28-SEP-1999 (first entry)

XX Rat brain specific potassium channel protein coding sequence.

DE Brain specific potassium channel; central nervous system disorder;
KW dementia; cerebral ischaemic sclerosis; therapy; probe; ss.

XX Rattus sp.

OS W09937677-A1.

XX 29-JUL-1999.

XX 20-JAN-1999; 99WO-JP000190.

XX 23-JAN-1998; 98JP-00011434.

XX 04-DEC-1998; 98JP-00346198.

XX (YAMA) YAMANOUCHI PHARM CO LTD.

XX Miyake A, Mochizuki S, Yokoi H;

XX WPI; 1999-458683/38.

XX Potassium channel protein expressed specifically in brain tissue and
PT method for its production.

XX Example 3; Page 54-57; 63pp; English.

XX This sequence encodes a rat potassium channel protein, and was used as a
CC probe to isolate DNA encoding the protein of the invention. The protein
CC of the invention is a human brain specific potassium channel protein. The

CC protein is used to treat and investigate disorders of the central nervous
CC system such as dementia and cerebral ischaemic sclerosis
XX
SQ Sequence 3715 BP; 735 A; 1167 C; 1090 G; 723 T; 0 U; 0 Other;

Query Match 81.9%; Score 2664.8; DB 2; Length 3715;
Best Local Similarity 89.0%; Pred. No. 0;
Matches 2905; Conservative 0; Mismatches 347; Indels 12; Gaps 2;

QY 1 ATGCCGGCCATGCGGGGCTCTCTGGCGCTCAGAACACCTTCTGACACCATCGGTACG 60
Db 156 ATGCCGGCCATGCGGGGCTCTCTGGCGCGAGAACCTTCTGACACCATCGGCACC 215
QY 61 CGCTTCGACGGCAGCAGCAGTAACCTTCTGGGCAACGCCAGGTGGCGGCTCTTC 120
Db 216 CGCTTCGACGGGACGACAGTAACCTTCTGGGCAACGCCAGGTGGCGGCTCTTC 275
QY 121 CGCGTGGTCTACTGCTCTGATGGCTTCTGACCTCAGGGGCTTCTCCGGGTGAGGTC 180
Db 276 CTGTGGTCTACTGCTCTGATGGCTTCTGACCTCAGGGGCTTCTCCAGAGCTGAGGTC 335
QY 181 ATGCAGCGGGGCTGTGCTCTCTTATGGGCCAGACACCATCGGTCTGTCGCGC 240
Db 336 ATGCAGCGGGGCTGTGCTCTCTTATGGGCCAGACACCATCGGTGAGTGGTCCG 395
QY 241 CAAACAGATCCGAAAGGCCCTGGATGAGCAACAAATTCMAAGGCTGAACTGATCCTGTAC 455
Db 396 CAAACAGATCCGAAAGGCCCTGGATGAGCAACAAATTCMAAGGCTGAACTGATCCTGTAC 455
QY 301 CGGAAGAGCGGCTCTCTCTCTCAAGGACATCAGCGAAACCAAGAACCGAGG 360
Db 456 CGGAAGAGCGGCTCTCTCTCTCAAGGACATCAGCGAAACCAAGAACCGAGG 360
QY 361 GGGGAGGTGGTCTCTCTCTCAAGGACATCAGCGAAACCAAGAACCGAGG 420
Db 516 GGGGAGGTGGTCTCTCTCTCAAGGACATCAGCGAAACCAAGAACCGAGG 420
QY 421 GGGCCCGACAGATGGAAGGAGAGGTGGTGGCGGCGCCGATATGGCGGCGACGATCC 480
Db 576 GGGCCCGACAGATGGAAGGAGAGGTGGTGGCGGCGCCGATATGGCGGCGACGATCC 480
QY 481 AAAGGCTTCAATGCAACCGCGGCGGAGCGCGGCTCTACCATCTGTCGGGCGAC 540
Db 636 AAAGGCTTCAATGCAACCGCGGCGGAGCGCGGCTCTACCATCTGTCGGGCGAC 540
QY 541 CTGAGAGGAGCCCAAGGGCAAGCAAGTCTCAATAAGGGGCTGTTGGGAGAGAACCA 600
Db 696 CTGAGAGGAGCCCAAGGGCAAGCAAGTCTCAATAAGGGGCTGTTGGGAGAGAACCA 600
QY 601 AACTTGCTGAGTACAAAGTAGCCGCAATCGGAAGTGGCCCTTATCTCTGTCACCTGT 660
Db 756 AACTTGCTGAGTACAAAGTAGCCGCAATCGGAAGTGGCCCTTATCTCTGTCACCTGT 815
QY 661 GGGGCACTGAGAGCCACCTGGGATGGCTTATCTCTGTCGGCCACACTCTATGCGGTGTC 720
Db 816 GGGGCACTGAGAGCCACCTGGGATGGCTTATCTCTGTCGGCCACACTCTATGCGGTGTC 720
QY 721 ACTGTGCCCTACAGCGTGTGTGTGAGCACAGCAGCGGAGCCAGTGGCGCGCGGCGCG 780
Db 876 ACTGTGCCCTACAGCGTGTGTGTGAGCACAGCAGCGGAGCCAGTGGCGCGCGGCGCG 780
QY 781 CCCAGGCTCTGACCTGGCGGCTCTTATCTCTGAGAGTGGCTCTGACATGTCGTAATTC 840
Db 936 CCTAGTGTCTGACCTGGCGGCTGTAAGTCTCTTATCTTAGATATGTCGTAATTC 995
QY 841 CGTACCACATTCGTGTCCCAAGTGGCGGAGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 900
Db 996 CGTACCACATTCGTGTCCCAAGTGGCGGAGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 900
QY 901 CACTAGCTCACCACCTGGTCTCTGCTGGATGTCTATCTCTGAGAGTGGCTGGCTGGCTGG 1055
Db 1056 CACTAGCTCACCACCTGGTCTCTGCTGGATGTCTATCTAGAGAGTGGCTGGCTGGCTGG 1115

961 CATGCTTCAAGGTCACAGTGTACTTGGGGGCCATCTGCTGAAGACGGTGGCCCTGCTG 1020
1116 CATGCTTCAAGGTCACAGTGTACTTGGGGGCCATCTGCTGAAGACGGTGGCCCTGCTT 1175
1021 CGCTGCTCGGCTGCTTCCGGGCTGGAACCGGTACTCGAGTACAGCGCGGTGCTGCTG 1080
1176 CGGCTGCTCGGCTACTACCAAGACTGGACCGGTACTCTCAGTATAGCGTGTGTGCTC 1235
1081 ACAGTCTATGGCGGTGTGCGCTGCTCGGCACTGGGTGCGCTGCTGCTGCTTAC 1140
1236 ACCTTCTCATGGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1295
1141 ATTGGCCAGCGGAGATCGAGACGACGAATCCGAGCTGCTCAGATTTGCTGCTGCTGCTG 1200
1296 ATCGGCGAGCAAGAGATTTGAGACAGGAGTCAAGAGTGTGCTGAGATCGGCTGCTGCTG 1355
1201 GAGTGGCGCGCGAGTGTGAGAGTCTCCTACTACTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
1356 GAGTGGCGCGCGAGTGTGAGAGTCTCCTACTACTGCTGCTGCTGCTGCTGCTGCTGCTG 1415
1261 AACAGTCTCGGCGAGAGTGTGAGAGTCTCCTACTACTGCTGCTGCTGCTGCTGCTGCTG 1311
1416 AACAGTCTCGGCGAGAGTGTGAGAGTCTCCTACTACTGCTGCTGCTGCTGCTGCTGCTG 1475
1312 ACGGGGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1371
1476 ACTGGGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1535
1372 TTGCGACTAGAGCTTACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1431
1536 TTGCGCTAGAGCTTACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1595
1432 GAGAGATCTTCCATCTGACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1491
1596 GAGAGATCTTCCATCTGACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1655
1492 GGAACCTGAGCGGCTATCATCCAGGATGTAGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 1551
1656 GGAATGTGACAGCATCATCCAGGATGTAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1715
1552 ACGCGGAGCTGCGGCTATCATCCAGGATGTAGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 1611
1716 ACCGCTGACCTGCGGATCATTCAGGATGTAGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 1775
1612 ATGCTGAGTACTTCCAGGCTATCATCCAGGATGTAGCGCGCTGCTGCTGCTGCTGCTGCTG 1671
1776 ATGCTGAGTACTTCCAGGCTATCATCCAGGATGTAGCGCGCTGCTGCTGCTGCTGCTGCTG 1835
1672 CTGAGAGCTTCCCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1731
1836 CTGAGAGCTTCCCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1895
1732 CTGAGAGCTTCCCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1791
1896 CTGAGAGCTTCCCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1955
1792 CTGAGAGCTTCCCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1851
1956 CTGAGAGCTTCCCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2015
1852 GCGCTTCTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1911
2016 GCTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2075
1912 ATCTAGGAGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1971
2076 ATCTAGGAGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2135
1972 GCGAATGCGAGCTGAGAGGGGCTGAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2031
2136 GCGAATGCGAGCTGAGAGGGGCTGAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2195
2032 CTGCGACGACAGCTTGGCTGTATACCGCGAGTTTGGCCCGCGCTTCAGTCTGCTGCTGCTG 2091

2196 CTGCGACGAGAGCTTGCAGTGTACCTGAGTTTGGCCCAAGCTTTAGCCGTGGCTCCGA 2255
2092 GGGGAGCTCAGCTACAACTCTGGGTGTGGGGAGGCTTTCAGAGGTGACACCACTCC 2151
2256 GGGGAGCTCAGCTACAACTCTGGGTGTGGGGAGGCTTTCAGAGGTGATACCACTCA 2315
2152 CTGAGCGGCGAATAATACCTTATTCACGCTGGAGGAGGAGGAGAGGAGGAGGAGCAG 2211
2316 CTGAGTGTGTGACAAACCTCTCATGTCCACACTGGAGGAGGAGGAGGAGGAGGAGCAG 2375
2212 GGGCCCAAGGCTTCCCGACCGCTGATGAGCCCTCCAGCCCTGCTGCTGCTGCTGCTGCTG 2271
2376 GGCACACAGATCTCACCGCCCGCAGAGATGAGCCCTCCAGCCCTGCTGCTGCTGCTGCTG 2435
2272 TGCACTCTCTCATCTCAGTGTCCAAAGCTCTATCCCAAGTCCCAAGTCCCAAGTCCCAAG 2331
2436 TGTACCTCTCTCTCTCAGCGGCCAACTACTCTCCCAAGTCCCAAGTCCCAAGTCCCAAG 2495
2332 CGTCTAGGTGGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2391
2496 AGGCTGGGTGGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2555
2392 TCTGCTTCCCGACCGGCTTAGAGGGGCTACGGCTGCCCCCATGCTGCTGCTGCTGCTGCTG 2451
2556 TCTGCTTCCCGACCGGCTTAGAGGGGCTACGGCTGCCCCCATGCTGCTGCTGCTGCTGCTG 2615
2452 CCAGATCTGAGCCCGCAGGAGTGTAGATGGATTTGAAGCGGCTGTGGCTCGGAGCAGCCC 2511
2616 CCAGATCTGAGCCCGCAGGAGTGTAGATGGATTTGAAGCGGCTGTGGCTCGGAGCAGCCC 2675
2512 AGTTCTCTTTTCGGCTGGGCGCAGTCTGCGCCCGGAGTGTAGCAGCAGCCCTTCCCTCGGA 2571
2676 AAGTTCTCTTTTCGGCTGGGCGCAGTCTGCGCCCGGAGTGTAGCAGCAGCCCTTCCCTCGGA 2735
2572 CCAGAGAGCGCTGCTGCTGCTTCCCGCAGCGAGGAGGAGGAGGAGGAGGAGGAGGAG 2631
2736 ACAGAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2795
2632 CTGAGCAAGCTTTCGGCAGGCGGTGACAGAGTGTGACAGCAGGAGTGTGAGATCGGAGAA 2691
2796 CTGAGCAAGCTTTCGGCAGGCGGTGACAGAGTGTGACAGCAGGAGTGTGAGATCGGAGAA 2855
2692 GGAAGTGTGAGTCTTCCCGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2751
2856 GGAAGTGTGAGTCTTCCCGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2915
2752 TGCCCTCGGCTATCGGAGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2811
2916 TGTCCCGGCTATCAGAGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2975
2812 CTGCTGTGAGTCTGAGGCGATCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2871
2976 CTGCTGTGAGTCTGAGGCGATCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3035
2872 AGTGGAGTGTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2928
3036 AGTGGAGTGTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3095
2929 TGGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2988
3096 TGGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3155
2989 ACCTCAGACTCAGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3048
3156 ACCTCAGACTCAGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3215
3049 TCCCTCTCTCTCTGAGAGGCGCTGAGTGTGGCGCGCAGAGCCTGTGAGCAGGCTGCT 3108
3216 TCACCCCTCTCTCTGAGAGGCGCTGAGTGTGGCGCGCAGAGCCTGTGAGCAGGCTGCT 3275
3109 GAGGCTACAGCAGTGTGAGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3168

Dd 3396 CAGGAGGGGCACAGGAGTCTCA 3419

RESULT 13
AAx84911

ID AAX84911 standard; DNA; 3064 BP.
XX AC AAX84911;
XX DT 28-SEP-1999 (first entry)
XX DE Human brain specific potassium channel protein coding sequence.
XX KW Brain specific potassium channel; human; central nervous system disorder;
XX KM dementia; cerebral ischaemic sclerosis; therapy; ss.
XX OS Homo sapiens.

EH Key Location/Qualifiers
FT CDS 4..3057
FT FT /*tag= a
XX PN WO9937677-A1.
XX PD 29-JUL-1999.
XX PF 20-JAN-1999; 99WO-JP000190.
XX PR 23-JAN-1998; 98JP-00011434.
XX PR 04-DEC-1998; 98JP-00346198.
XX PA (YAMA) YAMANOUCHI PHARM CO LTD.
XX PI Miyake A, Mochizuki S, Yokoi H;
XX RI WPI; 1999-458683/38.
XX DR P-FSDB; AAY22427.

PT Potassium channel protein expressed specifically in brain tissue and method for its production.
PX Claim 6; Page 44-49; 63pp; English.
PS CC This sequence encodes the potassium channel protein of the invention,
CC that is expressed specifically in brain tissue. The protein is used to
CC treat and investigate disorders of the central nervous system such as
CC dementia and cerebral ischaemic sclerosis
XX SQ Sequence 3064 BP; 554 A; 1042 C; 848 G; 620 T; 0 U; 0 Other;

Query Match 27.2%; Score 884.8; DB 2; Length 3064;
Best Local Similarity 65.5%; Pred. No. 6.4e-151;
Matches 1408; Conservative 0; Mismatches 622; Indels 120; Gaps 3;

Qy 1 ATCGCGGCCATGCGGGCCTTCGTGGCCCTTAGAACACTTCCTGGACACCATTGGCTACG 60
Dd |||||
Db 4 ATCGCGGTATGAAGGGTTGCTGGCCCCGAAAACAACCTTCCTGGACACCATGCCACC 63

Qy 61 CGCTTCGAGCGCACGCACAGTAACCTCGTGCTGGGGCAAGCCCAGGTGGGGGCTCTTC 120
Dd |||||
Db 64 CGTTTTGACGGGAACGCACACAACTTCCTGTGGCCAACGCACAGGGCACACCGGGGTTT 123

Qy 121 CCCGTGTCTACTGTCTCTGATGGCTTCGTGACCTCAGGGCTTCTCCCGGCTGAGGTC 180
Dd |||||
Db 124 CCCATCGTCTACTGTCTCCGAGGCTTCTGCGAGCTCAAGGCTACGCTGCGACCGAGGTC 183

Qy 181 ATCGAGCGGGCTGTGCTCTCTCTTCCTTTATGGGGCCAGACACCATGAGCTCGTCCGC 240
Dd |||||
Db 184 ATCGAAGAAGCCATGCAGTCCGGTTTCCTCTACGGCCAGAGACCATGAGCGAGGCTG 243

Qy 241 CACACATCCGAAGCCCTGGAGGAGCAAGAGGATGCAAGGCTGAGCTGATCCTGTAC 300
Dd |||||
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 2005 GTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2064
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 2065 GCCCGCGCTTTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2114
 2020 GGGGCTGCTTCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2069

RESULT 14
 AAX84918
 ID AAX84918 standard; DNA; 3736 BP.
 XX AC AAX84918;
 XX DT 28-SEP-1999 (first entry)
 XX DE Rat brain specific potassium channel protein coding sequence.
 XX DE Brain specific potassium channel; central nervous system disorder;
 XX DE dementia; cerebral ischaemic sclerosis; therapy; probe; ss.
 XX OS Rattus sp.
 XX PN W09937677-A1.
 XX PD 29-JUL-1999.
 XX PF 20-JAN-1999; 99WO-JP000190.

XX 23-JAN-1998; 98JP-00011434.
 PR 04-DEC-1998; 98JP-00346198.
 XX (YAMA) YAMANOUCI PHARM CO LTD.
 PA Miyake A, Mochizuki S, Yokoi H;
 PI WPI; 1999-458683/38.
 DR Potassium channel protein expressed specifically in brain tissue and
 PT method for its production.
 XX Example 3; Page 57-59; 63pp; English.
 PS This sequence encodes a rat potassium channel protein, and was used as a
 CC probe to isolate DNA encoding the protein of the invention. The protein
 CC of the invention is a human brain specific potassium channel protein. The
 CC protein is used to treat and investigate disorders of the central nervous
 CC system such as dementia and cerebral ischaemic sclerosis
 XX SQ Sequence 3736 BP; 706 A; 1210 C; 1000 G; 820 T; 0 U; 0 Other;
 Query Match 26.7%; Score 869.8; DB 2; Length 3736;
 Best Local Similarity 65.3%; Pred. No. 3.4e-148;
 Matches 1403; Conservative 0; Mismatches 627; Indels 117; Gaps 4;
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 DB 196 CGCTTTGACGGCAGCAGCAACTTCTTCTTGGCCAAATGCCAGGGGCCACCGGGGTTT 255
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 DB 256 CCATGCTCTACTGCTCTGACGCTTCTGTGAGTCTACAGGCTACGGCGCAGCAGGCTC 315
 QY 181 ATGCAGCGGGCTGTGCTCTCTCTTATGGGCGCAGACACAGTGTGCTGCTCGC 240
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 QY 301 CGGAAGAGCGGCTCCGCTCTCTGCTGTCTCTGTGATGTATACCATTAAGAATGAGAAA 360
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 QY 361 GGGGAGGTGCTCTCTCTTCTAGTCTCTCAAGGACATCAGCGAAACCAAGAACCGAGG- 419
 DB 496 GGGGAGGTGCTCTCTTCTTCTTCTTAAAGGACATCTCTAGAGTGGAGGCCAGGA 555
 QY 420 ---GGGCCCCGACAGTGGAGGAGACA-----GTTGTGGCGCGCGCTATATGGCGCG 471
 DB 556 CTTGGCTCACCAGGATCCATGGGACAAATTAATTAATTAATTAATTAATTAATTAATTA 615
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ADB53481

ID ADB53481 standard; DNA; 3736 BP.

XX ADB53481;

XX 04-DEC-2003 (first entry)

Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:4023.

toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;

toxicity marker; toxicity progression; drug screening;

primary rat hepatocyte toxicity modelling; gene; ds.

Rattus norvegicus.

XX WO2003065993-A2.

XX 14-AUG-2003.

XX 04-FEB-2003; 2003WO-US003482.

XX 04-FEB-2002; 2002US-0353171P.

XX 13-MAR-2002; 2002US-0363534P.

XX 08-APR-2002; 2002US-0370248P.

XX 10-APR-2002; 2002US-0371134P.

XX 10-APR-2002; 2002US-0371135P.

XX 10-APR-2002; 2002US-0371150P.

XX 11-APR-2002; 2002US-0371413P.

XX 19-APR-2002; 2002US-0373601P.

XX 19-APR-2002; 2002US-0373602P.

XX 22-APR-2002; 2002US-0374139P.

XX 08-MAY-2002; 2002US-0378370P.

XX 09-MAY-2002; 2002US-0378652P.

XX 09-MAY-2002; 2002US-0378653P.

XX 09-MAY-2002; 2002US-0378655P.

XX 09-JUL-2002; 2002US-0394230P.

XX 09-JUL-2002; 2002US-0394253P.

XX 04-SEP-2002; 2002US-0407688P.

XX 28-JAN-2003; 2003US-0442900P.

XX (GENE-) GENE LOGIC INC.

XX Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Orr M;

XX Elashoff M;

XX WPI; 2003-731472/69.


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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)

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Searched: 3237270 seqs, 2460713050 residues

Total number of hits satisfying chosen parameters: 6474540

Minimum DB seq length: 0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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3	3218	99.0	3857	15	US-10-121-746-19
4	3156	97.0	3355	9	US-09-119-855-1
5	3156	97.0	3355	15	US-10-185-867-1
6	3153	97.0	3249	15	US-10-185-867-3
7	2144	96.7	3240	9	US-09-119-855-3
8	2644.8	81.9	3715	9	US-09-965-830-9
9	884.8	27.2	3064	9	US-09-965-830-5
10	869.8	26.7	3736	9	US-09-965-830-10
11	844.4	26.0	870	9	US-09-119-855-9
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15	761.2	23.4	3321	15	US-10-185-867-17	Sequence 17, Appl
16	761.2	23.4	5107	15	US-10-185-867-15	Sequence 15, Appl
17	572.8	17.6	1626	9	US-09-119-855-6	Sequence 6, Appl
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43	342.8	10.5	3950	17	US-10-696-708-3	Sequence 3, Appl
44	342.8	10.5	4070	13	US-09-795-651-59	Sequence 59, Appl
45	342.8	10.5	4070	17	US-10-483-617-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-09-965-830-1
; Sequence 1, Application US/09965830
; Patent No. US20020177201A1
; GENERAL INFORMATION:
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd
; TITLE OF INVENTION: A novel potassium channel protein
; FILE REFERENCE: Y9903-PCT
; CURRENT APPLICATION NUMBER: US/09/965.830
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 09/600,776
; PRIOR FILING DATE: 2001-07-21
; PRIOR APPLICATION NUMBER: JP P1998-346198
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 12
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; SEQ ID NO 1
; LENGTH: 3323
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6) ..(3257)
US-09-965-830-1

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 3252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
US-10-121-746-19
; Sequence 19, Application US/10121746
; Publication No. US2003003648A1
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. US2003003648A1el Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/10/121,746
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US/09/336,643A
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 3857
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (249)...(3495)
; OTHER INFORMATION: K:Hnov14
US-10-121-746-19

Query Match 99.0%; Score 3218; DB 15; Length 3857;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3244; Conservative 0; Mismatches 5; Indels 3; Gaps 2;

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RESULT 4

US-09-119-855-1
; Sequence 1, Application US/09119855
; Patent No. US20020099197A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Roy A. J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR

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; FILE REFERENCE: mni-055
; CURRENT APPLICATION NUMBER: US/09/119,855
; CURRENT FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO. 1
; LENGTH: 3355
; TYPE: DNA
; ORGANISM: Monkey
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (113)..(3352)
US-09-119-855-1

Query Match
Best Local Similarity 97.0%; Score 3156; DB 9; Length 3355;
Matches 3192; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

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QY 121 CCGTGGGTCTACTGCTCTGATGGCTTCTGTGACCTCAGCGGCTTCTCCCGGGCTGAGGTC 180
Db 224 CCGTGGGTCTACTGCTCTGATGGCTTCTGTGACCTCAGCGGCTTCTCCCGGGCTGAGGTC 283

QY 181 ATGCAGCGGGGTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
Db 284 ATGCAGCGGGGTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 343

QY 241 CAACAGATCCGCAAGCCCTTGACAGACAGCAAGAGTTCAAGGCTGAGTGTCTGTAC 300
Db 344 CAACAGATCCGCAAGCCCTTGACAGACAGCAAGAGTTCAAGGCTGAGTGTCTGTAC 403

QY 301 CGGAAGAGCGGCTCCCGTCTCTGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
Db 404 CGGAAGAGCGGCTCCCGTCTCTGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 463

QY 361 GGGAGGTGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
Db 464 GGGAGGTGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 523

QY 421 GCGCCGACAGATGGAAGAGACAGTGTGTCGCGCGCGCGGATGAGTGTGCGGCGACATCC 480
Db 524 GCGCCGACAGATGGAAGAGACAGTGTGTCGCGCGCGCGGATGAGTGTGCGGCGACATCC 583

QY 481 AAAGGCTTCAATGCAACCGCGCGGAGCGCGGCGGTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
Db 584 AAAGGCTTCAATGCAACCGCGCGGAGCGCGGCGGTCTCTCTCTCTCTCTCTCTCTCTCTCT 643

QY 541 CTGAGAGAGCCCAAGGGCAAGCACAAGTCTCAATAGGGGGTGTGTTGGGAGAGAAACA 600
Db 644 CTGAGAGAGCCCAAGGGCAAGCACAAGTCTCAATAGGGGGTGTGTTGGGAGAGAGCA 703

QY 601 AACTTGCTGAGTCAAGATAGCGCCATCGGAAGTGTGCGGCTCTCTCTCTCTCTCTCTCTCT 660
Db 704 AACTTGCTGAGTCAAGATAGCTGCCATCGGAAGTGTGCGGCTCTCTCTCTCTCTCTCTCTCT 763

QY 661 GGGGCACTGAGAGCCACTCGGATGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
Db 764 GGGGCTGAGGGCCACTCGGATGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 823

QY 721 ACTGTGCCCTACAGGTGTGTGAGCAGCAGCAGGAGCCAGTGTGCGCGCGCGCGCGCG 780
Db 824 ACCGTGCCCTACAGGTGTGTGAGCAGCAGCAGGAGCCAGTGTGCGCGCGCGCGCGCG 883

QY 781 CCCAGGCTCTGTGACCTGGCGGTGGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
Db 884 CCCAGGCTCTGTGACCTGGCGGTGGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 943
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QY 361 GGGAGGTGGCTCTCTTCCTAGTCTCTCAAGAAGCATCAGCGAAACCAGAAACCGAGGG 420
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QY 421 GGGCCCGACAGATGGAAGGACAGAGTGGTGGCGCGCGCGATATGGCGGGCACGATCC 480
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QY 481 AAAGGCTTCAATGCCAACCGCGCGGAGCCGGCGGTGCTCTACACACCTGTCCGGGCAC 540
Db 584 AAAGGCTTCAATGCCAACCGCGCGGAGCGCGGCTGTGCTCTACACACCTGTCCGGGCAC 643
QY 541 CTGCGAAGCAGCCCAAGGGCAAGCAAGCTCAATPAAGGGGTGTGTTGGGAGAAACCA 600
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QY 601 AACTTGGCTGAGTACAAAGTAGCCGCATCCGGAAGTCCGCCCTTCACTCTGTGCACTGT 660
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Db 1004 CACTACGTACACACTGGTTCCTGTGGATGTATCGACGCGCTGCCCTTTGACCTGTGTG 1063
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Db 1064 CATGCTTCAAGGTCAAGTGTACTTCGGGGCCCATCTGCTGAAGACGTGGCGCTGTGTG 1123
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Db 1184 ACATGCTCATGGCGGTGTGCGCTGTGCGCACTGGGTGCGCTGCGTCTGTTTAC 1243
QY 1141 ATTGGCAGCGGGAGATCGAGACAGCGCAATCCGAGCTGCGCTGAGATTGGCTGGCTGAG 1200
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Db 1424 GAGCTGTGGCGCGCGCTGCTGGGACGCGCTTACATCACTCCCTCTACTTCCGACTC 1483
QY 1381 AGCAGCTTACAGCGTGGGTCTCGGCAACGTGTCCGCAACAGCAGCAGCAGCAAGTCTCT 1440
Db 1484 AGCAGCTTACAGCGTGGGTCTCGGCAACGTGTCCGCAACAGCAGCAGCAGCAAGTCTCT 1543
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QY 2521 TTCTCCATCTGACCACTGCTCATCGGCGCCCTGTATGACGAGCGCCCTCCCTGACCGAGAGC 2580

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Db 2684 GGCCTGCTCAGTGTTCCTCCATGGGCCCGGAGGGAAGAACACACACACACTGACACAG 2743
Qy 2641 CTTTGGCAGCGGTGACAGAGCTGTGACAGCAGGTGTGACAGATGGGGAAGACTGACAG 2700
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Qy 2701 TCACCTTCGCGAGGCTGTGACAGCTGTGCTGGGCCCGGACAGAGGAGGTGCTGCTCGG 2760
Db 2804 TCACCTTCGCGAGGCTGTGACAGCTGTGCTGGGCCCGGACAGAGGAGGTGCTGCTCGG 2863
Qy 2761 GCATCGGAGAGGGCGGTGCGACAGCAGCTCTCGGGCTTCTGAGCCTCTGTGTGTG 2820
Db 2864 GCATCGGAGAGGGCGGTGCGACAGCAGCTCTCGGGCTTCTGAGCCTCTGTGTGTG 2923
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Db 2924 GACACTGGGCGATCTCTACTGCTGACGCGCCCGGAGCTGCTCTGTGAGTGGGACT 2983
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Qy 3121 ACTGGAGAGCCCCACAGGCTCAGGGGGCTGCGCTTGGCTTGGCTTGGCTTGGCTTGG 3180
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Qy 3181 GAGATGCTGTATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3240
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Db 3344 ACAGGGGTCTGA 3355

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RESULT 6
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; Sequence 3, Application US/10185867
; Publication No. US20030104429A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, ROY A. J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-055CP
; CURRENT APPLICATION NUMBER: US/10/185,867
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: US/09/358,383
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: USSN 09/119,855
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 3249
; TYPE: DNA
; ORGANISM: Macaca sp.
; FEATURE:
; NAME/KEY: CDS

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; LOCATION: (1)..(3249)
US-10-185-867-3
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Best Local Similarity 98.2%; Pred. No. 0;
Matches 3189; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
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Db 121 CCGCTGCTTACTGCTCTGATGGCTTCTGAGACCTCAACGGGCTTCTCCGGGCTGAGGTC 180
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Qy 481 AAGGCTTCAATGCAACCGGCGGAGCGGCGGCTGTGCTCTACCACTGTCTCGGGGAC 540
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Qy 541 CTGAGAGAGCGGCGGAGGCAAGAGTCAATGAGGGGTGTTTGGGGAGAACCA 600
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Qy 601 AACTTGCTGAGTACAAAGTAGCGCCATCCGGAAGTCCGCTTTCATCTGTGCACTGT 660
Db 601 AACTTGCTGAGTACAAAGTAGCGCCATCCGGAAGTCCGCTTTCATCTGTGCACTGT 660
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QY	1690	GAGCTGCGCGCAGACATCGCCATGCACTGTGCACAAGGAGGTCTCTGCAGCTGCCACTGTTT	1740
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QY	1750	GAGGGCGCCAGCCGGGTGCTGCGGGCACTGTCTCTGGCCCTGCGGCGCGCCCTTCTGC	1809
DB	1741	GAGGGCAGCAGCCGGGTGCTGCGGGCACTGTCTCTGGGCACTGTCTCTGGGCGCTGCGGCGCGCCCTTCTGC	1800
QY	1810	ACGCCGGCGAGTACTCTCATCCACCAAGCGCATGCCCTGCAGGCGCCCTCTACTTTGTCTGCG	1869
DB	1801	ACGCCGGCGAGTACTCTCATCCACCAAGCGCATGCCCTGCAGGCGCCCTCTACTTTGTCTGCG	1860
QY	1870	TCTGGCTCCATGAGAGTGCTCAAGGGTGGCACCGTGTGCGCATCTCTAGGAAAGGGTGAC	1929
DB	1861	TCTGGCTCCATGAGAGTGCTCAAGGGTGGCACCGTGTGCGCATCTCTAGGAAAGGGTGAC	1920
QY	1930	CTGATCGGCTGTGAGCTGCCCGCGGGAGCAGTGTGTAAAGGCCAATGCGGACGTGAAG	1989
DB	1921	CTGATCGGCTGTGAGCTGCCCGCGGGAGCAGTGTGTAAAGGCCAATGCGGACGTGTGAAG	1980
QY	1990	GGGCTGACGTACTGCGTCTCTGCAGTGTCTGCAGTGGCTGCGCTGACGACGAGCTTTCG	2049
DB	1981	GGGCTGACGTACTGCGTCTCTGCAGTGTCTGCAGTGGCTGCGCTGACGACGAGCTTTCG	2040
QY	2050	CTGTACCCCGAGTTTGCCCGCGCTTCAGTGTGGCTCCGAGGGAGCTCAGCTACAAC	2109
DB	2041	CTGTACCCCGAGTTTGCCCGCGCTTCAGTGTGGCTCCGAGGGAGCTCAGCTACAAC	2100
QY	2110	CTGGGTCTCTGGGGAGGCTCTGCAGAGGTGGACACAGCTTCCTTGACGGCGGCAATACC	2169
DB	2101	CTGGGTCTCTGGGGAGGCTCTGCAGAGGTGGACACAGCTTCCTTGACGGCGGCAATACC	2160
QY	2170	CTTATGTCCACGTGTGAGGAAAGGACACAGATGGGGAGCAGGCGCCCAAGTCTCCCCA	2229
DB	2161	CTTATGTCCACGTGTGAGGAAAGGACACAGATGGGGAGCAGGCGCCCAAGTCTCCCCA	2220
QY	2230	GCCCGAGCTGATGAGCCCTTCAGCCCTCTGTCCCTGGCTGCACCTCTCATCTCTCA	2289
DB	2221	GCCCCAGCTGATGAGCCCTTCAGCCCTCTGTCCCTGGCTGCACCTCTCATCTCTCG	2280
QY	2290	GCTGTCCAAAGTGTATCTCCCACTCGAAGCAGCACCGCGCTCGTGTAGGTGCGCAGGG	2349
DB	2281	GCTGTCCAAAGTGTATCTCCCACTCGAAGCAGCACCGCGCTCGTGTAGGTGCGCAGGG	2340
QY	2350	AGGCCAGGCGGCGAGGGCTTTGAAGGCTGAGGCTGGCCCTCTGCTCCCCCAGCGGCC	2409
DB	2341	AGACCAGGCGGCGAGGGCTTTGAAGGCTGAGGCTGGCCCTCTGCTCCCCCAGCGGCC	2400
QY	2410	CTAGAGGGGTACGGCTGCCCCCATGCGAATGTGCGCCCATGATCTGAGCCGCCAGG	2469
DB	2401	CTAGAGGGGTACGGCTGCCCCCATGCGAATGTGCGCCCATGATCTGAGCCGCCAGG	2460
QY	2470	GTAGTAGATGGCAATGAAGACGCTGTGGCTCGGACCGCCCAAGTCTCTTTTCGCGTG	2529
DB	2461	GTAGTAGATGGCAATGAAGACGCTGTGGCTCGGACCGCCCAAGTCTCTTTTCGCGATG	2520
QY	2530	GGCCAGTCTGGCCCGGAATGTAGCAGCAGCCCTCCCTTGGACCGAGAGCGGCTGTCTC	2589
DB	2521	GGCCAGTCTGGCCCGGAATGTAGCAGCAGCCCTCCCTTGGACCGAGAGCGGCTGTCTC	2580
QY	2590	ACTGTTTCCCCATGGGCGCCAGGAGGCAAGAACACAGACACTGGAACAAGCTTCGGCAG	2649
DB	2581	ACTGTCCCCCATGGGCGCCAGCGAGGCAAGGAACACAGACACTGGAACAAGCTTCGGCAG	2640
QY	2650	CGCGTCACAGCTGTTCAGACAGGCTGTGCAGATGCGGGAGGACTGCAGTCACTTTCG	2709
DB	2641	CGCGTCAGTGCAGCTGTTCAGAACAGGCTGTGCAGATGCGGGAGGACTGCAGTCACTTTCG	2700
QY	2710	CAGGCTGTGCAGCTTGTCTCTGGCGCCCAACAGGAGGGGTCCGCTCGGCACTCGGGA	2769
DB	2701	CAGGCTGTGCAGCTTGTCTCTGGCAACCCCATAGGGAGGTTCCATGCCCTCGGGCTCAGGA	2760
QY	2770	GAGGGCGGTGCCACCCAGCACTCCGGGCTTTCGACGCTCTGTGTGTGGACACTGGG	2829

Db	2761	GAGGGGCCATGCCAGCAGACCTCGGGCTTCTGAGCCTCTGTGTGTGGACACTGGG	2820
QY	2830	GCATCTCTACTGAGCCCCAGCTGGCTCTGCTTGTAGTGGGACATTGCCCCAC	2889
Db	2821	GCATCTCTACTGAGCCCCAGCTGGCTCTGCTTGTAGTGGGACATTGCCCCAC	2880
QY	2890	CCTGTCGGGGCTCTCTCCCTCATGGACCTCTGGCCCTGGGTCCTCCAGCGTCTCAG	2949
Db	2881	CCTGTCGGGGCTCTCTCCCTCATGGACCTCTGGCCCTGGGTCCTCCAGCATCTCAG	2940
QY	2950	AGTCCCCCTTGGCTCGAGCCACAGCTTCTTGGACCTTCACCTCAGACTCAGAGCCCTC	3009
Db	2941	AGTCCCCCTTGGCTCGAGCCACAGCTTCTTGGACCTTCACCTCAGACTCAGAGCCCTC	3000
QY	3010	GGCTCAGGAGACCTCTGCTCGAGCCAGACCCCTGCCTCCCTCTCTCTCTGAGGAA	3069
Db	3001	GGCTCAGGAGACCTCTGCTCGAGCCAGACCCCTGCCTCTCTCTCTGAGGAA	3060
QY	3070	GGGGCTAGGACTGGGGCCGAGACCTTGTAGCCAGAGCTGAGGCTACCGACTGGAGAG	3129
Db	3061	GGGGCTAGGACTGGGGCCGAGACCTTGTAGCCAGAGCTGAGGCTACCGACTGGAGAG	3120
QY	3130	CCCCACACAGGTCAGGGGGCTTGGCCCTTGGCCCTGGGACCCGACAGCTTGAGATGGTG	3189
Db	3121	CCCCCGCAGTGTGAGGGGGCTTGGCCCTTGGCCCTGGGACCCGACAGCTTGAGATGGTG	3180
QY	3190	CTTATTGGCTGCCATGGCTCTGGGCACAGTCCAGTGGACCCAGAGAAAGGCACAGGGTC	3249
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RESULT 8
 US-09-965-830-9
 ; Sequence 9, Application US/09965830
 ; Patent No. US20020177201A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
 ; TITLE OF INVENTION: A novel potassium channel protein
 ; FILE REFERENCE: Y9903-PCT
 ; CURRENT APPLICATION NUMBER: US/09/965,830
 ; CURRENT FILING DATE: 2001-10-01
 ; PRIOR APPLICATION NUMBER: 09/600,776
 ; PRIOR FILING DATE: 2001-07-21
 ; PRIOR APPLICATION NUMBER: JP P1998-346198
 ; PRIOR FILING DATE: 1998-12-04
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 9
 ; LENGTH: 3715
 ; TYPE: DNA
 ; ORGANISM: Rattus sp.
 ; US-09-965-830-9

	Query Match	81.9%;	Score 2664.8;	DB 9;	Length 3715;
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Qy	61	CGCTTCGACGGCAGCAGTAGTAATCTTGCTGGGCAACGCCCAAGTCGGGGCTCTTTC	120		
Db	216	CGCTTCGACGGGACGACAGTAATCTTGCTGGGCAACGCCCAAGTCGAGGGCTCTTC	275		
Qy	121	CCCGTGGTCTACTGCTCTCATGGCTTCTGTGACCTTCACGGGCTTCTCCCGGGCTGAGTTC	180		
Db	276	CCGTGCTGTCTACTGCTCCGATGGCTTCTGTGACCTTCA CGGGTTTCTCAGAGCTGAGTTC	335		
Qy	181	ATGCAGGGGGCTGTGCTGCTCTCTTTATGGGCCAGACACAGTGAAGTCGTCCGC	240		
Db	336	ATGCAGGAGGCTGTGCTGCTCTCTTCTATGGGCCAGACACAGTGAAGTGTGTCGC	395		

QY	241	CAACAGATCCGACGAGCCCTGACGAGCAACAGGAGTTCAAGGCTGAGTGTATCTCTGTAC	300
Db	396	CAACAGATCCGAAAGCCCTGGATGAGCAAAAGAAATTCAGGCTGATGATCTCTGTAC	455
QY	301	CGGAAGAGCGGGCTCCCGTTCTGTTCTCTCTGATGTGATACCCATAAAGAAATGAGAAA	360
Db	456	CGGAAGAGCGGGCTCCATCTCTGTTCTCTCTGATGTGATACCTATAAAGAAACGAGAAG	515
QY	361	GGGAGGTTGGCTCTCTCTGATGTCTCTCAAGAGCATCAGCGAAACCAAGAACCGAGG	420
Db	516	GGGAGGTTGGCTCTCTCTGATGTCTCTCAAGAGCATCAGTGAGCAACCAAGAACCGAGGA	575
QY	421	GGCCCCGACAGATGGAAGGAGACAGGTGTGGCGCGCATATGGCGGGGACCATCC	480
Db	576	GGCCCCGACAACTGGAAGGAGAGAGGTGTGGCGCGCATATGGTGGGCGAGATCC	635
QY	481	AAAGGCTTCAATGCCAAACCGCGCGGAGCCGGGCGGTGTCTTACCACTGTCTCGGGCAC	540
Db	636	AAAGGCTTAAATGCCAAATCGAGGCGCGAGCGCGGCGGTCTCTTACCACTCTCTGGTCC	695
QY	541	CTGCAAGAGCGCCCAAGGCGAGCAACAGCTCAATAGGGGGTGTGGGAGAGAACCA	600
Db	696	CTGCAAGAACCAACCAAGGCGAGCAACAACTCAATAGGGGTGTGGGAGAGAACCA	755
QY	601	AACCTTGCTGAGTACAAAGTAGCGCCCATCCGGAAGTGGCGCTTCACTCTGTGTGCACTGT	660
Db	756	AAATTTGCCGAAATAAAGTCTGTCTATCGGAAGTCACTCTTATCTCTGTGCACTGT	815
QY	661	GGGGCACTGAGAGCACCTGGATGTGCTTCACTCTGTCTGCGCACACTCTATGTGGCTGT	720
Db	816	GGGGCTCTGAGAGCACCTGGATGTGCTTCACTCTGTCTGCGCACACTCTAGTGGCTGT	875
QY	721	ACTGTGCCCTACAGCGTGTGTGACACAGCAGCGAGCCCGAGTGGCGCGCGGCGCG	780
Db	876	ACTGTGCCCATACAGCGTGTGTGACACAGCAGCGAGCCCGAGTGGCGCGCGGCGCG	935
QY	781	CCAGCGCTGTGACCTGGCGGTGGAGTCTCTTCACTCTGATGATGTGCTGAATTT	840
Db	936	CTTATGTGTGTGACCTGGCGGTGGAGTCTCTTCACTCTAGATATGTGCTGAATTT	995
QY	841	CGTACCACTTGTGTCAAGTGGCGGCAAGTGTGTGTGGCCCAAGTCAATTTGGCTC	900
Db	996	GGTACTACTTGTGTCAAGTCAAGGCGAGTGTGTGTGGCCCAAGTCAATTTGGCTC	1055
QY	901	CACCTAGTCACTGTTCTGTGTGATGTCTATCGCAGCGTCCCTTTGACTGCTA	960
Db	1056	CACCTAGTCACTGTTCTGTGTGATGTCTATCGCAGCACTGCCCCCTTTGACTGCTA	1115
QY	961	CATGCTTCAAGGTCAACGTGTACTTGGGGCCCATCTGCTGAAGACGCTGCGCTGCTG	1020
Db	1116	CATGCTTCAAGGTCAATGTGTACTTGGGGCTCACCTACTGAAGACGCTGCGCTGCTT	1175
QY	1021	CGCTGTGCGCTGCTTCCGGGCTGACCGGTAATCGGATCTCGAGTACAGCGCGCTGCTG	1080
Db	1176	CGGCTGTGCGCTTACTACCAAGACTGGACCGGTACTCTCAGTATAGCGCTGTTGTGCTC	1235
QY	1081	ACACTGCTCATGGCGGTGTGGCCCTGCTCGGCACTGGGTGCGCTGCTGCTGTTTAC	1140
Db	1236	ACCTGTGCTATGGGTGTGTGGCCCTGCTCGCCCACTGGGTGGCGCTGCTGTTTCTAC	1295
QY	1141	ATTGGCCAGCGGAGATCGAGAGCAGCGAAATCCGAGCTGCTGAGATTTGGCTGGTGCAG	1200
Db	1296	ATGGCCAGCAAGAGATTGAGACAGCGAGTCAGAGTGCCTGAGATCGGCTGGCTGCAG	1355
QY	1201	GAGTGGCGCGCGACTGGAGCTCCCTACTACTGTGTGGCGGAGCGGCGAGCTGGAGG	1260
Db	1356	GAGTGGCGCGCGAGCTGGAGCGCCCTATTACTGTGTGAGCGGAGTCCAGATGGAGG	1415
QY	1261	ACAGCTCGGCGAGGTGACAACTGACGACGCA-----GCAGCGAGCCCAACGGG	1311
Db	1416	AACAGCTTGGCCAGAGTGAANAATGCAAGTAGCAGTGGCGGCGGAGCGCAACGGG	1475
QY	1312	ACGGGGCTGGAGCTGCTGGGGCGCGCTGCTGGCGAGCGCTTACATCACCTCCCTCTAC	1371
Db	1476	ACTGGGCTGGAGCTGCTGGGTGGCGCCATCCCTACGAGCGCTTACATCACCTCTGTAC	1535
QY	1372	TTTCGCACTCAGCAGCTCACCAGCGTGGGCTTCGGCAAGTGTCCGCCCAACACGACAC	1431
Db	1536	TTTCGCGCTCAGCAGCTCACCAGTGTGGGCTTCGGCAATGTGTCCGCTAACACAGACT	1595
QY	1432	GAGAAGATCTTCTCCATCTGCACCAATGCTCATCGGCGCCCTGATGACCGGGTGTGTTT	1491
Db	1596	GAGAAGATTTTCTCCATCTGCACCAATGCTTATTTGGAGCTCTGATGATGAGTGTGTTT	1655
QY	1492	GGGAAGCTGACGGCGATCATCCAGCGCATGTAGCGCGCGCTTCTGTACCAACAGCGC	1551
Db	1656	GGGAATGTGACAGCCATCATCCAGCGCATGTAGCTCGCGGCTTCTGTACCAACAGCGC	1715
QY	1552	ACGCGGACTCGCGCACTACATCCGATCCACCGTATCCCAAGCCCTTCAAGCAGCGC	1611
Db	1716	ACCGTGAACCTGGAGACTACATTCGATCCACCGCATCCCAAGCCCTTCAAGCAGCGC	1775
QY	1612	ATGCTGGAGTACTTTCAGGCGCACTGGGGGTGAAACAAATGGCATTCGACACCCAGAGCTG	1671
Db	1776	ATGCTGGAGTACTTTCAGGCGCACTGGGGGTGAAACAAACGSCATTCGATACCTGAGCTG	1835
QY	1672	CTGCAAGCTCCTGACGAGCTCGCGAGCATCGCATGACCTGCACCAAGGAGGTC	1731
Db	1836	CTGCAAGCTTTCGGATGAGCTTCGAGCAGACATCGCATGACCTGCACCAAGGAGGTC	1895
QY	1732	CTGCAAGCTGCACTGTTTGAAGCGCGCAGCGCGGCTGCTGCGGGCACTGTCTTGCC	1791
Db	1896	CTGCAAGCTGCACTGTTTGAAGCGCAGCGCGGCTGCTGCGGGCACTGTCTTGCC	1955
QY	1792	CTGCGGCCCTTCTGACCGCGGCGAGTACTTATTCACCAAGCGAGTCTCTCCAG	1851
Db	1956	CTGAGGCCCTTCTGACCGCGGCGAGTACTTATTCACCAAGCGAGTCTCTCCAG	2015
QY	1852	GCCTCTACTTGTCTGCTCTGCTCCATGAGGTGCTCAAGGTGTCACCGTCTGCGC	1911
Db	2016	GCTCTCTACTTGTGTGCTCAGGTTCCATGGAGTCTCTCAAGGTGTCACCGTCTGCGC	2075
QY	1912	ATCCTAGGAGGCGGCACTGATCGGCTGTGAGCTGCGCGCGGCGGAGCGTGGTAAAG	1971
Db	2076	ATCCTAGGAGGCGGCACTGATCGGCTGTGAGCTGCGCGCGGCGGAGCGTGGTAAAG	2135
QY	1972	GCCAAATGCCAGCTGAAGAGGCTGACGTACTGCTCTGAGTGTCTGACGCTGGCTGGC	2031
Db	2136	GCCAAATGCCAGCTGAAGAGGCTGACGTACTGCTCTGAGTGTCTGACGCTGGCTGGC	2195
QY	2032	CTGCAACGACGCTTGGCTGACCCCGAGTTCGCCCGCGCTTCAGTCTGCTGCGC	2091
Db	2196	CTGCAACGAGGCTTGGCTGACCCCTGAGTTCGCCCGCGCTTCAGTCTGCTGCGC	2255
QY	2092	GGGAGGCTCAGCTAACCTGGGTGCTGGGGAGGCTCTGAGAGGTGGACACCAAGCTCC	2151
Db	2256	GGGAGGCTCAGCTAACCTGGGTGCTGGGGAGGCTCTGAGAGGTGGACACCAAGCTCA	2315
QY	2152	CTGAGCGCGCAATACCTTATGTCTCAAGTGTGAGAGAGGAGACAGATGGGGAGAG	2211
Db	2316	CTGAGTGTGCAACACCTTATGTCTCACTGGAGGAGAGGAGACAGATGGGGAGAG	2375
QY	2212	GGCCCCAGGCTTCCAGCGCCAGCTGATGAGCGCTCCAGCGCCCTGCTGCTGCGCTGGC	2271
Db	2376	GGACACAGATCTTCCAGCGCCAGCTGATGAGCGCTCCAGCGCCCTGCTGCTGCGCTGGC	2435
QY	2272	TGCACCTCTCATCTCAGCTGCCAAGCTGTATCCCACTGCGAAGACAGCCCGGCT	2331
Db	2436	TGTACCTCTCTCTCTCAGCGCCCAAACTACTCTCTCCCACTGCAACTGCAACCGGCGG	2495
QY	2332	CGTCTAGTGGAGAGGAGCGCAGCGAGGCTTTTGAAGCTTGAAGCTGAGCTGCGCC	2391
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QY 2512 AAGTTCTTTCGCGTGGGCCAGTCTGGCCCGGAATGTAGCAGCAGCCCTCCCTGGA 2571
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QY 3109 GAGGCTACGACTGAGAGGCGCCCGACAGGCTCAGGGGCGCTGGCTTGGCTTGGGAC 3168
Db 3276 GAGGCTACGACTGAGAGGCGCCCGACAGGCTCAGGGGCGCTGGCTTGGCTTGGGAT 3335
QY 3169 CCCACAGCTTGGAGATGGTGTCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3228
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QY 3229 CAGGAAGAGGACAGGGGCTCTGA 3252
Db 3396 CAGGAGGAGGACAGGAGTCTGA 3419
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RESULT 9

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US-09-965-830-5
; Sequence 5, Application US/09965830
; Patent No. US20020177201A1
; GENERAL INFORMATION:
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: A novel potassium channel protein
; FILE REFERENCE: Y9903-PCT
; CURRENT APPLICATION NUMBER: US/09/965,830
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 09/600,776
; PRIOR FILING DATE: 2001-07-21
; PRIOR APPLICATION NUMBER: JP P1998-346198
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; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 3064
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(3057)
US-09-965-830-5
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Query Match

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Best Local Similarity 27.2%; Score 884.8; DB 9; Length 3064;
Matches 1408; Conservative 0; Mismatches 622; Indels 120; Gaps 3;
QY 1 ATGCCCGCCATGCGGGGCTCTCTGGCGCTCAGAACACCTTCTGTCGACACCATCGCTACG 60
Db 4 ATGCCCGCTCATGAGGGGTTGCTGGCCCGCAACACCTTCTGTCGACACCATCGCCACC 63
QY 61 CGCTTCGACGGCAGCAGCAGTAATCTGCTGGGCAACCGCCAGGTGGCGGCTCTTC 120
Db 64 CGTTTGAAGCAACGACAGCACTTCTGCTGGCCAAACGACAGGCGCACGCGGCTTT 123
QY 121 CCCTGTGCTACTGCTGATGGCTTCTGTGACCTCAGGGCTTCTCCGGGCTGAGGTC 180
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QY 181 ATGCAAGCGGGGCTGCTCTCTCTCTTATGGCCAGACACCATGAGTGGCTCGCCGC 240
Db 184 ATGCAAGAGACCTGAGCTGCGGTTCTCTACGCGCCAGAGACCATGAGCAGCCCTG 243
QY 241 CACAGATCCGCAAGGCTTGAACGAGCAGCAAGAGTTCAAGGCTGAGTGTATCTGTAC 300
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QY 301 CGGAGAGGGGCTCCCGTCTGCTGCTCTGCTGATGTATACCATTAAGATGAGAAA 360
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QY 415 CGAGGGGCGCCGACAGATGGAAGAGAGACAGTGGTGGCGCGCGATATGGCGGGCA 474
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QY 475 CGATCCAAAGGCTTCAATGCGCAACCGGGCGGAGCGCGGCGGTCTCTACCATGTCC 534
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QY 535 GGGCAGCTTGCAGAGAGCGCCCAAGGCAAGCACAAGCTCAATAAGGGGCTCTTTGGG 594
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QY 595 AAACCAAACTTGTCTGAGTACAAAGTAGCCGCAATCCGGAAGTCCGCTTCTCATCTG 654
Db 604 AAGCATCATGCGCGAGTACAAAGTGGCTCTCGTGGGGGCTCTCGTCTCTCTCTCT 663
QY 655 CACTGTGGGCACTGAGAGGCACTGGGATGGCTTCTCTCTCTCTCTCTCTCTCTCTCT 714
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QY 715 GCTGTCACTGTGCCCTACAGCGTGTGTGAGCAGCAGCAGGAGCGGAGCGGCGCCGC 774
Db 724 GCGGTACCGTCCCTTACATGTCTGTTCTCGGTGAGGATGAGACCGCCCATCACTTC 783
QY 775 GGGCGGCGGAGCTGTGTACCTGGCGTGGAGGTCTCTTCTCTCTCTCTCTCTCTCT 834
Db 784 CGACACACCTTGTGAGCGACATCGCGGTGAAATGCTCTTCTCTCTCTCTCTCTCT 843
QY 835 AATTTCCGTACCACTCTGCTGTCAGTGGGCGAGGTGGTGTGTTGTTGTTGTTGTTG 894
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QY 472 GCAGATCCAAAGCTTCAATGCCAACCGCGCGGAGCGCGCGTGTCTTACCCAGCTG 531
Db 616 GGAGCTAGCTCAAGACTTAGTGTCCACGAGGAGGAGAAACGGACAGTTCTACACCGGTG 675
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Db 676 ACTGGCCATTGTGTGCGCGGAGACCGAGGAAGCGTGAAGGCCAATAGTAACGTTGTGAG 735
QY 592 GAGAAACCAAACTTGCCTGAGTACAAAGTAGCCGCATCCGGAAGTCGCCCTTCACTCG 651
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QY 772 CGCGCCCGCCAGGGTCTGTGACCTGGCGCGTGGAGGTCTTCTTCACTTGCACATTGG 831
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Db 1386 ----- 1385
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QY 1372 TTCCACTACGACGCTCACAGCGTGGGCTTCGGCAACGTGTCCGCCAACACGACAC 1431
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QY 1552 ACGCGGACCTGGCGACTAATCCGCATCCACCGTATCCCAAGCCCTCAAGCAGCG 1611
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Db 1972 ATCTTGAAGAGGGGCACTTGTGCTGCGGAGATCTTCTGCTGCTGCTGCTGCTGCTGCT 2031
QY 1963 -----GTGTAAGGCCAATGCCAGCTGAAAGGGCTGACGTACTGCGTC 2007
Db 2032 GCAGGGCGAGGCTGCTGCTGAAGACCGAGCGCTGATGTGAAGCACTGACTTACTGCGC 2091
QY 2008 CTGCAGTGTCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2067
Db 2092 CTGCAGCAGCTGAGCAGCGGCGTGGCGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 2151
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RESULT 11

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US-09-119-855-9
; Sequence 9, Application US/09119855
; Patent No. US20020099197A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A. J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: mmi-055
; CURRENT APPLICATION NUMBER: US/09/119,855
; CURRENT FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 9
; LENGTH: 870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(870)
US-09-119-855-9
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Query Match 26.0%; Score 844.4; DB 9; Length 870;
Best Local Similarity 99.9%; Pred. No. 1.4e-204;
Matches 845; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 ATGCGCGCCATCGGGGCTCTGCGGCTCAGAACCTTCTTGGACACCATCGCTACG 60
Db 1 ATGCGCGCCATCGGGGCTCTGCGGCGCGGAGAACCTTCTTGGACACCATCGCTACG 60
QY 61 CGCTTCGACGGCAGCAGTAACTTCTGCTGCGGCAACGCCAGGTGGCGGGCTCTTC 120
Db 61 CGCTTCGACGGCAGCAGTAACTTCTGCTGCGGCAACGCCAGGTGGCGGGCTCTTC 120
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841 CGTACC 846
841 CGTACC 846

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US-10-185-867-9
; Sequence 9, Application US/10185867
; Publication No. US20030104429A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A. J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-055CP
; CURRENT APPLICATION NUMBER: US/10/185,867
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: US/09/358,383
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: USN 09/119,855
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 870
; TYPE: DNA
; ORGANISM: Homo sapiens

FEATURE:
NAME/KEY: CDS
LOCATION: (1)... (870)
US-10-185-867-9
Query Match 26.0%; Score 844.4; DB 15; Length 870;
Best Local Similarity 99.9%; Pred. No. 1.4e-204;
Matches 845; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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61 CGCTTCAGCGCACGACAGTAACTTCCTGCTGGCAACGCCAGCTGGCGGCTCTTC 120
61 CGCTTCAGCGCACGACAGTAACTTCCTGCTGGCAACGCCAGCTGGCGGCTCTTC 120
121 CCGCTGCTCTACTGCTCTGATGGCTTCTGCTGACCTCACGGGCTTCTCCGGGCTGAGGTC 180
121 CCGCTGCTCTACTGCTCTGATGGCTTCTGCTGACCTCACGGGCTTCTCCGGGCTGAGGTC 180
181 ATGACGCGGGCTGCTGCTGCT 240
181 ATGACGCGGGCTGCTGCTGCT 240
241 CAACAGATCCGAAGGCCCTTGACAGAGCAACAGAGTTCAGAGTGTGATCCATGATGAT 300
241 CAACAGATCCGAAGGCCCTTGACAGAGCAACAGAGTTCAGAGTGTGATCCATGATGAT 300
301 CGGAAGAGCGGGCTCCGCTTCTGCTGCTCTCTGATGATGATCCATGATGATGATGATGAT 360
301 CGGAAGAGCGGGCTCCGCTTCTGCTGCTCTCTGATGATGATCCATGATGATGATGATGAT 360
361 GGGAGGTGCT 420
361 GGGAGGTGCT 420
421 GGGCCGACAGATGGAAGGAGACAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
421 GGGCCGACAGATGGAAGGAGACAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
481 AAAGGCTTCAATGCCAAACCGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540
481 AAAGGCTTCAATGCCAAACCGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540
541 CTGAGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600
541 CTGAGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600
601 AACTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
601 AACTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
661 GGGGCACTGAGAGCACTGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
661 GGGGCACTGAGAGCACTGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
721 ACTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
721 ACTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
841 CGTACC 846
841 CGTACC 846

RESULT 13
US-09-119-855-7
; Sequence 7, Application US/09119855

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; Patent No. US20020099197A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: mni-055
; CURRENT APPLICATION NUMBER: US/09/119,855
; CURRENT FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1132
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (263)..(1132)
US-09-119-855-7

Query Match      26.0%; Score 844.4; DB 9; Length 1132;
Best Local Similarity 99.9%; Pred. No. 1.4e-204;
Matches 845; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCGGGCCATGCGGGGCTCTCGGCGCTCAGAACACCTTCTCGGACACCATCGCTACG 60
DB 263 ATGCGGGCCATGCGGGGCTCTCGGCGCGGAGAACACTTCTCGGACACCATCGCTACG 322
QY 61 CGCTTCGACGGACGACAGTAACCTTCTGTGGGCAACGCCAGGTGCGGGGCTCTTC 120
DB 323 CGCTTCGACGGACGACAGTAACCTTCTGTGGGCAACGCCAGGTGCGGGGCTCTTC 382
QY 121 CCCGTGGTCTACTGCTCTGATGGCTTCTGACCTCAGGCTTCTCCGGGCTGAGGTC 180
DB 383 CCCGTGGTCTACTGCTCTGATGGCTTCTGACCTCAGGCTTCTCCGGGCTGAGGTC 442
QY 181 ATGCGGGGCTGTGCTGCTCTCTTCTTATGGGCGACACACAGTGAGCTGCTCGC 240
DB 443 ATGCGGGGCTGTGCTGCTCTCTTCTTATGGGCGACACACAGTGAGCTGCTCGC 502
QY 241 CAACAGATCCGACAGGCTTGGACGAGCAAGAGTTCAAGGTGAGCTGATCTGTAC 300
DB 503 CAACAGATCCGACAGGCTTGGACGAGCAAGAGTTCAAGGTGAGCTGATCTGTAC 562
QY 301 CGGAAGAGCGGCTCCCGTCTCTGTGTCTCTGTGATGTATACCATTAAGAAATGAGAAA 360
DB 563 CGGAAGAGCGGCTCCCGTCTCTGTGTCTCTGTGATGTATACCATTAAGAAATGAGAAA 622
QY 361 GGGGAGGTGGCTCTCTTCTTAGTCTCTCAAGAGACATCAGCGAAACCAAGAACCGAGGG 420
DB 623 GGGGAGGTGGCTCTCTTCTTAGTCTCTCAAGAGACATCAGCGAAACCAAGAACCGAGGG 682
QY 421 GGCCCCGACAGATGGAAGGAGACAGGTGGTGGCGCGCGATATGCGCGGACGATCC 480
DB 683 GGCCCCGACAGATGGAAGGAGACAGGTGGTGGCGCGCGATATGCGCGGACGATCC 742
QY 481 AAAGGCTTCAATGCCAACCGGCGGAGCGGGCGGTGCTTCTACACCTGTTCGGGCGAC 540
DB 543 AAAGGCTTCAATGCCAACCGGCGGAGCGGGCGGTGCTTCTACACCTGTTCGGGCGAC 600
QY 541 CTGCAAGAGCGCCCAAGGGCAAGCAAGCTCAATAGGGGGTGTGTTGGGAGAACCA 660
DB 803 CTGCAAGAGCGCCCAAGGGCAAGCAAGCTCAATAGGGGGTGTGTTGGGAGAACCA 862
QY 601 AACTTGCTGAGTCAAGAGTACCGCCATCCGGAAGTCGCGCTTCTATCTGCTGCTGTC 660
DB 863 AACTTGCTGAGTCAAGAGTACCGCCATCCGGAAGTCGCGCTTCTATCTGCTGCTGTC 922
QY 661 GGGGCACTGAGAGCACTGGGATGGCTTCTCTGCTCGCCACACTCTATGTGGCTGTC 720
DB 923 GGGGCACTGAGAGCACTGGGATGGCTTCTCTGCTCGCCACACTCTATGTGGCTGTC 982
QY 721 ACTGTGCTTACAGGCTGTGTGAGCAGCAGCAAGGAGCCAGTGGCGCCCGGCGCG 780
DB 983 ACTGTGCTTACAGGCTGTGTGAGCAGCAGCAAGGAGCCAGTGGCGCCCGGCGCG 1042
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QY 781 CCAGCGCTCTGTGACCTGGCCGTGGAGGTCTCTTCTATCTTGCATGTGCTGAATTC 840
DB 1043 CCAGCGCTCTGTGACCTGGCCGTGGAGGTCTCTTCTATCTTGCATGTGCTGAATTC 1102
QY 841 CGTACC 846
DB 1103 CGTACC 1108
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RESULT 14
US-10-185-867-7
; Sequence 7, Application US/10185867
; Publication No. US20030104429A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-055CP
; CURRENT APPLICATION NUMBER: US/10/185,867
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: US/09/358,383
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: USSN 09/119,855
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1132
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (263)..(1132)
US-10-185-867-7
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Query Match      26.0%; Score 844.4; DB 15; Length 1132;
Best Local Similarity 99.9%; Pred. No. 1.4e-204;
Matches 845; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCGGGCCATGCGGGGCTCTCGGCGCTCAGAACACCTTCTCGGACACCATCGCTACG 60
DB 263 ATGCGGGCCATGCGGGGCTCTCGGCGCGGAGAACACTTCTCGGACACCATCGCTACG 322
QY 61 CGCTTCGACGGACGACAGTAACCTTCTGTGGGCAACGCCAGGTGCGGGGCTCTTC 120
DB 323 CGCTTCGACGGACGACAGTAACCTTCTGTGGGCAACGCCAGGTGCGGGGCTCTTC 382
QY 121 CCCGTGGTCTACTGCTCTGATGGCTTCTGACCTCAGGCTTCTCCGGGCTGAGGTC 180
DB 383 CCCGTGGTCTACTGCTCTGATGGCTTCTGACCTCAGGCTTCTCCGGGCTGAGGTC 442
QY 181 ATGCGGGGCTGTGCTGCTCTCTTCTTATGGGCGACACACAGTGAGCTGCTCGC 240
DB 443 ATGCGGGGCTGTGCTGCTCTCTTCTTATGGGCGACACACAGTGAGCTGCTCGC 502
QY 241 CAACAGATCCGACAGGCTTGGACGAGCAAGAGTTCAAGGTGAGCTGATCTGTAC 300
DB 503 CAACAGATCCGACAGGCTTGGACGAGCAAGAGTTCAAGGTGAGCTGATCTGTAC 562
QY 301 CGGAAGAGCGGCTCCCGTCTCTGTGTCTCTGTGATGTATACCATTAAGAAATGAGAAA 360
DB 563 CGGAAGAGCGGCTCCCGTCTCTGTGTCTCTGTGATGTATACCATTAAGAAATGAGAAA 622
QY 361 GGGGAGGTGGCTCTCTTCTTAGTCTCTCAAGAGACATCAGCGAAACCAAGAACCGAGGG 420
DB 623 GGGGAGGTGGCTCTCTTCTTAGTCTCTCAAGAGACATCAGCGAAACCAAGAACCGAGGG 682
QY 421 GGCCCCGACAGATGGAAGGAGACAGGTGGTGGCGCGCGATATGCGCGGACGATCC 480
DB 683 GGCCCCGACAGATGGAAGGAGACAGGTGGTGGCGCGCGATATGCGCGGACGATCC 742
QY 481 AAAGGCTTCAATGCCAACCGGCGGAGCGGGCGGTGCTTCTACACCTGTTCGGGCGAC 540
DB 543 AAAGGCTTCAATGCCAACCGGCGGAGCGGGCGGTGCTTCTACACCTGTTCGGGCGAC 600
QY 541 CTGCAAGAGCGCCCAAGGGCAAGCAAGCTCAATAGGGGGTGTGTTGGGAGAACCA 660
DB 803 CTGCAAGAGCGCCCAAGGGCAAGCAAGCTCAATAGGGGGTGTGTTGGGAGAACCA 862
QY 601 AACTTGCTGAGTCAAGAGTACCGCCATCCGGAAGTCGCGCTTCTATCTGCTGCTGTC 660
DB 863 AACTTGCTGAGTCAAGAGTACCGCCATCCGGAAGTCGCGCTTCTATCTGCTGCTGTC 922
QY 661 GGGGCACTGAGAGCACTGGGATGGCTTCTCTGCTCGCCACACTCTATGTGGCTGTC 720
DB 923 GGGGCACTGAGAGCACTGGGATGGCTTCTCTGCTCGCCACACTCTATGTGGCTGTC 982
QY 721 ACTGTGCTTACAGGCTGTGTGAGCAGCAGCAAGGAGCCAGTGGCGCCCGGCGCG 780
DB 983 ACTGTGCTTACAGGCTGTGTGAGCAGCAGCAAGGAGCCAGTGGCGCCCGGCGCG 1042
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Db 743 AAAGGCTTCAATGCCAACCGGCGGAGCGCGCGTCTCTACCACTGTCCGGGCAC 802
Qy 541 CTGCAGAACGCCCAAGCGGACACAGCTCAATAAGGGGTGTTTGGGGAGAACCA 600
Db 803 CTGCAGAACGCCCAAGCGGACACAGCTCAATAAGGGGTGTTTGGGGAGAACCA 862
Qy 601 AACTTCGCTGAGTACAAAGTAGCCGCATCCGGAAGTCGCCCTTCTATCTCTGTCAGTGT 660
Db 863 AACTTCGCTGAGTACAAAGTAGCCGCATCCGGAAGTCGCCCTTCTATCTCTGTCAGTGT 922
Qy 661 GGGGCACTGAGACGCCACCTGGGATGCTTCATCTCTGTCGACACACTCTATGTCGCTGTC 120
Db 923 GGGGCACTGAGACGCCACCTGGGATGCTTCATCTCTGTCGACACACTCTATGTCGCTGTC 982
Qy 721 ACTGTGCTTACAGCGTGTGTGTGACACAGCAGCGGAGCCAGTGCAGCGCCGCCGCCG 780
Db 983 ACTGTGCTTACAGCGTGTGTGTGACACAGCAGCGGAGCCAGTGCAGCGCCGCCGCCG 1042
Qy 781 CCCAGCGCTGTGACCTGGCGGTGGAGTCTCTTCTATCTCTGACATTTGCTGAATTC 840
Db 1043 CCCAGCGTGTGACCTGGCGGTGGAGTCTCTTCTATCTCTGACATTTGCTGAATTC 1102
Qy 841 CGTACC 846
Db 1103 CGTACC 1108

RESULT 15
US-10-185-867-17
; Sequence 17, Application US/10185867
; Publication No. US20030104429A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A. J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MN-055CP
; CURRENT APPLICATION NUMBER: US/10/185,867
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: US/09/358,383
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: US/09/119,855
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 3321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3321)
US-10-185-867-17

Query Match 23.4%; Score 761.2; DB 15; Length 3321;
Best Local Similarity 62.2%; Pred. No. 2.3e-183;
Matches 1319; Conservative 0; Mismatches 708; Indels 93; Gaps 4;

Qy 1 ATGCGGCGCATGCGGGGCTCTCTGCGCTCAGAACACTTCTCTGGACACCATCCTCTACG 60
Db 1 ATGCGGCTATGAAGGATTTACTGGCGCGGAACACACTTCTCTGGACACCATCCTCCACC 60
Qy 61 CGCTTCGACGCGCAGCAGTAATCTGTGTGGGCAACGCCAGCGGCGGCTCTTC 120
Db 61 CGTTTTGACGGAACACATAGCAACTTCTCTTCCATGCAATGCGGAGTGGCTGAAGGTTTC 120
Qy 121 CCCGTGGTCTACTGCTGTGAGGCTCTGTGACCTCAGGGCTCTCCGGGCTCAGATC 180
Db 121 CCCATAGTCTACTGCTTCGATGGCTTCTGCGAGCTTGTGTGATTTGCCCGAATCTGAGTC 180
Qy 181 ATGCGAGCGGGCTGTGCTGTCTCTTCTTATGGGCCAGACACCATGAGCTCGTCCGC 240
Db 181 ATGCGAGAGGTTGTAGTGTGAAGTCTTATTTGGGGTTGAACCAATGAGCAACTGATG 240
Qy 241 CAACAGATCCGCAAGGCCCTGGACGAGCAAGAGGATTCGAAGCTGATCCTGTATC 300

Db 241 CTTCAAATAGAAAGTCACTGGAGGAGAAAACAGATTCAGAGGAGAAATTAATGTTCTAC 300
Qy 301 CGGAAGAGCGGGCTCCCGTTCTGGTGTCTCTGGATGTGATACCCATAAGATAGAGAAA 360
Db 301 AAGAAAACCGGCTCTCCATTTTGGTGTCTACTGGATATTGTTCCCAATAAGATAGAGAAA 360
Qy 361 GGGAGGCTGGCTCTCTCTCTAGTCTCTACAGGACATCAGCGAAACCAAGAACCCAGAGGG 420
Db 361 GGAGATGTAGTACTTTTCTGGCTCTGTTCAAAGATATAACAGATA-CAAAAAGTGAAGAT 419
Qy 421 GGGCCCGACAGATGGAAGGAGACAGGTGTGGCGCGCGCGATATATGCGCGGCGACCATCC 480
Db 420 TATCCAGAAAGATAAAAAGAGACAAAGTCAAAGGAAGATCAAGAGCAGGAGGCCCA 476
Qy 481 AAAGGCTTCAATGCCAACCGGCGGAGCGCGGTCTCTACCACTGTCCGGGCAC 540
Db 477 -----CTTTGACTCAGCCCGGAGACGAGTGTGAGCAGTCTCTTATCACAATCTCTGGGCAC 531
Qy 541 CTCGAGAGCAGCCCAAGGCGACGACCAAGCTCAATAAGGGGTGTTTGGGGAGAAACCA 600
Db 532 CTGCAAGAGAGAGAAAGAACAAATGAAATAAATAAATGTTTGTAGATAAACCA 591
Qy 601 AACTTGTGCTGAGTACAAAGTAGCCGCATCCGGAAGTGCCTCTTCTGTGCACTGT 660
Db 592 GCAATTCGGAGTATAAAGTTCTGTGACAAAAGTCCAAATTCATACTTCTGCAATTT 651
Qy 661 GGGGCACTGAGACGCCACCTGGGATGCTTCCTGTCTGCCACACTCTATGTCGCTGTC 720
Db 652 AGCACATTTTAAAGCTGGCTGGGACTGGCTTATTTTGTGGCAAGTGTATGTTGCTGTG 711
Qy 721 ACTGTGCCCTACAGCGTGTGTGTGACACAGCAGGAGCCAGTGCAGCGCGCGGCCG 780
Db 712 ACTGTACTTACAAACGTTTGTCTTATTTGGCAATGACGACCTGTCCCAACTCGGAGC 768
Qy 781 CCCAGCGTCTGTGACCTGGCGGTGGAGTCTCTTCTATCTCTGACATTTGCTGAATTC 840
Db 769 ACAACCGTCACTGACATTTGAGTGGAGATCTTTTATATAGATATTAATTTAAATTC 828
Qy 841 CGTACCACTTCTGTCTCAAGTCCGAGTGGGTGTGTTTGGCCCAAGTCCATTTGCTC 900
Db 829 CGAACTTATGTGACGAACTTGTGCGCAAGTATCTTTGAAGCAAGATCAATTTGCACT 888
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Db 889 CACTATGTCAACCTGTTCTATGATTTAATGCTGCTGCCCTGCTTGTGATCTTCTG 948
Qy 961 CATGCTTCAAGGTCAAGCTGATCTTCTGGGCGCCATCTGTGAAAGACGTCGCGCTGCTG 1020
Db 949 TATGCTTCAACGTCACAGTGTGTCTCTCGTGCATCTTCTAAAGACAGTGCCTCTCTG 1008
Qy 1021 GCGTGTGCGCTGCTTCTCGCGGTGGACCGGTACTCGAGTACAGAGCGCGGTGGTGTGCTG 1080
Db 1009 GGTCTTTTGGCTGTGCTGACAGAGTTAGACCGCTATTCCCAACACAGTACTATGCTGCTG 1068
Qy 1081 ACATGCTCATGGCGGTGTTCCGCTGCTCGGCACTGGGTGCTGCTGCTGCTGTTTAC 1140
Db 1069 ACTGTGCTCATGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1128
Qy 1141 ATTTGCCAGCGGGAGATCGAGAGCAGCAATCCGAGTGCCTGAGATTTGGTGTGCTGAG 1200
Db 1129 ATTGGAATAATGGAGAGGAGAGACAAACAGCTTCTGAAAGTGGGAAGTTGGTTGGCTTCA 1188
Qy 1201 GAGTGGCGCGGCTGAGTCTGAGTCTCTTACTACCTGTTGGGCGGAGCCAGCTGGAGGG 1260
Db 1189 GAGTTGGGAAGAGACTGGAATCTCATACTAT----- 1221
Qy 1261 AACAGTCCGGCCAGTGAACACTGACAGCAGCAGCGAGGCCAACGGGACGGGGCTG 1320
Db 1222 -----GGCAAC 1227
Qy 1321 GAGCTGTGGCGGCGCGCTGCTGCGAGCGCTTACATCACTCCTCTACTTGGCACTC 1380

Db 1228 AATACCTTGGGGGCCGTCGATCCGAAGTGCCTATATTGCGCTCTGTACTTTCAGCGTG 1287
QY 1381 AGCAGCCTCACACGCTGGGCTTTCGCAACGTCGTCCGCCAAACACGACACCGAGAGATC 1440
Db 1288 AGCAGCCTCACACGCTGGGCTTTCGCAACGTCGTCCGCCAAACACGACACCGAGAGATC 1347
QY 1441 TTCTCATCTGCAACCATGCTCATCGCGCCCTGATGACGCGGTGGTGGTGGAAACGTG 1500
Db 1348 TTCTCATCTGCAACCATGCTCATCGCGCCCTGATGACGCGGTGGTGGTGGAAACGTG 1407
QY 1501 ACGGCCATCATCCAGCGCATGACGCGCGCGCTTCTGTACACAGCCGACGCGCGGAC 1560
Db 1408 ACAGCAATCATACAGAGATGACTCCAGATGGTCCCTCTATCACATGAACATAAGGAT 1467
QY 1561 CTGCGGACTCATCCGCGATCCACCGCTATCCCAAGCCCTCAAGCAGCGCATGCTGGAG 1620
Db 1468 CTGAAGAATTCATCCGTGCCATCACTTGCCCCACAACTCAAGCAGAGATGCTCGAA 1527
QY 1621 TACTTCCAGGCCACCTGGCGGGTGAAATGGCATCGACACCAACCGAGTGTGTCAGAGC 1680
Db 1528 TATTTTCAACAACCTGGTCAGTCAACAATGGAATAGATTCAATGAGCTTTTGAAGAC 1587
QY 1681 CTCCTGTGACGAGTGCAGCGCAGACATCGCCATGCGCTGCACTGCAACGAGATCTGCGAGCTG 1740
Db 1588 TTTCAGATGAATCTGGTTCTGACATCACTATGCACTTGAAACAAGGAGATCTTACAGTTG 1647
QY 1741 COACTGTTTGGGCGGCCAGCGCGGCTGCTCGGGGCACTGTCTCTGGCCCTGGGGCC 1800
Db 1648 TCCCTTTTGAATGCGCAGCGGGGCTGCTCAGGTCTCTGTCTTACATCAAAACC 1707
QY 1801 GCCTTCTGACCGCGGCGAGTACTCTATCCACCAAGCGATGCCCTGCAGGCCCTCTAC 1860
Db 1708 TCTTTCTGTGCTCCGGGGAGTATCTGCTGCGTCAAGGGATGCTTTGCAGGCCATCTAC 1767
QY 1861 TTTGTCTGCTGTGGCTCCATGAGGTGCTCAAGGGTGGCACCGTGTCTGCCATCCTAGGG 1920
Db 1768 TTTGTATGCTCGGGCTCCATGGAATCTTAAAGACAGCATGGTGTGCTGCTTCTTGGG 1827
QY 1921 AAGGCGACCTGATCGGCTGTGAGCTGCCCGGGGAGCAGTGTAAAGGCCAATGCC 1980
Db 1828 AAAGGGATTTAATTGGAGCAATCTATCAATTAAGGACCAAGTGATCAAGACCAATGCA 1887
QY 1981 GACGTGAAGGGGCTGACGTACTGCTGTCAGTGTCTGCAAGTGTGGCTGGCCCTGCACGAC 2040
Db 1888 GATGTAAAGGCTTTAAACCTACTGTGATCTCCAGTGTATCATCTCAAAGGACTCTTTGAA 1947
QY 2041 AGCCTTGGCTGTACCCGAGTTTGGCCCGGCTTTCAGTGTGGCTCGAGGGGAGCTC 2100
Db 1948 GTGCTAGACCTTTACCCAGATATGCTCACAAATTCGTGGAAGACATTCAGCATGACCTC 2007
QY 2101 AGCTACAACTGGGTGCTGG 2120
Db 2008 ACATACAACTCCGAGAAGG 2027

Search completed: September 1, 2004, 21:04:19
Job time : 982 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 1, 2004, 15:01:21; Search time 107.5 Seconds
(without alignments)
5819.811 Million cell updates/sec

Title: US-09-965-830-1_COPY_6_3257

Perfect score: 6089

Sequence: 1 atgcggccatcggggctc.....aagaaggcacaggggtctga 3252

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5

Ygapop 10.0, Ygapext 0.5

Fgapop 6.0, Fgapext 7.0

Delop 6.0, Delext 7.0

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 566732

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/cgn2.1/USPTO spool_p/US0965830/runat_01092004_160110_4809/app_query.fasta_1.3399
-DB=PIR 78 -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US0965830@cgn 1.1.163 @runat_01092004_160110_4809 -NCPU=6 -ICPU=3
-NO_MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRAD=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: PIR 78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5428	89.1	1087	2 T31100	probable potassium channel
2	2515	41.3	1102	2 T17367	potassium channel
3	2439.5	40.1	1017	2 T31354	probable potassium channel
4	1901	31.2	1284	2 T13168	probable potassium channel
5	1551	25.5	1159	2 T38465	probable potassium channel
6	1390	22.8	1174	2 A40853	potassium channel
7	1380.5	22.7	962	2 T31197	potassium channel
8	1371.5	22.5	989	2 T48912	potassium channel
9	1257	20.6	934	2 T42394	potassium channel
10	1029.5	16.9	514	2 T19579	hypothetical protein
11	439	7.2	706	2 A55251	cyclic nucleotide
12	423.5	7.0	735	2 I50630	alpha subunit of c
13	421.5	6.9	665	2 S52072	DmCNC protein - f
14	421.5	6.9	691	2 JG6509	rod cyclic nucleot

15	420	6.9	695	2	S74179	cyclic nucleotide
16	416.5	6.8	732	2	S35691	cyclic nucleotide
17	414.5	6.8	682	1	JH0560	cyclic nucleotide
18	414	6.8	688	2	B42161	cyclic nucleotide
19	413.5	6.8	690	1	S07103	cyclic nucleotide
20	413	6.8	686	1	A44842	cyclic nucleotide
21	411	6.7	645	2	I50680	cyclic nucleotide
22	407	6.7	690	2	A42161	cyclic nucleotide
23	401	6.6	1414	1	S23809	cyclic nucleotide
24	393	6.5	664	2	S11517	cyclic nucleotide
25	391.5	6.4	663	2	S11521	cyclic nucleotide
26	391	6.4	1453	2	S21626	cyclic nucleotide
27	389.5	6.4	1454	1	CGH15	cyclic nucleotide
28	386.5	6.3	787	2	S68699	cyclic nucleotide
29	371	6.1	3570	2	T45025	cyclic nucleotide
30	370	6.1	1464	1	CGH15	cyclic nucleotide
31	369.5	6.1	575	2	I59327	cyclic nucleotide
32	368.5	6.1	733	2	E85357	cyclic nucleotide
33	367.5	6.0	1042	1	CGH15	cyclic nucleotide
34	365	6.0	738	2	E86294	cyclic nucleotide
35	361	5.9	880	2	F85381	cyclic nucleotide
36	361	5.9	916	2	T05360	cyclic nucleotide
37	361	5.9	1106	2	JQ0405	cyclic nucleotide
38	360	5.9	1042	1	CGH15	cyclic nucleotide
39	358.5	5.9	1453	2	S21626	cyclic nucleotide
40	357	5.9	1418	2	T45467	cyclic nucleotide
41	356.5	5.9	710	2	T52573	cyclic nucleotide
42	356.5	5.9	1486	1	B40333	cyclic nucleotide
43	354.5	5.8	1414	1	S23809	cyclic nucleotide
44	353.5	5.8	747	2	T52572	cyclic nucleotide
45	352	5.8	1806	1	CGH15	cyclic nucleotide

ALIGNMENTS

RESULT 1

T31100

probable potassium channel 2 - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999

C:Accession: T31100

C:Engelard, B.; Neu, A.; Ludwig, J.; Roepke, J.; Pongs, O.

A:Description: Identification of three rat potassium channel genes homologous to D. melanogaster

A:Reference number: Z20983

A:Accession: T31100

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1087 <ENG>

A:Cross-references: EMBL:AJ007627; NID:ei329995; PID:ei329996; PIDN:CAA07586.1

A:Experimental source: cortex

C:Genetics:

A:Gene: elk2

C:Keywords: potassium channel

Alignment Scores:

Pred. No.: 6.73e-274

Score: 5428.00

Percent Similarity: 96.60%

Best Local Similarity: 95.58%

Query Match: 89.14%

DB: 2

US-09-965-830-1_COPY_6_3257 (1-3252) x T31100 (1-1087)

QY 1 ATGCGCGCCATGGGGCCCTCGCGCCCTCAGACCTTCCTGGACACCATCGCTACG 60

Db 1 MetProMetArgGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20

QY 61 CGCTTCGACGCGCACGACAGTAACCTCGTGTGGCAACGCCAGGTCGGGGGCTCTTC 120

Db 21 ArgPheAspGlyThrHisSerAsnPheValGlyAsnAlaGlnValAlaGlyLeuPhe 40

121	CCCGTGTCTACTCTCTGATGGCTTCTGTGACCTCACGGCTTCTCCCGGGCTGAGGTC	180
41	ProValValTyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal	60
181	ATGCAGCGGGCTCTGCTGCTCTCTCTCTCTTATGGCGCAGACACACAGTGAGCTCGTCCGC	240
61	MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArg	80
241	CAACAGATCCCGAAGGCCCTGGAGCAGACACAAGAGATTCAAGCTGAGCTGATCCTCTAC	300
81	GlnGlnIleArgLysAlaLeuAspGluHisLysGluPheLysAlaGluLeuIleLeuTyr	100
301	CGGAGAGCGGGCTCCCGCTCTGTTGTTCTCTGATGTGATACCCATAAAGAAATGAGAAA	360
101	ArgLysSerGlyLeuProPheTyrCysLeuLeuAspValIleProlIleLysAsnGluLys	120
361	GGGAGGTGGCTCTCTCTCTAGTCTCTCACAGGACATCACGGAACACCAAGAACCGAGGG	420
121	GlyGluValAlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGly	480
421	GGCCCGGACAGATGGAAGAGACAGTGGTGGCGCGCGCATATGGCGCGGACGATCC	540
141	GlyProAspAsnTrpLysGluArgGlyGlyArgArgGlyArgGlyArgAlaGlySer	160
481	AAAGGCTCAATGCCAACCGCGCGGAGCGCGGCGGTGCTCTACCACTGTCCGGGCAC	540
161	LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis	180
541	CTGCAGAAGCAGCCCCAAGGGCAAGCACAAAGCTCAATAAGGGGGTGTGGGGAGAAACA	600
181	LeuGlnLysGlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyGluLysPro	200
601	AACTTGCCTGAGTACAAAGTAGCCCATCCGGAAGTCGCCCTTCATCTCTGTGCACTGT	660
201	AsnLeuProGluTyrLysValAlaIleArgLysSerProPheIleLeuLeuHisCys	220
661	GGGGCACTGAGAGCCACCTGGAGTGGCTTCATCCTGCTCGGCACACTCTATGTGGCTGTC	720
221	GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal	240
721	ACTGTCCCTTACAGCTGTGTGTGAGCACAGCACGGGAGCCAGATGCCCGCGCGCGCG	780
241	ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro	260
781	CCGAGCGTGTGACCTGCGCGTGGAGGTCCTTTCATCTCTGACATTGCTGTAATTTC	840
261	ProSerValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPhe	280
841	CGTACCACATTCGTGTCCAAAGTCGGGCGCAGGTGGTGTTCGCCCCAAAGTCCATTGGCTC	900
281	ArgThrThrPheValSerLysSerGlyGlnValValPheAlaProLysSerIleCysLeu	300
901	CATCTAGTCACACCTGTTCTCTGCTGATGTATCGCAGCGCTGCCCTTCACCTGCTA	960
301	HisTyrValThrThrTrpPheLeuLeuAspValIleAlaAlaLeuProPheAspLeuLeu	320
961	CATGCTTCAAGTCAACGTTACTTTCGGGGCCCATCTGTCTGAAGACGGTGGCGCTCTG	1020
321	HisAlaPheLysValAsnValTyrValGlyAlaHisLeuLeuLysThrValArgLeuLeu	340
1021	CGCTGTGCTGCTGCTTCCGCGGCTGGACCGGTACTTCGAGTACAGCGCGCTGGTGGCTG	1080
341	ArgLeuLeuArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValValLeu	360
1081	ACACTGCTCATGCCGTTGTCGCCCTGCTCGCGCACTGGGTGCGCTGCTCGTCTGGTTTAC	1140
361	ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValLacCysValTrpPheTyr	380
1141	ATTGGCAGCGGAGATCGAGACGAGCAATCCGAGCTGCTGAGATTGCTGGCTGCAG	1200
381	IleGlyGlnGlnGluIleGluAsnSerGluSerGluLeuProGluIleGlyTrpLeuGln	400
1201	GAGCTGGCGCCGAGCTGGAGACTCCCTCTACTGCTGGCGCGGAGCCAGCTGGAGGG	1260

[illegible]

Db 761 CysThrSerSerSerSerAlaLysLeuLeuSerProArgArgThrAlaProArgPro 780
QY 2332 CTTCTAGTGGCAGAGAGGCGCAGGCGAGGAGGCTTTGAGGCTGAGGCTGCGCC 2391
Db 781 ArgLeuGlyGlyArgGlyArgProSerArgAlaGlyValLeuLysProGluAlaGlyPro 800
QY 2392 TCTGCTCCCGCCAGCGGCGCTAGAGGGCTACGGCTGCCCGCCCATGCGATGTGCGCC 2451
Db 801 SerAlaHisProArgThrLeuAspGlyLeuGlnLeuProMetProTrpAenValPro 820
QY 2452 CCAGATCTCAGCCCGAGGCTAGTAGTGCATGATGATGAGAGCGCTGCTGCGCAGCAGCC 2511
Db 821 ProAspLeuSerProArgValValAspGlyLeuGlnLeuProMetProTrpAenValPro 840
QY 2512 AAGTTCTCTTCCGCTGGCGCAGTCTGCGCGGAATGTAGCAGAGCCCTCCCTCGA 2571
Db 841 LysPheSerPheArgValGlyGlnSerGlyProGluCysSerSerSerProSerProGly 860
QY 2572 CCAGAGAGCGGCTGCTACTGTTCCCGATGGCCCGCAGGAGGCAAGAACACACACACA 2631
Db 861 ThrGluSerGlyLeuLeuThrValProLeuValProSerGluAlaArgAsnThrAspThr 880
QY 2632 CTGGACAACTTCGCGAGCGGCTGACAGCTGTGACAGAGTGTGCTGAGATGGCGAA 2691
Db 881 LeuAspLysLeuArgGlnAlaValThrGluLeuSerGluGlnValLeuGlnMetArgGlu 900
QY 2692 GGACTGCGACTCTGCGCAGGCTGTGACAGTGTGCTGCGCGCCCGCAGAGGAGGTCCG 2751
Db 901 GlyLeuGlnSerLeuArgGlnAlaValGlnLeuLeuValProGlnGlyGln 920
QY 2752 TGCCCTCGGGCATCGGAGAGGGCGTGCAGCCAGCCAGCCTCGGGCTTCTGAGCCT 2811
Db 921 CysProArgValSerGlyGluGlyProCysProAlaThrAlaSerGlyLeuLeuGlnPro 940
QY 2812 CTGTGTGGACACTGGGGCATCTCTACTGCTGAGCCCGCCCGAGCTGCTGTCTG 2871
Db 941 LeuArgValAspThrGlyAlaSerSerTyrCysLeuGlnProProAlaGlySerValLeu 960
QY 2872 AGTGGAGCTTGGCCCGCCAGCTCGTCCGGGG---CCTCTCCCTCATGGCAGCCCTGGCC 2928
Db 961 SerGlyThrTrpProHisProArgProGlyHisProProProLeuMetAlaProTrpPro 980
QY 2929 TGGGTCCCGCAGCTCTCAGAGTCCCGCTCGGCTCGAGCCAGCAGCTTCTGAGCCTCC 2988
Db 981 TrpGlyProProAlaSerGlnSerSerProTrpProArgAlaThrAlaLeuTrpThrSer 1000
QY 2989 ACCTCAGACTCAGAGCCCGCTGCTCAGAGACCTCTCTCTGAGCCCGCAGCAGCCCTGCC 3048
Db 1001 ThrSerAspSerGluProProGlySerGlyAspLeuCysSerGluProSerThrProAla 1020
QY 3049 TCCCTCTCTCTCTGAGAGGGGCTAGGACTGGGCGCGCAGAGCCTGTGAGCCAGGCT 3108
Db 1021 SerProProProGluGluGlyAlaArgThrGlyThrProAlaProValSerGlnAla 1040
QY 3109 GAGCTACAGACTGAGAGCCCGCCAGGGTCAAGGGCTGAGGGGCTGCTCCCTGGGAC 3168
Db 1041 GluAlaThrSerThrGlyGluProProProGlySerGlyGlyArgAlaLeuProTrpAsp 1060
QY 3169 CCCACAGCCTGAGAGTGGTCTATTGGCTGCCATGCTGCTGAGCAGTCCAGTGGAC 3228
Db 1061 ProHisSerLeuGluMetValLeuLeuGlyCysHisGlyProGlySerValGlnTrpThr 1080
QY 3229 CAGGAAGAAGGACAGGGGCTC 3249
Db 1081 GlnGluGluGlyThrGlyVal 1087

RESULT 2

Tl7367

potassium channel protein elk1 - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: Tl7367

R;Shi, W.; Wang, H.S.; Pan, Z.; Wymore, R.; Cohen, I.S.; McKinnon, D.; Dixon, J.E.

J. Physiol. 511, 675-682, 1998
A;Title: Cloning of a mammalian elk potassium channel gene and EAG mRNA distribution in
A;Reference number: Z18731; MUID:98382545; PMID:9714851
A;Accession: Tl7367
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1102 <SHI>
A;Cross-references: EMBL:AF061957; NID:g3659689; PID:g3659690; PIDN:AA061520.1
C;Genetics:
A;Gene: elk1
C;Function:
A;Description: may play a role in the sympathetic nervous system
C;Keywords: potassium channel

Alignment Scores:

Pred. No.:	5,97e-123	Length:	1102
Score:	2515.00	Matches:	551
Percent Similarity:	62.00%	Conservative:	149
Best Local Similarity:	48.80%	Mismatches:	295
Query Match:	41.30%	Indels:	134
DB:	2	Gaps:	24

US-09-965-830-1_COPY_6_3257 (1-3252) x Tl7367 (1-1102)

QY 1 ATGCGCGCCATCGGGGCTCTGCGGCTCAGAACACCTTCTGAGACACCTCGCTAGC 60
Db 1 MetProValMetLysGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20
QY 61 CGCTTCGAGCGGACACACAGTAACTTCGTGCTGGGCAAGCCGAGGTGGGGGCTCTTC 120
Db 21 ArgPheAspGlyThrHisSerAsnPhelleLeuAlaAsnAlaGlnValAlaLysGlyPhe 40
QY 121 CCCGTGCTACTGCTGATGGCTTCTGTACCTCAGCGGCTTCTCCCGGCTGAGGTC 180
Db 41 ProIleValTyrCysSerAspGlyPheCysGluLeuAlaGlyPheAlaArgThrGluVal 60
QY 181 ATGAGCGGGGCTGCGCTGCTCTTCTTTATGGCCAGACACCCAGTGAGCTCTGCGC 240
Db 61 MetGlnLysSerCysSerCysLysPheLeuPheGlyValGluThrAsnGluGlnLeuMet 80
QY 241 CAACAGATCCGACGAGCCCTGACGAGCACAGGAGTTCAGGCTGAGTGTATCTGTAC 300
Db 81 LeuGlnIleGluLysSerLeuGluGluLysValGluPheLysGlyGluIleMetPheTyr 100
QY 301 CGAAGAGCGGCTCCCTTCTGCTGCTCTCTGATGTATACCCATAAAGATGAGAAA 360
Db 101 LysLysAsnGlyAlaProPheTrpCysLeuLeuAspIleValProIleLysAsnGluLys 120
QY 361 GGGGAGGTGGCTCTCTCTCTAGTCTCTCACAGGACATCAGCGAAACCAAGAACCGA 417
Db 121 GlyAspValValLeuPheLeuAlaSerPheLysAspIleThrAspThrLysValLysIle 140
QY 418 GGGGCGCCCGACAGATGGAAGAGACAGGTGCTGCGCGCGCCGATATGGCGGSCACGA 477
Db 141 ThrSerGluAspLysLysGluAspArgAlaLysGlyArgSerArgAlaGly----- 157
QY 478 TCCAAAGCTTCAATGCGCAACCGCGCGGCGCGGCGCTCTACACCTGTCTCCGG 537
Db 158 ---SerHisPheAspSerAlaArgArgSerArgAlaValLeuTyrHisIleSerGly 176
QY 538 CACCTGAGAGAGCCCGGAGGCAACAGTCAATAGGGGGTGTGGGGAGAAA 597
Db 177 HisLeuGlnArgArgGluLysAsnLysLeuLysIleAsnAsnValPheValAspLys 196
QY 598 CCAAACTTGCTGAGTACAAAGTAGCGCCATCCGGAAGTCGCCCTTCATCTCTGTCAC 657
Db 197 ProAlaPheProGluTyrLysValSerAspAlaLysSerLysPheIleLeuLeuHis 216
QY 658 TGTGGGCACTGAGAGCCACTGGATGGCTTCTATCTGCTCGCCACACTCTATGTGGCT 717
Db 217 PheSerThrPheLysAlaGlyTrpAspTrpLeuLeuLeuAlaThrPheTyrValAla 236
QY 718 GTCACTGTGCCCTACAGCGTGTGTGTGAGCACAGCAGCGGAGCCCGAGTGGCGCGCGCG 777

QY	241	CAACAGATCCGCAAGGCCCTCGACGACACCAAGAGGTTCAAGGCTGAGCTGATCCTGTAC	300
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QY	80	AlaGlnIleAlaGlnAlaLeuLeuGlyAlaGluGluArgLysValGluIleAlaPheTyr	99
Db		: : : : : : : : : : : : :	
QY	301	CGAAGAGCGGGTCCCGTTCTCGTGTCTCTGGATGTGATACCCATGAAGATGAGAAA	360
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QY	100	ArgLysAspGlySerCysPheLeuCysLeuValAspValProValLysAsnGluAsp	119
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QY	361	GGGAGGTGGCTCTCTTCCTA-----GTCTCTCACAGGACATC-----	399
Db		: : : : : : : : : : : : :	
QY	120	GlyAlaValIleMetPheIleLeuAenPheGluValValMetGluLysAspMetValGly	139
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QY	400	-----AGCGAAACCAAGAACCGAGGGGGCCCGACAGATGG-----	435
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QY	140	SerProAlaHisAspThrAsnHisArgGlyProProThrSerTrpLeuAlaProGlyArg	159
Db		: : : : : : : : : : : : :	
QY	435	-----	435
Db		: : : : : : : : : : : : :	
QY	160	AlaLysThrPheArgLeuLysLeuProAlaLeuLeuAlaLeuThrAlaArgGluSerSer	179
Db		: : : : : : : : : : : : :	
QY	436	---AAGGACACAGTGGTGGCGCGCCGATATGGCCGGC---ACGATCCAAAGCTTC	489
Db		: : : : : : : : : : : : :	
QY	180	ValArgSerGlyAlaGly-GlyAlaGlyAla-ProGlyAlaValValAspValA	199
Db		: : : : : : : : : : : : :	
QY	490	ATGCCAACCGCG-----	503
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QY	199	spLeuThrProAlaAlaProSerSerGluSerLeuAlaLeuAspGluValThrAlaMetA	219
Db		: : : : : : : : : : : : :	
QY	504	-----GGGAGCCGGCGCGTCTCTA-----	524
Db		: : : : : : : : : : : : :	
QY	219	spAsnHisValAlaGlyLeuGlyProAlaGluLysArgAlaLeuValGlyProGlyS	239
Db		: : : : : : : : : : : : :	
QY	525	--CCACCTGTCCGGCACCCTGCAGAGCAGCCCAAGGCCAAG---CACAGTCAAT---	576
Db		: : : : : : : : : : : : :	
QY	239	erProProArgSerAlaProGlyGlnLeu-ProSerProArgAlaHisSerLeuAsnPro	258
Db		: : : : : : : : : : : : :	
QY	576	-----	576
Db		: : : : : : : : : : : : :	
QY	259	AspAlaSerGlySerCysSerLeuAlaArgThrArgSerArgGluSerCysAlaSer	278
Db		: : : : : : : : : : : : :	
QY	577	-----AAGGGGTCTTTTGGGAG	594
Db		: : : : : : : : : : : : :	
QY	279	ValArgArgAlaSerSerAlaAspAspIleGluAlaMetArgAlaGlyValLeuProPro	298
Db		: : : : : : : : : : : : :	
QY	595	AAACCACAAAC-----	603
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QY	299	ProProArgHisAlaSerThrGlyAlaMethHisProLeuArgSerGlyLeuLeuAsnSer	318
Db		: : : : : : : : : : : : :	
QY	603	-----	603
Db		: : : : : : : : : : : : :	
QY	319	ThrSerAspSerAspLeuValArgTyrArgThrIleSerLysIleProGlnIleThrLeu	338
Db		: : : : : : : : : : : : :	
QY	603	-----	603
Db		: : : : : : : : : : : : :	
QY	339	AsnPheValAspLeuLysGlyAspProPheLeuAlaSerProThrSerAspArgGluIle	358
Db		: : : : : : : : : : : : :	
QY	603	-----	603
Db		: : : : : : : : : : : : :	
QY	359	IleAlaProLysIleLysGluArgThrHisAsnValThrGluLysValThrGlnValLeu	378
Db		: : : : : : : : : : : : :	
QY	604	-----TTGCCTGAGTCAAAAGTAGCCGCATCCGGAAGTCGCCCTTC	645
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QY	379	SerLeuGlyAlaAspValLeuProGluTyrLysLeuGlnAlaProArgIleHisArgTrp	398
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QY	646	ATCTGTTCACACTGTGGGGCACTGAGGACACCTGGGATGGCTTCATCTGTCTGCCACA	705
Db		: : : : : : : : : : : : :	
QY	399	ThrIleLeuHisTyrSerProPheLysAlaValTrpAspTrpLeuI	

QY	757	GAGCCCAAGTGC	-----GCCCGCGCGCGCCAGCGCTGTGACCTGC	801
Db	439	GlyProAlaThrGluCysGlyTyrAlaCysGlnProLeuAlaValValAspLeu	 	458
QY	802	GTCGAGGTCTCTTCATCTTCACATTGCGTGAATTTCCGTTACACAAATCGTCCAAAG	 	861
Db	459	ValAspIleMetPheIleValAspIleLeuIleAsnPheArgThrThrTyrValAsnAla	 	478
QY	862	TCGGCGCAGGTGTGTTCGCCCAAGTCCATTTCCTCCACTAGTCCACCACTGGTTC	 	921
Db	479	AsnGluGluValValSerHisProGlyArgIleAlaValHisTyrPheLysGlyTyrPhe	 	498
QY	922	CTGCTGGATGTCATCGCAGCGCTGCCCTTGCCTGTACATGCTTCAAGGTCAACGTG	 	981
Db	499	LeuIleAspMetValAlaAlaIleProPheAspLeuLeu	 	511
QY	982	TACTTCGGGGCC	-----CATCTGTGAAGACGGTGGCGCTGCTCGC	1023
Db	512	IlePheGlySerGlySerGluGluLeuLeuIleGlyLeuLeuTyrThrAlaArgLeuLeuArg	 	531
QY	1024	CTGCTGCGCGTCTTCCCGCGGTGGACCGGTACTCGAGTACACGCGGTGGTCTGACACA	 	1083
Db	532	LeuValArgValAlaArgLysLeuAspArgTyrSerGluTyrGlyAlaAlaValLeuPhe	 	551
QY	1084	CTGCTCATGGCGTGTTCGCTCTCGCGACACTGGTTCGCTCGCTGTGTTTACATT	 	1143
Db	552	LeuLeuMetCysThrPheAlaLeuIleAlaHisTrpLeuAlaCysIleTrpTyrAlaIle	 	571
QY	1144	GSCCAGCGGAGATCGAGACGAGCGAATCCGAGCTGCCTGAGATTGGCTGGCTGAGG	 	1203
Db	572	GlyAsnMetGluGlnProHisMetAspSer	 	588
QY	1204	CTGGCCCGCCGACTGGAGACTCCCTACTACTCTGTGTGGCGGAGCCAGCTGGAGGGAAC	 	1263
Db	589	LeuGlyAspGlnIleGlyLysProTyr	 	598
QY	1264	AGTCCGGCGAGTGTCAACTGCAGCAGCAGCAGCGAGGCCAACCGGCGGTGGAG	 	1323
Db	599	SerSerGly	-----	601
QY	1324	CTGCTGGCGCGCGTCTGCTGGCAGCGCCCTACATCACCTCCCTTACTTCGCATCTCAGC	 	1383
Db	602	--LeuGlyGlyProSerIleLysAspLysTyrValThrAlaLeuTyrPheThrPheSer	 	620
QY	1384	AGCCTCACCAAGCGTGGCTTCGGCAACGTCTCGCCCAACACGACACCCAGAGATCTTC	 	1443
Db	621	SerLeuThrSerValGlyPheGlyAsnValSerProAsnThrAsnSerGluLysIlePhe	 	640
QY	1444	TCGATCTGCACCATGTCTATCGCGCGCTGATGCAGCGGTGGTGTTCGGAACTGACG	 	1503
Db	641	SerIleCysValMetLeuIleGlySerLeuMetTyrAlaSerIlePheGlyAsnValSer	 	660
QY	1504	GCAATCATCAGCGCATGTACGCCCGCTTCTGTACACAGCGGCACGGCGGACTG	 	1563
Db	661	AlaIleIleGlnArgLeuTyrSerGlyThrAlaArgTyrHisThrGlnMetLeuArgVal	 	680
QY	1564	CGCAGTACATCCGCATCCACCGTATCCCAAGCCCTCAAGCAGCATGTCTGGAGTAC	 	1623
Db	681	ArgGluPheIleArgPheHisGlnIleProAsnProLeuArgGlnArgLeuGlnGluTyr	 	700
QY	1624	TTCAGCGCCACTGGCGGTGAACATGGCATCGACACCGAGCTCTCTGCAGCGCTC	 	1683
Db	701	PheGlnHisAlaIleTrpSerTyrThrAsnGlyIleAspMetAsnAlaValLeuLysGlyPhe	 	720
QY	1684	CTGACGAGCTGGCGCAGACATGCCCATGCACTGCACAGGAGGTCTCTGAG---CTG	 	1740
Db	721	ProGluCysLeuGlnAlaAspIleCysLeuHisLeuAsnArgSerLeuLeuGlnHisCys	 	740
QY	1741	CCACTGTTTGGCGCGCCAGCGCGCTGCTGGGGCAGCTGTCTGGCCCTCGGCC	 	1800
Db	741	LysProPheArgGlyAlaThrLysGlyCysLeuArgAlaLeuAlaMetLysPheLysThr	 	760
QY	1801	GCCTTTCGACCGCGGGCGAGTACCTCATCCCAAGCGCATGCCCTCGAGGCCCTCTAC	 	1860

Db 100 IleLeuLeuTyrHisLysAsnAsnLeuGlnCysGlyCysAlaLeuSerGlnPheGlyLys 119
QY 316 -----CCTTCTCTGGTGTCTCTGGATGTGATACCATTAAGAATGAG 357
Db 120 AlaGlnThrGlnGluThrProLeuTyrPheLeuLeuGlnValAlaProIleArgAsnGlu 139
QY 358 AAAGGGAGGTGGCTCTCTCTAGTCTCTCACAGGACATCAGCGAAACCAAGACCGA 417
Db 140 ArgAspLeuValValLeuPheLeuLeuThrPheArgAspIleThrAlaLeuLysGln--- 158
QY 418 GGGGGCCCCACAGATGGAAGGACAGCTGGT-----GGCGGCGCGGATGGCCGG 471
Db 159 -----ProIleAspSerGluAspThrLysGlyValLeuGlyLeuSerLysPheAlaLys 176
QY 472 ---GCACGATCCAAAGCTTCAATGCCAACCGCGGGAGCGCGGCTGTCTACCAC 528
Db 177 LeuAlaArgSerVal-----ThrArgSerArg-----Gln 186
QY 529 CTGTCGGGGCACTGTGAG-----AAGCAGCCCAAGGGCAAGCTCAATAAGGGG 582
Db 187 PheSerAlaHisLeuProThrLeuLysAspProThrLysGlnSerAsnLeuAlaHisMet 206
QY 583 GTCTTTGGGGAGAAACCAACTTGCCTGAGTACAAAGTAGCCGCCATPCGGAAAGTCGCC 642
Db 207 MetSerLeuSerAlaAspIleMetProGlnTyrArgGlnGluAlaProLysThrProPro 226
QY 643 TTATCTCTGTGCACTGTGGGGCACTGAGAGCCACCTGGGATGGCTTCCTCTCGTCGCC 702
Db 227 HistLeuLeuHisTyrCysAlaPheLysAlaIleTyrAspTrpValIleLeuCysLeu 246
QY 703 ACACCTATATGTGGTGTCTAGTGCCTACAGCGTGTGTG-----AGCACAGCACGG 756
Db 247 ThrPheTyrThrAlaIleMetValProTyrAsnValAlaPheLysAsnLysThrSerGlu 266
QY 757 GAGCCAGTGGCGCGCGCGCGCGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGTCTTC 816
Db 267 AspValSerLeuLeu-----ValValAspSerIleValAspValIlePhe 281
QY 817 ATCTTGTACATGTGTGAATTTCCGTACCATATTGCTTCCAGTTCCTCCAGTCGGCGG 876
Db 282 PheIleAspIleValLeuAsnPheHisThrThrPheValGlyProGlyGlyValVal 301
QY 877 TTTGCCCAAGTCCATTGCTCCTCACTAGTCACCACTGTGCTCTCTGCTGATGTCTATC 936
Db 302 SerAspProLysValIleArgMetAsnTyrLeuLysSerTyrPheIleIleAspLeuLeu 321
QY 937 GCAGGCTGCCCTTTGACCTGTACATGCCTTCAG-----GTCAACGTG 981
Db 322 SerCysLeuProTyrAspValPheAsnAlaPheAspArgAspGluAspGlyIleGlySer 341
QY 982 TACTTCGGGGCCCATCTGCTGAAGACGGTGGCGCTGTGCTGCTGCTGCTGCTGCTTCCG 1041
Db 342 LeuPheSerAla-----LeuLysValValArgLeuLeuArgLeuGlyArgValValArg 359
QY 1042 CGGTGGACCGGTACTCGCATAGCGCCCTGGTGTGACACTGCTCATGCGCGCTGTTC 1101
Db 360 LysLeuAspArgTyrLeuGluTyrGlyAlaAlaMetLeuIleLeuLeuLysPheTyr 379
QY 1102 GCCCTGTCTGCGCACTGGGTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1161
Db 380 MetLeuValAlaHisTyrPheLeuAlaCysIleTyrPheSerIleGlyArgSerAspAlaAsp 399
QY 1162 AGCAGCGAAATCCGAGCTGCTGAGATGGCTGGCTGCTGAGAGCTGGCGCGCGCTGAG 1221
Db 400 AsnGly-----IleGlnTyrSerTyrLeuTyrLysLeuAlaAsnValThrGln 415
QY 1222 ACTCCCTACTACCTGGTGGCGGAGCGCCAGCTGGAGGGAACAGCTCCGCGCAGAGTGAC 1281
Db 416 SerProTyrSerTyrIleTyr----- 422
QY 1282 AACTGCAGCAGCAGCAGCGGCAACCGGACGGGGCTGTGAGCTGTGGCGCGCGCTGCG 1341

Db 423 -----SerAsnAspThrGlyProGluLeuValAsnGlyProSer 435
QY 1342 CTGCGCAGCGCTACATCACCTCCCTTACTTCCACTCAGCAGCTCACCAGCGTGGGC 1401
Db 436 ArgLysSerMetTyrValThrAlaLeuTyrPheThrMetThrCysMetThrSerValGly 455
QY 1402 TTGGGCAACCTGTCCGCCAACACGACACCGAGAGATCTTCTCCATCTGCACCATGTC 1461
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QY 1462 ATCGCGCCCTGTATGACGCGGTGTGTGGGAACTGAGCGGCATCATCCAGCGCATG 1521
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QY 1759 AGCGCGGCTGCTGCGCGCATGCTCTCTGCGCCCTGCGCGCGCTTCTGACGCGCGCG 1818
Db 576 SerAspGlyCysLeuArgAlaLeuAlaMetHisPheMetMetSerHisSerAlaProGly 595
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QY 1879 ATGGAGGTGCTCAAGGTGGCACCGTGTCTGCGCATCTTAGGAAAGCGGCGCATCTGCGC 1938
Db 616 LeuGluValIleGlnAspAspValValAlaIleLeuGlyLysGlyAspValPheGly 635
QY 1939 TGTGAGTGTCCCGCGCGGAGCAGGTGTAAAGCCAATGCCAGTGAAGGGGTGACG 1998
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2109 ----- 2109
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 I48912
 potassium channel subunit - mouse
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 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
 C:Accession: I48912
 R:Wamke, J.W.; Ganetzky, B.
 Proc. Natl. Acad. Sci. U.S.A. 91, 3438-3442, 1994
 A:Title: A family of potassium channel genes related to eag in Drosophila and mammals.
 A:Reference number: A54953; MUID:94211879; PMID:8159766
 A:Accession: I48912
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-389 <RES>
 A:Cross-references: EMBL:U04294; NID:9487739; PIDN:AAA62474.1; PID:9487740
 C:Genetics:
 A:Gene: m-eag
 Alignment Scores:
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 Score: 1371.50 Matches: 341
 Percent Similarity: 50.14% Conservative: 189
 Best Local Similarity: 32.26% Mismatches: 310
 Query Match: 22.52% Indels: 217
 DB: 2 Gaps: 31
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 Db 28 Thr-----AsnPheValLeuGlyAsnAlaGlnIleValAsp---TrpProIleValTyr 44
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 Db 45 SerAsnAspGlyPheCysLysLeuSerGlyTyrHisArgAlaGluValMetGlnLysSer 64
 QY 193 TGTGCTGCTCTCTTATGATGGCGCAGACACAGTGTAGCTGTCTGTCGCGCAACAGATCCGC 252
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 QY 253 AAGGCGCTTCTGATGGCGTCAAGGCTGAGTGTATGATGCTGTATGATGATGATGATGATG 312
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 QY 550 ---CAGCCCAAGGGCAAGCAC-----AAGTCAATAGGGGGGTG 585
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749	ValLysSerProArgSerLysProLysArg-----	758		
2437	CCATGGNAATGCCCCCAGATCTGAGCCCAAGGCTAGATGCGATTGAAGACGCGCTGT	2496		
759	-----ProProLeuMetLysArgGlnThrValAsp-----GluAsp-AlaLe	772		
2497	GGCTCGACACAGC-----CCAAATTCTTTCCGCTGGCCAGCTGCGCCCGGAA	2547		
772	uSerArgThrSerTrpLysMetAspLysLysAspArgGluTrpSerSerLeuSerAsn--	791		
2548	TGTAGCAGACGCCCTCCCTCGACCCAGAGCGGCTGCTCACTGTCCCATGGGCCC	2607		
791	-----	791		
2608	AGCGAGCAAGAAACACAGACACACTGGACAAGCTTCGGCAGCGGG-----TGACA	2658		
792	-IleLysThrGluMetLysSerLysPheAspIleIleGlyGluArgLeuThrIleIleG	811		
2659	GAGCTGTACAGACGATGCTGCAGATGCGGGAAGAGACTGCGAGTCTGCCAGGCTGTG	2718		
811	uGlnIleAsnSerArg-LeuAlaLeuLeuGluArgValLeuIleGlyAsnAsnGly----	829		
2719	CAGCTTGTCTTGGGCCCCACAGGAGGGTCCGTGCCCTCGGGCATCGGAGAGGGCCG	2778		
830	-----GlyAlaAsnThrProSerThrMetProValGlySerP	842		
2779	TGCCCCAGCACCTCCGGGCTTCTGCAAGCCTCTGTGTGACACTGGGCATCCCTCC	2838		
842	he-----SerAlaLeuAsnGluSerGlyAsn-----ArgLeuT	853		
2839	TACTGCTCGAGCCCCAGCTGGCTCTGTCTTGAGTGG-----	2876		
853	hrLeuAspAlaAlaProValAlaArgSerValSerTrpSerGluGlnHisGlnProHisT	873		
2877	-----GACTTGGCCCCACCTCGTCGGGGCCCTCCCTCCCTC-----ATG	2916		
873	rpGlnArgPheValGluIleTyrSerGluThrSerThrVal-ProProLeuArgGluLeu	892		
2917	GCACCTGGCCCTGGGGTCCCCAGCGTCTCAGAGCTCCCTCGGCTCGAGCCAGCT	2976		
893	GluAlaGlyGluTrpGluProProIleArgGluProThrProAsnPro-----	908		
2977	TTCGTGACCTCCACCTCAGACTCAGAGCCCTT	3009		
909	-----SerThrSerSerArgValPro	916		

C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T19579
R;Mortimore, B.
submitted to the EMBL Data Library, August 1994
A;Reference number: Z19145
A;Accession: T19579
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-514 «WILL»
A;Cross-references: EMBL:Z35596; PIDN:CAAB84644.1; GSPDB:GN00021; CESP:C30D11.1
A;Experimental source: clone C30D11
C;Genetics:
A;Gene: CESP:C30D11.1
A;Map position: 3
A;Introns: 49/3; 77/2; 151/3; 192/3; 244/2; 264/1; 366/3; 435/2; 479/1

Alignment Scores:
Pred. No.: 5.45e-46 Length: 514
Score: 1029.50 Matches: 215
Percent Similarity: 61.78% Mismatches: 84
Best Local Similarity: 44.42% Indels: 138
Query Match: 16.91% DB: 47
Gaps: 10

US-09-965-830-1_COPY_6_3257 (1-3252) x T19579 (1-514)

QY 604 TTGCCTCAGTACAAAGTAGCGCATCCGGAGTCGCCCTTCATCCTGTGCACGTGGG 663
Db |||||||TTTTTTTTTT||| : : : : :
58 LeuProGluThrLysLeuGlnProThrArgIleHisHisCysThrIleValHisTySer 77
QY 664 GCACGTGAGAGCACCTGGGTGGCTTCATCTCTGCTCGGCACACACTATGTGGCTGTCACT 723
Db : : : : : ||||||| : : : : :
78 ProPheLysAlaValTPAspTrpIleIleLeuLeuValIleTyThrAlaValPhe 97
QY 724 GTGCCCTACAGCGTGTTGTGTGAGCACAGCAGCGGAG-----CCCAGT 765
Db ||||| ||||| |||||
98 ThrProTyr---ValAlaAlaPheLeuAeuArgIleLeuGlnAspThrAlaLysLysSer 116
QY 766 GCCGCCCGCGCGCCCGCAGCGGTCTGTGACTGCGCGGTGGAGGTCTCTTCATCCTTGAC 825
Db ||||| ||||| : : : : :
117 ArgPheThrGluProLeuGluIleValAspLeuIleValAspIleMetPheIleValAsp 136
QY 826 ATTGTGTCGAATTCCGTACCACATTCGTGTCCAAAGTCGGGC-----CAGGTGGTG 876
Db : : : : : ||||||| : : : : :
137 IleIleIleAsnPheArgThrThrTyrValAsnGluAsnAspGluAlaCysGlnValVal 156
QY 877 TTTGCCCCAAAGTCCANTTCCTCCACACGTCAACCACCTGGTTCCTGCGATGTCA TC 936
Db ||||| ||||| |||||
157 SerAspProGlyLysIleAlaThrHisTyThrPhenylsGlyTrpPheIleIleAspMetVal 176
QY 937 GCACGGCTGCCTTTTCACCTGCTA-----CATGCCTCAAGGTCAACGTGTAC 984
Db ||||| : : : : : ||||| : : : : :
177 AlaAlaValProPheAspLeuLeuValSerThrAsnSerAspGluThrThrThrLeu 196
QY 985 TTCGGGCCCCATCTGCTGAGACGGTGGCGCTGTGCGCCTGTGCGCCTGCTTCCGCGG 1044
Db ||||| : : : : : ||||| : : : : :
197 IleGly-----LeuLeuLysThrAlaArgLeuLeuArgValAlaAlaArgLys 214
QY 1045 CTGGACCGGTACTCGCAGTACAGCGCGTGGTGTGTGACACTGTCTCATGGCGGTTCGCC 1104
Db ||||| : : : : : ||||| : : : : :
215 LeuAspArgTyrSerGluTyrGlyAlaAlaValLeuLeuLeuMetAlaThrPheAla 234
QY 1105 CTGCTCGGCACCTGGTCCGCTCGGTCTGGTTTACATTTGGCCAGCGGAGATCGAGGC 1164
Db ||||| : : : : : ||||| : : : : :
235 LeuIleAlaHisTrpLeuAlaCysIleTrpTyrAlaIleGlySerAlaGluLeuSerHis 254
QY 1165 AGCGAATCCGAGTGCCTGAGATTGGCTGCTCAGAGAGTGC CGCCGCTGGAGACT 1224
Db ||||| ||||| ||||| : : : : : ||||| : : : : :
255 Lys-----GluTyrThrTrpLeuHisGlnLeuSerLysGlnLeuAlaGln 269
QY 1225 CCTACTACCTGGTGGCGCGGAGCCAGCTGGAGGGAAACAGCTCCGCGCCAGAGTGACAAC 1284
Db ||||| ||||| |||||


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QY 894 TTGGCTCCACTAGCTCACCACC-----TGTTCTCTGATGTCATCGCAGCGTGCC 947
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 178 uArgArgHisTyrPheHisThrLysGlyTyr---LeuAspValLeuSerMetLeuP 197
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 948 CTTTGACTCTCATACCCCTTC-----AAGTCAACGTGTACTTTCGGGGC 992
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 197 oThrAspLeuAlaTyrIleTyrTrpProGluThrCysSerSerLeuTyrLeuProCy 217
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 993 CCAT---CTGCTGAAGCGGTGGCGCTGCTGCGCTGCTGCGCTGCTTCCGCGGTGGA 1049
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 217 sProValIleValArgLeuAsnArgLeuLeuArgIleAsnArgLeuTrpGluTrpPheAs 237
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1050 CCGGTACTCG-----CAGTACAGCGCGGTGGTGTGAC 1082
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 237 pArgThrGluThrAlaThrGlyTyrProAsnAlaPheArgIleCysLysValValLeuAl 257
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1083 AATGCTCATGGCCGTGTTCGCCCTGCTGCGCATGGGTGGCTGCTGCTGCTGCTTACAT 1142
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 257 alleLeu-----ValLeuIleHisTrpAsnAlaCysMetTyrPheAlaI 272
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1143 TGGCCAGCGGAGATCGAGACGCGAATCCGAGCTGCTGAGATTGGCTGCTGAGGA 1202
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 272 eSerTyrGluIleGlyPheSerSerAspSer-----TrpValTyrAs 286
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1203 GCTGGCCCGCGACTGAGACTCCCTACTACTGCTGGCGCGGAGCCAGCTGAGGGAA 1262
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 286 nLeu----- 287
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1263 CAGCTCGGCGAGAGTGACAACTGCAGCAGCAGCGAGCGCAACGGGAGCGGGCTGGA 1322
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 288 -----AsnGlyThr----- 290
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1323 GCTGCTGGCGCGCGTGGCTGCGCGCGCTAGCATCACCTCCCTACTTTCGCACTCAG 1382
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 291 -----ArgAsnAsnThrLeuGlnArgGlnTyrIleTyrSerPheTyrTrpSerThrLe 308
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1383 CAGCTCACCAGCGTGGCTTCGGCTTCGCAAGTGTCCGCCAAACGACGACCGAGAAGATCTT 1442
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 308 uThrLeuThrIleGlyGluThrProThrProGluAsn---AspValGluTyrLeuPh 327
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1443 CTCATCTGCACCATGCTCATCGCGCGCTGATGACGCGGTGGTGTGGTGGAACTGAC 1502
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 327 eValValAlaAspPheLeuAlaGlyValLeuIlePheAlaThrIleValGlyAsnIleGl 347
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1503 GGCCATCATCCAGCGCATGTAGCCCGCGCTTCTGTACACAGCGCGCAGCGCGACCT 1562
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 347 ySerMetIleSerAsnMetAsnValAlaArgValGluPheGlnAsnArgMetAspGlyVa 367
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1563 GCGGACTATACCTCCGCTATCCACCTATCCCAAGCCCTCAAGCAGCGCATGCTGGAGTA 1622
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 367 lLysGlnTyrMetAlaPheArgArgValGlyHisGluLeuGluAlaArgValIleArgTr 387
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1623 CTTCCAGGCCACTGGCGGTGAACAATGGCATCGACACCAAGCGGTGTGTGAGAGCT 1682
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 387 pPheAlaTyrThrTrpSerGlnSerGlyAlaLeuAspGluArgValLeuAlaAlaLe 407
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1683 CCCTGACGAGTGGCGGCGAGATCGCATCCATCCAGCGCGAGGTCTG---CAGCT 1739
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 407 uProAspLysLeuLysAlaGluIleAlaIleGlnValHisMetAspThrLeuLysGlnVa 427
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1740 GCCACTGTTTCAGCGGCGCGCGGTGCTGCGGCGACTGCTGCGCTGCGGCG 1799
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 427 lArgIlePheHisAspThrGluProGlyLeuLeuGluAlaValLeuLysLeuLysLe 447
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1800 CGCCTTCTGCGCGCGGAGTACCTCATCCCAAGCGATGCTTCGAGGCGCTCTA 1859
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 447 uGlnValPheSerProGlyAspTyrIleCysArgLysGlyAspValGlyLysGluMetTy 467
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1860 CTTTGTCTGCTCTGCTCCATGGAGGTGCTC-----AAGGGTGGCACCCTGCTGCGCAT 1913
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 467 rIleValLysArgGlyLysLeuSerValValGlyAspAspGlyIleThrValLeuAlaTh 487
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1914 CTTAGGGAAGGCGGACCTGATCGGC-----TGTGAGCTGCCCGCGCGGAGCA 1961
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 487 rLeuGlyAlaGlySerValPheGlyGluValSerValLeuGluIleAlaGlyAsnArgTh 507
QY 1962 GTGGTAAAGCCCATCCGACGTGAAGGGCTGACGTACTGCTCTCTGACGTGTCTGCA 2021
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 507 rGlyAsnArgArgThrAlaAsnValArgSerLeuGlyTyrSerAspLeuPheCysLeuAl 527
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2022 GCTGGCTGGCTGACGACGACGCTTGGCTGTACCCGAG 2061
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 527 aLysArgAspLeuTrpGluThrLeuSerAspTyrProGlu 540
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
RESULT 14
JC6509
rod cyclic nucleotide-gated cation channel protein alpha-chain - dog
C:Species: Canis lupus familiaris (dog)
C:Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jul-2000
C:Accession: JC6509
R:Vske, A.; Nilsson, S.E.G.; Gal, A.
Gene 202, 115-119, 1997
A:Title: Characterization of canine rod photoreceptor cGMP-gated cation channel alpha-su
A:Reference number: JC6509; MUID:98087425; PMID:9427553
A:Accession: JC6509
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-691 <VES>
A:Cross-references: EMBL:X99914; NID:g1488571; PIDN:CAA68186.1; PID:g1488572
C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-
F:478-602/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>
Alignment Scores:
Pred. No.: 1,77e-14 Length: 691
Score: 421.50 Matches: 145
Percent Similarity: 42.54% Conservative: 126
Best Local Similarity: 22.76% Mismatches: 265
Query Match: 6.92% Indels: 101
DB: 2 Gaps: 17
US-09-965-830-1_COPY_6_3257 (1-3252) x JC6509 (1-691)
QY 343 CCCATAAAGAAATGAGAAA-----GGGAGGTGGCTCTCTTCTAGTCTCTCACAAG 393
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 74 ProSerGlnArgGluGlnTyrLeuProGlyAlaIleAlaLeuPheAsnValAsnSer 93
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 394 GACATCAGCAACCAAGAACCGAGGGGGCCCGACAGATGGAAGGACAGAGTGGTGGC 453
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 94 SerAsnLysGluGluGluProLysGluLysLysLysLysLysLysLysLysLysLys 110
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 454 CGGCGCGATATGGCGGCGACGATCCAAAGGCTTCAATGCCAACCGCGCGGAGCGG 513
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 111 -----LysSerLysSerGlyAspLysAsnGluAsnLysLysAspSerGlu 125
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 514 GCGGTGCTTACACCTGTGCGGCACCTGCAGAGCAGCCCAAGGACCAAGCACAAGCTC 573
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 126 -----LysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 137
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 574 AATAAGGGGGTGTGTTGGGAGAAACCAACTTGCCTGAGTACAAAGTAGCGCATCCGG 633
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 138 AsnLysGluGluLysGlyLysAspLysGluGlu-----Lys 151
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 634 AAGTCGCGCTTTCATCTGTTGCACTGTGGGCGACCTGAGAGCCACTGGGATGGCTTCATC 693
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 152 LysGluValMetValIleAspProAlaGlyAsnMetTyrTyrAsnTrpLeuPheCysIle 171
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 694 CTGCTGCCACACTCTATGTGGTGTCTACTGTGCGCTTACAGCGTGTGTGTGAGCAGCA 753
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 172 ThrLeuProValMetTyrAsnTrpThrMetValIleAlaArgAlaCysPheAspGluLeu 191
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 754 CGGAGCGCCAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 813
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 192 GlnSerAspTyrLeuGluTyrTrp-----IleIlePheAspTyrLeuSerAspIleVal 209
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 814 TTCATCTCTGACATGTGTGAATTTCCGTACCATTCGTGTCTCAAGTCGCGCGAGGTG 873
Db : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

Db	210	TyrLeuLeuAspMetPheValArgThrArgThrGlyTyrLeuGluGlnGlyLeuLeuVal	229
Qy	874	GTGTTTCCCCAAAGTCCATTTCCTCCACCTACCTACACCTGGTTCTGCTGGAGTGC	933
Db	230	ArgGluGluAlaLysLeuLeuGlyLeuValTyrLysSerAsnLeuGlnPheLysLeuAspPhe	249
Qy	934	ATCCGACGGCTGCCCTTTGACCTGCTACCTGCTCAAGGTCAAC---GTGTACTTCGGG	990
Db	250	LeuSerValIleProThrAspLeuLeuTyr---PheLysLeuGlyTyrAsnTyrProGlu	268
Qy	991	GCCCATCTGCTGAAGACGGTGCCTGCTGGCTGCTGCGCCTGCTTCGCGCGTGGAC	1050
Db	269	IleArgLeuAsnArgLeuLeuArgIleSerArgMetPheGluPhePheGlnArgThrGlu	288
Qy	1051	CGGTACTCGAGTACAGCGCGCTGGTG---CTGACACTGCTCATGCGCGCTGTTCGCCCTG	1107
Db	289	ThrArgThrAsnTyrProAsnIlePheArgIleSerAsnLeuValMetTyrIleValIle	308
Qy	1108	CTGCGGACCTGGGTGGCTGGCTGGTGTATATGGCCAGCGGGAGATCGAGAGCAGC	1167
Db	309	IleIleHisTrpAsnAlaCysValTyrPheSerIleSerLysAlaIleGlyPheGlyAsn	328
Qy	1168	GAATCCGACGTG-----CCTCAGATTGGCTGGCTGCAGGAGCTGGCC	1209
Db	329	AspThrTrpValTyrProAspValAsnAspProGluPheGly-----ArgLeuAla	345
Qy	1210	CGCGACTGGAGACTCCCTACTACTCTGGTGGCGCGAGGCAGCTGGAGGAAACAGTCC	1269
Db	346	ArgLys-----	347
Qy	1270	GGCGAGTGCACAACTGCAGCAGCAGCAGCGGCCAACCGGACGGGGCTGGAGCTGCTG	1329
Db	347	-----	347
Qy	1330	GGCGGCGGCTGCTGCGCAGGGCTACATCACCTCCTCTACTTCGCACCTCAGACGCTC	1389
Db	348	-----TyrValTyrSerLeuTyrTrpSerThrLeuThrLeu	359
Qy	1390	ACCAGCGTGGCTTCGGCAACGTGTCGCGCAACACGACGACCCAGGAGATCTTCTCCATC	1449
Db	360	ThrThrIleGly---GluThrProProValArgAspSerGluTyrValPheValVal	378
Qy	1450	TGCACCATGCTCATCGCGCGCTTGAGCAGCGCGGTGTGTGGTGGAACTGACGGCGCATC	1509
Db	379	ValAspPheLeuIleGlyValLeuIlePheAlaThrIleValGlyAsnIleGlySerMet	398
Qy	1510	ATCCAGCGCATGACGCGCGCGTCTTCTGTACACAGCGCGACGCGCGACCTCGCGGAC	1569
Db	399	IleSerAsnMetAsnAlaAlaArgAlaGluPheGlnAlaArgIleAspAlaIleLysGln	418
Qy	1570	TACATCGCATCCACCGCTATCCCCAACCCCTCAAGCAGCGCATGCTGGAGTACTTCCAG	1629
Db	419	TyrMetHisPheArgAsnValSerLysAspMetGlnLysArgValIleLysTrpPheAsp	438
Qy	1630	GCCACCTGGCGGTGAACAATGGCATCGACACACCCAGCTGCTGCAGACCTCCCTGCAC	1689
Db	439	TyrLeuTrpThrAsnLysLysThrValAspLysLysGluValLeuLysTyrLeuProAsp	458
Qy	1690	GAGTGGCGGACAGATCGCATGCACCTGCACAAAGGAGTCTCTG---CAGCTGCCCATCTG	1746
Db	459	LysLeuArgAlaGluIleAlaIleAsnValHisLeuAspThrLeuLysLysValArgIle	478
Qy	1747	TTTGAGCGCGACGCGCGCTGCTGCGGGCACTGCTCTGGCCCTGCGCGCGCGCTTC	1806
Db	479	PheAlaAspCysGluAlaGlyLeuLeuValGluLeuValLeuLysLeuGlnProGlnVal	498
Qy	1807	TGCACCGCGCGAGTAGTACCTCATCCCAAGGGCGATCCCTCGACGGCCCTCTACTTTGTG	1866
Db	499	TyrSerProGlyAspTyrIleCysLysLysGlyAspIleGlyArgGluMetTyrIleIle	518
Qy	1867	TGCTCTGGCTCCATGAGGTGCTC-----AAGGTGGCACCGTGTCTGCGCATCTTAGGG	1920
Db	519	LysGluGlyLysLeuAlaValAlaAspAspGlyIleThrGlnPheValValLeuSer	538

QY	1921	AAGGGGACCTGATCGGC-----TGTGAGCTGCCCGCGGAGCAGGTTGGTA	1961
Db	539	AspGlySerTyrPheGlyGluIleSerIleLeuAsnIleLysGlySerTyrSAlaGlyAsn	558
QY	1969	AAGGCCAATGCCGAGCTGAAGGGCTGACCTACTCGCTCTCGCAGTGTCTGCAGCTGGCT	2028
Db	559	ArgArgThrAlaAsnIleLysSerIleGlyTyrSerAspLeuPheCysLeuSerLysAsp	578
QY	2029	GGCCTGCACGACAGCCCTGGCGTGTACCCGAGTTTGCCCGCGCTTCAGTCTGGCGCTC	2088
Db	579	AspLeuMetGluAlaLeuThrGluTyrProAsp-----AlaLysThrMet	593
QY	2089	CGAGGGAGCTCAGCTACAACCTGGTGTGGGGAGGCTCTGCAGAGGTGGACACCGC	2148
Db	594	LeuGluGluLysGlyLysGlnIleLeuMetLysAspGlyLeuLeuAspIleAsnIleAla	613
QY	2149	TCCCTGAGCGCGACAATACCTTATGTCACGCTGGAGGAGAGGAGACA	2199
Db	614	AsnAlaGlySerAsp-----ProLysAspLeuGluGluLysValThr	627
RESULT 15			
QY	S74179	cyclic nucleotide-gated channel protein - human	
Db	C:Species: Homo sapiens (man)		
QY	C:Date: 14-Apr-1998	#sequence_revision 24-Apr-1998	#text_change 16-Jul-1999
Db	C:Accession: S74179		
QY	R:Yu, W.P.; Grunwald, M.E.; Yau, K.W.		
Db	FEBS Lett. 393, 211-215, 1996		
QY	A:Title: Molecular cloning, functional expression and chromosomal localization		
Db	A:Reference number: S74179; MUID:96409310; PMID:8814292		
QY	A:Accession: S74179		
Db	A>Status: not compared with conceptual translation		
QY	A:Molecule type: mRNA		
Db	A:Residues: 1-695 <YUW>		
QY	A:Experimental source: retina		
Db	C:Genetics:		
QY	A:Map position: 2		
Db	C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nu		
QY	C:Keywords: ion channel; ion transport; membrane protein		
Db	F:482-607/Domain: cAMP receptor protein cyclic nucleotide-binding domain homolo		
Alignment Scores:			
Pred. No.:	2,12e-14	Length:	695
Score:	420.00	Matches:	141
Percent Similarity:	42.25%	Conservative:	96
Best Local Similarity:	25.13%	Mismatches:	218
Query Match:	6.90%	Indels:	106
DB:	2	Gaps:	17
US-09-965-930-1_COPY_6_3257 (1-3252) x S74179 (1-695)			
QY	787	GTCTGTGACCTGGCGGTGGAGGTCTCTTCATCCTCTGACATTTGCTGTAATTTCCGTACC	846
Db	205	ValLeuAspTyrSerAlaAspValLeuTyrValLeuAspValLeuValArgAlaArgThr	224
QY	847	ACATTGCTGTCAGTGGCGGCCAGGTGGTGTGGCCCCAAGTCCATTTCCTCCCTAC	906
Db	225	GlyPheLeu---GluGlnGlyLeuMetValSerAspThrAsnArgLeuTrpGlnHisTyr	243
QY	907	---GTCACCACTGTTTCCTGCTGGATGTTCATCGCAGCGCTGCCCTTTGACCTGCTACAT	963
Db	244	LysThrThrThrGlnPheLysLeuAspValLeuSerLeuValProThrAspLeuAlaTyr	263
QY	964	GCCTTCAAGTTCACGTGTACTTCGGGGCCCATCTCTGCTGAAGACGGTGGCGCTGCTGC	1023
Db	264	---LeuLysValGlyThrAsnTyrProGlu-----ValArgPheAsnArgLeuLeuLys	280
QY	1024	CTGCTGGCGCTGCTTCGCGGCTGGACCGGTACTCG-----	1059
Db	281	PheSerArgLeuPheGluPhePheAspArgThrGluThrArgThrAsnTyrProAsnMet	300
QY	1060	---CAGTACAGCGCGGTGGTGGTGCACACTGCTCATGGCCGTGTTCGCCCTGTCGGCAC	1116

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Db 301 PheArgIleGlyAsnLeuValLeuTyrIleLeu-----IleIleIleHis 315
QY 1117 TGGTCCCTCGTCTGTTTTCATTGGCCAGCGGAGATCGAGACGAGATCCGAG 1176
Db 316 TrpAsnAlaCysIleTyrPheAlaIleSerLys----- 326
QY 1177 CTGCCTCAGATTGGCTGGCTGCAGGAGCTGGCCCGCGAGACTCCCTACTACTG 1236
Db 327 -----PheIleGlyPhe----- 330
QY 1237 GTGGCCCGGAGCCAGCTGGAGGGAACAGCTCCCGCCAGAGTGACAACTGCAGCAGCAGC 1296
Db 331 -----GlyThrAspSerTrpValTyrProAsnIleSerIlePro 343
QY 1297 AGCAGAGCCCAACGGGACGCGGCTGGAGCTGTGGGCGCGCTGCTGCGCAGCGCCTAC 1356
Db 344 GluHisGlyArg-----LeuSerArgLysTyr 352
QY 1357 ATCACCTCCCTACTTTCGCACTCAGCAGCTCACCAGCTGCGGTGGCTTCGCGCAAGCTGTCC 1416
Db 353 IleTyrSerLeuTyrTrpSerThrLeuThrLeuThrIleGly-----GluThrProPro 371
QY 1417 GCCAACACGACGACCGGAGAGATCTTCTCCATCTGCACCATGCTCATCGGCGCCCTGATG 1476
Db 372 ProValLysAspGluLeuTyrLeuPheValValValAspPheLeuValGlyValLeuIle 391
QY 1477 CAGCGGTGTGTGGTGGAGCGTGAACGCGCATATCCAGGCGCATGTACGCCCGCGCTTT 1536
Db 392 PheAlaThrIleValGlyAsnValGlySerMetIleSerAsnMetAsnAlaSerArgAla 411
QY 1537 CTGTACCACAGCCGACGCGGAGCTGGCGGACTACATCCGCATCCACCGTATCCCAAG 1596
Db 412 GluPheGlnAlaLysIleAspSerIleLysGlnTyrMetGlnPheArgLysValThrLys 431
QY 1597 CCCCTCAAGCAGCATGCTGGAGTACTTCCAGGCCACCTGGCGGTGAACAATGGCATC 1656
Db 432 AspLeuGluThrArgValIleArgTrpPheAspTyrLeuTrpAlaAsnLysLysThrVal 451
QY 1657 GACACACCGAGTGTGTCGAGAGCTCCCTGACGAGTGGCGCGCAGACATCGCCATGCAC 1716
Db 452 AspGluLysGluValLeuLysSerLeuProAspLysLeuLysAlaGluIleAlaIleAsn 471
QY 1717 CTGCACAGGAGGTCCTG---CAGCTGCCACTGTTTGAGGCGGCCAGCGCGGTGCTG 1773
Db 472 ValHisLeuAspThrLeuLysLysValArgIlePheGlnAspCysGluAlaGlyLeuLeu 491
QY 1774 CGGCACTGTCTGCGCCCTGCGCGCCGCTTCTGCACGCGCGGAGTACTCATCCAC 1833
Db 492 ValGluLeuValLeuLysLeuArgProThrValPheSerProGlyAspTyrIleCysLys 511
QY 1834 CAAGCGATGCCGTGACGGCCCTTACTTTGTCTGTGCTCGCTCCATGGAGGTGCTC--- 1890
Db 512 LysGlyAspIleGlyLysGluMetTyrIleIleAsnGluGlyLysLeuAlaValAla 531
QY 1891 ---AAGGTTGGCAGCTGCTCGCCATCTAGGGAAGGGCGACCTGATCGGC----- 1938
Db 532 AspAspGlyValThrGlnPheValValLeuSerAspGlySerTyrPheGlyGluIleSer 551
QY 1939 ---TGTGAGTGTCCCGCGGAGCAGGTGTGTAAGGCCAATGCCAGCTGAAGGGGCTG 1995
Db 552 IleLeuAsnIleLysGlySerLysSerGlyAsnArgArgThrAlaAsnIleArgSerIle 571
QY 1996 ACGTACTGCGTCTGTCAGTGTCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2055
Db 572 GlyTyrSerAspLeuPheCysLeuSerLysAspAspLeuMetGluAlaLeuThrGluTyr 591
QY 2056 CCCGAGTTTGGCCGCTTCAGTCTGCTGGCTCCGAGGGGAGCTCAGCTACACCTGGGT 2115
Db 592 ProGlyGlnAlaLysLys----- 597
QY 2116 GCTGGGGGAGGCTCTGCGAGAGGTGGACACAGCTCCCTGAGCGGCGCAATACCTTATG 2175
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Db 598 -----AlaLeuGluGluLysGlyArgGlnIleLeuMetLysAspAsnLeuIleAsp 614
QY 2176 TCACAGCTGAGGAGAGAGACAGATGGGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGG 2235
Db 615 GluGluLeuAlaArgAlaGlyAlaAsp-----ProLysAsp 626
QY 2236 GCTGATGAGCCCTCCAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2295
Db 627 LeuGluGluLysValGluGlnLeuGlySerSerLeuAspThrLeuGlnThrArgPheAla 646
QY 2296 AAGCTGTCTATCCCCACGCTCGAACAGCACCC-----CGGCTCTGCTA----- 2337
Db 647 ArgLeuLeuAlaGluTyrAsnAlaThrGlnMetLysMetLysGlnArgLeuSerGlnLeu 666
QY 2338 -----GGTGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2382
Db 667 GluSerGlnValLysGlyGlyAspLysProLeuAlaAspGlyGluValProGlyAsp 686
QY 2383 GCT 2385
Db 687 Ala 687
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Search completed: September 1, 2004, 15:40:30
Job time : 225.5 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 1, 2004, 14:38:36 ; Search time 5277 Seconds
(without alignments)
18402.845 Million cell updates/sec

Title: US-09-965-830-1_COPY_6_3257

Perfect score: 3252

Sequence: 1 atgcggccatgcccgcct.....aagaaggcacaggggtctga 3252

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST:*

1: em_estab:*

2: em_estum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_estl:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_man:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gssl:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	844.4	26.0	1114	14	U69184
2	802.4	24.7	896	12	BM452074
3	783.4	24.1	4015	11	AK048629
4	675.6	20.8	862	13	BU187340

5	662.8	20.4	766	10	BE795800
6	658.4	20.2	714	10	BE778330
7	608.6	18.7	617	10	AW249035
8	582.4	17.9	704	14	CD354565
9	550.6	16.9	651	9	AL134774
10	492	15.1	501	10	AW249298
11	477	14.5	865	14	CD106245
12	470	14.7	482	10	BE266788
13	424	13.0	424	9	AI272282
14	369.8	11.4	682	13	BQ444229
15	361	11.1	522	12	BI975332
16	345	10.6	710	12	BQ045257
17	337.4	10.4	387	14	R35526
18	328.4	10.1	463	14	R73353
19	315.6	9.7	572	14	CB055396
20	313	9.6	391	14	RI3511
21	305.8	9.4	765	13	BU291269
22	305.6	9.4	328	9	AA325048
23	301.4	9.3	1076	12	BM561167
24	294.4	9.1	1115	12	BM547060
25	284.2	8.7	351	14	R35105
26	278.8	8.6	839	12	BI737339
27	271.4	8.3	438	14	CB751495
28	261.8	8.1	337	10	BF449484
29	259.8	8.0	909	13	BX391570
30	258.8	8.0	924	14	CA454037
31	256	7.9	878	13	BU170580
32	255.8	7.9	615	14	CB579755
33	250.2	7.7	438	29	CG479581
34	246.6	7.6	635	10	BF589083
35	246	7.5	661	12	BI390873
36	242.8	7.5	4059	11	AK032438
37	242.2	7.4	749	13	BU07188
38	242.2	7.4	784	13	BU07166
39	239.6	7.4	815	12	BM948237
40	238.8	7.3	853	13	BU164703
41	234	7.2	558	9	AI450906
42	232.6	7.2	315	13	BY363096
43	228	7.0	926	13	EX327696
44	227.8	7.0	475	9	AW082228
45	227.4	7.0	2894	29	AY409916

ALIGNMENTS

RESULT 1	U69184	U69184	1114 bp	mRNA	linear	EST 27-OCT-1999
LOCUS	U69184	Soares infant brain INIB	Homo sapiens	cdna	clone 37299	mrna
DEFINITION	U69184	Soares infant brain INIB	Homo sapiens	cdna	clone 37299	mrna
ACCESSION	U69184	sequence.				
VERSION	U69184.1	GI:2739408				
KEYWORDS	EST.					
SOURCE	Homo sapiens					
ORGANISM	Homo sapiens					
REFERENCE	1	(bases 1 to 1114)				
AUTHORS	Volorio, S., Simon, G., Repetto, M., Cucciard, M., Banfi, S., Borsani, G., Ballabio, A. and Zollo, M.					
TITLE	Sequencing analysis of forty-eight human image cDNA clones similar to drosophila mutant protein					
JOURNAL	DNA Seq. 9 (5-6), 307-315 (1998)					
MEDLINE	99452388					
PUBMED	10524757					
COMMENT	Contact: Zollo, Massimo Telethon Institute of Genetics and Medicine Via Olgettina 58, Milan, MI 20132, Italy Email: zollo@tigem.it. Location/Qualifiers 1. .1114 /organism="Homo sapiens"					
FEATURES	source					

Db	965	ACTGTGCCCTACAGCGTGTGTGTGAGCACAGCAAGCGGAGCCAGAGTGCCTGCGCGCGGCCG 102
Qy	781	CCAGCGTCTGTGACCTGGCCGCTGGAGTCTCTTTCATCTTTCACATTTGCTGCTGAATTC 840
Db	1025	CCAGCGTCTGTGACCTGGCCGCTGGAGTCTCTTTCATCTTTCACATTTGCTGCTGAATTC 1084
Qy	841	CGTACC 846
Db	1085	CGTACC 1090
RESULT 2		
LOCUS	BM452074	896 bp mRNA linear EST 05-FEB-2002
DEFINITION	AGENCOURT_6397332 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5492993	
ACCESSION	5', mRNA sequence.	
VERSION	BM452074	
KEYWORDS	BM452074.1 GI:18501114	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
TITLE	1 (bases 1 to 896)	
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/ .	
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabs-r@mail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LHAM2115 row: p column: 18 High quality sequence stop: 610. Location/Qualifiers 1..896 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:5492993" /tissue_type="retinoblastoma" /lab_host="DH10B (phage-resistant)" /clone_lib="NIH MGC 67" /note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.75 kb. Library constructed by Life Technologies."	
FEATURES	source	
ORIGIN		
Query Match	24.7%;	Score 802.4; DB 12; Length 896;
Best Local Similarity	95.2%;	Pred. No. 2.7e-120;
Matches 849;	Conservative	0; Mismatches 41; Indels 2; Gaps 2;
Qy	292	ATCTGTACCGAAGAGCGGCTCCCGTTCTGGTGTCTCTGGATGTATCCCATTAAG 351
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Db	61	AATGAGAAAGGGAGTGGTCTCTCTCTAGTCTCTCACAGGACATCAGCGAAACCAAG 120
Qy	412	AACCGAGGGGCCCCCGACAGATGAAGAGACAGGTGGTGGCCCGCGCCGATATGGCCGG 471
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Qy	472	GCAGATCCAAAGGCTCAATGTCACCGCGCGGAGCCGGGCCGTCTTACACCTG 531
Db	181	GCAGATCCAAAGGCTCAATGTCACCGCGCGGAGCCGGGCCGTCTTACACCTG 240

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Db 301 GAGAAACCAACTTGCCTGAGTCAAAAGTAGCCGCCATCCGGAAGTCCGCCCTTCATCTGT 360
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Db 361 TTGCACGTGGGCACTGAGAGCCACCTGGATGGCTTCATCCCTGCGCCACACTCTAT 420
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Db 421 GTGGCTGTCACTGTGCCCTACAGCGTGTGTGTGACACAGCAGCGGAGCCAGTCCGCC 480
QY 772 CGCGGCCCGCCAGCGTGTGTGACCTGGCGGTGGAGTGCCTTTCATCTTGCATTTGTG 831
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QY 832 CTGAATTTCCGTACCACTTCGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCC 891
Db 541 CTGAATTTCCGTACCACTTCGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCC 600
QY 892 ATTTGCCCTCCACTACGTCCACACCTGGTTCCTGCTGGATGTCATCGCAGCGCTGCCCTTT 951
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QY 952 GACCTGTGATGCTTCAAGGTCAAGTGTGATCTTGGGGGCCATCTGCTGAAGACGGTG 1011
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QY 1012 CGCTGCTGGCGCTGCTGCGCTGCTTCCGGCGTGGACCGGCTGCTGCTGCTGCTGCTGCT 1070
Db 721 CGCTGCTGGCGCTGCTGCGCTGCTTCCGGCGTGGACCGGCTGCTGCTGCTGCTGCTGCT 780
QY 1071 CGTGGTGTGACACTGTCTCAT-GGCCGTGTTCCGCTGCTGCGCACTGGGTGCGCTGCG 1129
Db 781 CGTGGGCTGACACTGTCTCATGGGCGCTGTTCCGCTGCTGCGCATTTGGGCCCTTGGC 840
QY 1130 TCTGTTTTCATTTGCGCAGCGGAGATCGAGACGGAATCCGAGCTGCC 1181
Db 841 GTCTGTTTTCATTTGCGCAGCGGAGATCGAGACGGAATCCGAGCTGCC 892

RESULT 3
AK048629
LOCUS Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library, clone:CI30090D05 product:ELK CHANNEL 3 (FRAGMENT) homolog [Rattus norvegicus], full insert sequence.
ACCESSION AK048629
VERSION AK048629.1 GI:26339459
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
```

AUTHORS

Shibata,K., Itoh,M., Aizawa,K., Nagaoaka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsuunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,K., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multipillar sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861

TITLE

The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection

Nature 409, 685-690 (2001)

REFERENCE

AUTHORS

The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

REFERENCE

AUTHORS

Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imoto,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL:http://genome.gsc.riken.go.jp/

URL:http://fantom.gsc.riken.go.jp/.

FEATURES

source

1. .4015
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:CI30090D05"
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/clone="CI30090D05"
/tissue_type="head"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="16 days embryo"
<1. .3294
/note="unnamed protein product; ELK CHANNEL 3 (FRAGMENT) homolog [Rattus norvegicus] (SPTR|Q9QWS8, evidence: FASTY, 98.4%ID, 100length, match=1098) putative"
/codon_start=1
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/translation="GLLAPQNTFLDTIATFRDGTSHNSFILANQAVKGFPIVYCGDGF"

CDS


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Qy      1876  TCCATGAGGTGTCCTAAGAGTGGACCGTGTCCCATCTCCTAGGGAAGGCGACCTGATC 1935
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Qy      1936  GCGTGTGAGTGTCCCGGGGAGCAGGTGGTAAAGCCCAATGCGCAGCTGAAGGGCTG 1995
Db      1828  GGAGCAAAATTATCAATTAAGACCAAGTGATCAAGACCAACGCTGATGAAGGCGCTG 1887
Qy      1996  ACGTACTGCGTCTCCAGTGTCTGCAGTGTCTGCAGTGTCTGCCTGCACGACAGCTTGCCTGTAC 2055
Db      1888  ACCTACTGTGATCTACAGTGCATCATCTTGAAGGTCTCTTTGAGTGTCTGGGCTTTAC 1947
Qy      2056  CCCAGTGTGCGCGCGCTTCAGTGTGCGCTCCGAGGGAGCTCAGTACAACTGGGT 2115
Db      1948  CCAAGTATGCACAAATTCGTAGAAGACATCCAGCAGCACTTACATACAACTTCGA 2007
Qy      2116  GCTGG 2120
Db      2008  GAAGG 2012

RESULT 4
BUI87340 862 bp mRNA linear EST 04-SEP-2002
LOCUS AGENCOURT 788853 NIH_MGC_67 Homo sapiens cdna clone IMAGE:6140620
5', mRNA sequence.
ACCESSION BUI87340
VERSION BUI87340.1 GI:22701324
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 862)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL NIH-MGC http://mgc.nci.nih.gov/
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cdna Library Preparation: Life Technologies, Inc.
cdna Library Arrayed by: The I.M.A.G.E. Consortium (LMLL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMLL at:
http://image.llnl.gov
Plate: L1AM13459 row: i column: 05
High quality sequence stop: 522.
Location/Qualifiers
1. .862
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6140620"
/lab_host="DH10B (phage-resistant)"
/tissue_type="retinoblastoma"
/clone_lib="NIH MGC 67"
/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 Kb. Library constructed by Life
Technologies."

FEATURES
source
Query Match 20.8%; Score 675.6; DB 13; Length 862;
Best Local Similarity 94.5%; Pred. No. 1.1e-99;
Matches 763; Conservative 0; Mismatches 37; Indels 7; Gaps 6;

ORIGIN
545 AGAAGCAGCCCAAGGCGAAGCAGCAGCTCAATAAGGGGGTGTTCGGGAGAAACCAACT 604
Db      1 AGAAGCAGCCCAAGGCGAAGCAGCAGCTCAATAAGGGGGTGTTCGGGAGAAACCAACT 60


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Qy      605  TGCTGAGTACAAAGTAGCCGCATCCGGAAGTCGCCCTTCATCCTCTGTGCACTGTGGG 664
Db      61  TGCTGAGTACAAAGTAGCCGCATCCGGAAGTCGCCCTTCATCCTCTGTGCACTGTGGG 120
Qy      665  CACTGAGAGCCACTGGGATGGCTTCATCCTGTCTGCCACACTATATGTGGCTGTCACTG 724
Db      121  CACTGAGAGCCACTGGGATGGCTTCATCCTGTCTGCCACACTATATGTGGCTGTCACTG 180
Qy      725  TGCCTACAGCGTGTGTGAGCACAGCAGGAGCCAGTGCCTGCGGCGGCGGCGGCCCA 784
Db      181  TGCCTACAGCGTGTGTGAGCACAGCAGGAGCCAGTGCCTGCGGCGGCGGCGGCCCA 240
Qy      785  GCGTCTGTGACCTTGGCGGTGGAGTCTCTTCACTCTTGACATTTGCTGAATTTCCGTA 844
Db      241  GCGTCTGTGACCTTGGCGGTGGAGTCTCTTCACTCTTGACATTTGCTGAATTTCCGTA 300
Qy      845  CCACATTCGTGTCCAACTCGGGCCAGGTGTGTTTGGCCCAAGTCCATTTGCTCCACT 904
Db      301  CCACATTCGTGTCCAACTCGGGCCAGGTGTGTTTGGCCCAAGTCCATTTGCTCCACT 360
Qy      905  ACGTCACCACTGTTCTCTGCTGATGTCTCGAGCGCTGCCCTTTGACCTGTACATG 964
Db      361  ACGTCACCACTGTTCTCTGCTGATGTCTCGAGCGCTGCCCTTTGACCTGTACATG 420
Qy      965  CTTTCAAGGTCAACGTGTACTTTCGGGGCCCATCTGCTGAAGACGCTGCGCTGTGCGCC 1024
Db      421  CTTTCAAGGTCAACGTGTACTTTCGGGGCCCATCTGCTGAAGACGCTGCGCTGTGCGCC 480
Qy      1025  TGTGTCGCCCTGCTTTCGGCGGTGGACCGGTACTCGCAGTACAGCG - CCGTGGTGTGACA 1083
Db      481  TGTGTCGCCCTGCTTTCGGCGGTGGACCGGTACTCGCANACAAAGCGCGCTGTGCTGACA 540
Qy      1084  CTGCTATAGCGGTGTTGCGCCCTGCTCGCGCACTGGGTGCGCT - GCGTCTGTTTACAT 1142
Db      541  CTGCTATAGCGGTGTTGCGCCCTGCTCGCGCACTGGGTGCGCTGCGCTGTGTTTACAT 600
Qy      1143  TGGCCAGC - GGGAGATCGAGACGAGCAATCCGAGCTGCCT - GAGATTGGCTGGCTGCAG 1200
Db      601  TGGCCAGCNGGGAGATCGAGACGAGCAATCCGAGCTGCCTGAGATGGTGGCTGCAG 660
Qy      1201  GAGCTGGCCCGCCGACTGGAGACTCCCTACTACCTGGTGGG - CCGGAGGCCAGCTGAG 1258
Db      661  GAGCTGGCCCGCCGACTGGAGACTCTANTTTACTGGGGGGGGCGGAGCCAGCAGCTGAG 720
Qy      1259  GGAACAGC - TCGGCGCAGTGAACACTGAGCAGCAGCAGCGAGGCGCAAGCGACGGG 1317
Db      721  GGAACAGCTTCCGGCCAGAGTGACAACCTGCAGCAGCAGCAGCGAGGCGCAAGCGACGG 780
Qy      1318  CTGGAGCTGTGTGGCGCCCGCTGCTG 1344
Db      781  GGCTGGAACCTGTGTGGCGCGGCGCCCG 807

RESULT 5
BUI795800
LOCUS BE795800
DEFINITION 601590834F1 NIH_MGC_7 Homo sapiens cdna clone IMAGE:3944793 5',
mRNA sequence.
ACCESSION BE795800
VERSION BE795800.1 GI:10216998
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 766)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL NIH-MGC http://mgc.nci.nih.gov/
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP


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CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLC802 row: d column: 10
High quality sequence start: 5
High quality sequence stop: 763.
Location/Qualifiers
1. .766
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3944793"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; CDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5',
adaptor: GGACAGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 20.4%; Score 662.8; DB 10; Length 766;
Best Local Similarity 96.4%; Pred. No. 1.3e-97;
Matches 744; Conservative 0; Mismatches 17; Indels 11; Gaps 6;

QY 2219 CGGTCTCCCGAGCCCGAGCTGATGAGCCCTCCAGCCCGCTGTCTCCCTGGCTGCACCT 2278
DB 4 CGGTCTCCCGAGCCCGAGCTGATGAGCCCTCCAGCCCGCTGTCTCCCTGGCTGCACCT 63
QY 2279 CCTCATCTCAGTGCAGCTGCTATCCAGCTCGAAGCAGCACCAGCCGCTCTGCTAG 2338
DB 64 CCTCATCTCAGTGCAGCTGCTATCCAGCTCGAAGCAGCACCAGCCGCTCTGCTAG 123
QY 2339 GTGGCAGAGGAGGCGCAGGCGAGGGGCTTTGAAGCTGAGGCTGGCCCTCTGCTC 2398
DB 124 GTGGCAGAGGAGGCGCAGGCGAGGGGCTTTGAAGCTGAGGCTGGCCCTCTGCTC 183
QY 2399 CCCCACGGGCGCTAGAGGGGCTACGGCTGCCCCCATGCCATGCAATGTGCCCCAGATC 2458
DB 184 CCCCACGGGCGCTAGAGGGGCTACGGCTGCCCCCATGCCATGCAATGTGCCCCAGATC 243
QY 2459 TGAGCCCCAGGCTAGTAGTGGATTGAAGCGGCTGTGGCTCGGACGACCCAGATTCT 2518
DB 244 TGAGCCCCA-GTAGTAGATGGATTGAAGCGGCTGTGGCTCGGACGACCCAGATTCT 302
QY 2519 CTTTCGGCTGGGCGCAGTCTGGCCCGAATGTAGCAGAGCCCTCCCTGGACACAGAGA 2578
DB 303 CTTTCGGCTGGGCGCAGTCTGGCCCGAATGTAGCAGAGCCCTCCCTGGACACAGAGA 362
QY 2579 GCGGCTGTCTACTGTTTCCCATGGCCCGCAGGAGCAAGGAACACAGACACTGGACA 2638
DB 363 GCGGCTGTCTACTGTTTCCCATGGCCCGCAGGAGCAAGGAACACAGACACTGGACA 422
QY 2639 AGCTTCGCGAGCGGCTGACAGAGCTGTGACAGAGGTGTGACAGTCCGGGAGGACTGC 2698
DB 423 AGCTTCGCGAGCGGCTGACAGAGCTGTGACAGAGGTGTGACAGTCCGGGAGGACTGC 482
QY 2699 AGTCACTTCGCGAGGCTGTGACAGTGTCTGCGCGCCACACAGGAGGCTTCGTGCCCTC 2758
DB 483 AGTCACTTCGCGAGGCTGTGACAGTGTCTGCGCGCCACACAGGAGGCTTCGTGCCCTC 542
QY 2759 GGGCATTCGGGAGAGGGGCGTGTGCCACGACCACTTCCGGGCTTTCGACGCTCTGTGTG 2818
DB 543 GGGCATTCGGGAGAGGGGCGTGTGCCACGACCACTTCCGGGCTTTCGACGCTCTGTGTG 602
QY 2819 TGGACACTTGGGCGATCTCTCTACTGCTTCGACCCCCAGCTGGCTCTGTCTTGTAGTGGGA 2878

Db 603 TGCACACTGGGGCATCTCTACTGCTGCAG-CCCAGCTGGCTGTCTTGTAGTGGGA 661
QY 2879 CTTTGGCCCCACCTCTCTCGGGGCTCTCCCTCATGGCACCTGGCCCTGGGTCCTCC 2938
Db 662 CTTTGG-CCCACTCTCTCGGGGCTCTCTCTCC-TCATGCACCTGGCCCTGGGCT-CCC 715
QY 2939 CAGCGTCTCAGAGCTCCCTCGCTCGAGCCACAGCTTCTGACCTCCAC 2990
Db 716 CAGCGTCTCAGAGCTCGCTGCTCGAG---CACAGCTTCTGAGACTTCCAC 764

RESULT 6

BE778330
LOCUS BE778330 714 bp mRNA linear EST 20-OCT-2000
DEFINITION G01463723F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3867076 5',
mRNA sequence.

ACCESSION

BE778330

VERSION

BE778330.1 GI:10199528

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ARCC

COMMENT

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM9612 row: n column: 05
High quality sequence stop: 691.

FEATURES

Location/Qualifiers
1. .714
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3867076"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_67"
/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."

ORIGIN

Query Match 20.2%; Score 658.4; DB 10; Length 714;
Best Local Similarity 99.3%; Pred. No. 6.4e-97;
Matches 703; Conservative 0; Mismatches 1; Indels 4; Gaps 4;

QY 377 TCCTAGTCTCTCACAGGACATCAGGAACCAAGAACCGAGGGGGCCCCGACAGATGGA 436
Db 1 TCCTAGTCTCTCACAGGACATCAGGAACCAAGAACCGAGGGGGCCCCGACAGATGGA 60
QY 437 AGGAGACAGGTGGTGGCCCGCCGATATGGCCGGGACGATCCAAAGCTTCAATGCCA 496
Db 61 AGGAGACAGGTGGTGGCCCGCCGATATGGCCGGGACGATCCAAAGCTTCAATGCCA 120
QY 497 ACCGGGGCGAGCCGGCCGTGTCTACCACTGTCCGGGCACTTCGACAGAGACGCCA 556
Db 121 ACCGGGGCGAGCCGGCCGTGTCTACCACTGTCCGGGCACTTCGACAGAGACGCCA 180
QY 557 AGGGCAAGCACAAAGCTCAATAGGGGGTGTGTTGGGGAGAAACCAACTTGCCTGAGTACA 616
Db 181 AGGGCAAGCACAAAGCTCAATAGGGGGTGTGTTGGGGAGAAACCAACTTGCCTGAGTACA 240

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QY 617 AAGTAGCGCCATCCGGAAGTCGCCCTTTCATCCGTGTTGCACTGTGGGGCACTGAGAGCCA 676
Db 241 AAGTAGCGCCATCCGGAAGTCGCCCTTTCATCCGTGTTGCACTGTGGGGCACTGAGAGCCA 300
QY 677 CTTGGGATGCTTCATCTGCTGCCACACTCTATATGTGGTGTCACTGTGCGCTTACAGCG 736
Db 301 CTTGGGATGCTTCATCTGCTGCCACACTCTATATGTGGTGTCACTGTGCGCTTACAGCG 360
QY 737 TGTGTGTGAGACAGACAGCGAGCCCACTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 796
Db 361 TGTGTGTGAGACAGACAGCGAGCCCACTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
QY 797 TGGCGGTGG-AGTCCCTTCATCTGACATCTGCTGCAATTCCTGACACATTCGTG 855
Db 421 TGGCGGTGGAGGTTCCTTCATCTGACATCTGCTGCAATTCCTGACACATTCGTG 480
QY 856 TCCAAAGTCGGGCGCCAGGTGTGTTTGGCCCCAAAGTCCATTTTGCTTCCACTAGTCACCAACC 915
Db 481 TCCAAAGTCGGGCGCCAGGTGTGTTTGGCCCCAAAGTCCATTTTGCTTCCACTAGTCACCAACC 540
QY 916 TGGTTCCTGCTGATGATCATCGAGCGTGCCTTTTGACCTGTACATGCTTCAAGGTC 975
Db 541 TGGTTCCTGCTGATGATCATCGAGCGTGCCTTTTGACCTGTACATGCTTCAAGGTC 600
QY 976 AAGCTGTACTTTCGGGGCCCTCTGCTGAAGACGCTGCGCTGCTGCGCTGCTGCGCTG 1035
Db 601 AAGCTGTACTTTCGGGG-CCATCTGCTGAAGACGCTGCGCTGCTGCGCTGCTGCGCTG 659
QY 1036 CTTCCGGCGGTGGACCGGTACTCGCAGTA-CAGCGCGCTGTGCTGTGAC 1082
Db 660 CTTACGCGG-TGGACCGGTACTCGCAGTACCAGCGCGGTGTGCTGTGAC 706
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RESULT 7
AW249035 617 bp mRNA linear EST 07-JAN-2000
LOCUS 2820908.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820908 5',
DEFINITION mRNA sequence.
ACCESSION AW249035
VERSION AW249035.1 GI:6592028
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2820908.3prime
Contact: Robert Strausberg, Ph.D.
Email: csapbs-remail.nih.gov
Tissue Procurement: DCTD/BTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross match from University of Washington Genome Center
PHRAP suite. Poly-T Identification: PatMatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu
Plate: LLCMS5 row: G column: 21
High quality sequence stop: 569.
FEATURES
source 1..617
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="IMAGE:2820908"
/tissue_type="small cell carcinoma"
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/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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ORIGIN	Query Match	18.7%	Score 608.6;	DB 10;	Length 617;
	Best Local Similarity	99.3%	Pred. No. 7.5e-89;		
	Matches 611;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;
QY	2431	CCCATGCGCATGGAATGTGCCCCAGATCTCAGCCCCAGGCTAGTGTGATGATGCAATTAAGAC	2490		
Db	3	CACGAGGCATGGAATGTGCCCCAGATCTCAGCCCCAGGCTAGTGTGATGATGCAATTAAGAC	62		
QY	2491	GGCTGTGGCTCGGACACAGCCCAAGTTCTCTTTCCGCGTGGGCCAGTCTGGCCCCGAATGT	2550		
Db	63	GGCTGTGGCTCGGACACAGCCCAAGTTCTCTTTCCGCGTGGGCCAGTCTGGCCCCGAATGT	122		
QY	2551	AGCAGCAGCCCTCCCTCGGACACAGAGCGGCTGTCTCACTGTTCCTCCATGGGCCACAGC	2610		
Db	123	AGCAGCAGCCCTCCCTCGGACACAGAGCGGCTGTCTCACTGTTCCTCCATGGGCCACAGC	182		
QY	2611	GAGCAAGGAACACAGACACACTGGCAAGCTTCGGCAGCGGTGACAGAGCTGTCTCAGAG	2670		
Db	183	GAGCAAGGAACACAGACACACTGGCAAGCTTCGGCAGCGGTGACAGAGCTGTCTCAGAG	242		
QY	2671	CAGGTGTCTCAGATGCGGGAAGACTCGAGTCACTTCGCCAGGCTGTGCAGCTTGTCTCTG	2730		
Db	243	CAGGTGTCTCAGATGCGGGAAGACTCGAGTCACTTCGCCAGGCTGTGCAGCTTGTCTCTG	302		
QY	2731	GCGCCCCACAGGAGGCTCGGTGCCCTCGGCAATCGGAGAGGCGCGTGCAGCCACAGC	2790		
Db	303	GCGCCCCACAGGAGGCTCGGTGCCCTCGGCAATCGGAGAGGCGCGTGCAGCCACAGC	362		
QY	2791	ACCTCCGGGCTTTCGACGCTCTGTGTGACACTGTGGGCACTGGGGCATCTCTACTGTGCTG	2850		
Db	363	ACCTCCGGGCTTTCGACGCTCTGTGTGACACTGTGGGCACTGGGGCATCTCTACTGTGCTG	422		
QY	2851	CCCCAGCTGTCTGTCTTGTAGTGGACACTTGGCCCCACCTCTCTCGGGGCTCTCTCCC	2910		
Db	423	CCCCAGCTGTCTGTCTTGTAGTGGACACTTGGCCCCACCTCTCTCGGGGCTCTCTCCC	482		
QY	2911	CTCATGGCACCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCT	2970		
Db	483	CTCATGGCACCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCT	542		
QY	2971	ACAGCTTTTGGACCTCCACTCAGACTCAGAGCCCCCTGTGCTCAGGAGACCTCTGTCTCT	3030		
Db	543	ACAGCTTTTGGACCTCCACTCAGACTCAGAGCCCCCTGTGCTCAGGAGACCTCTGTCTCT	602		
QY	3031	GAGCCCCAGACCCCT 3045			
Db	603	GAGCCCCAGACCCCT 617			

RESULT 8
CD354565 704 bp mRNA linear EST 15-JUL-2003
LOCUS UI-M-GMO-cgd-j-01-0-UI.r1 NIH_BMAP_GMO Mus musculus cDNA clone
DEFINITION IMAGE:30361272 5', mRNA sequence.
ACCESSION CD354565
VERSION CD354565.1 GI:31147066
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;


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Db 1 AGGAGTTCAAGCTGAGCTGATCTCTGTACGGAAGAGCGGCTCCGCTTCTGGTGTCTCC 60
QY 332 TGGATGTGATACCCATAAAGATGAGAAAGGAGGTGGTCTCTTCTAGTCTCTCACA 391
Db 61 TGGATGTGATACCCATAAAGATGAGAAAGGAGGTGGTCTCTTCTAGTCTCTCACA 120
QY 392 AGGACATCAGCGAAGCAAGAACCGAGGGGGCCCGACAGATGCAAGAGGACAGGTGGTG 451
Db 121 AGGACATCAGCGAAGCAAGAACCGAGGGGGCCCGACAGATGCAAGAGGACAGGTGGTG 180
QY 452 GCCGGCGCCGATATGCGCGGACGATCCAAAGGCTTCAATGCAACCGCGCGCGAGCC 511
Db 181 GCCGGCGCCGATATGCGCGGACGATCCAAAGGCTTCAATGCAACCGCGCGCGAGCC 240
QY 512 GGGCGGTGCTTACACCTTCTCGGGGACCTGAGAGAGAGCCCAAGGGCAAGCAGCAGC 571
Db 241 GGGCGGTGCTTACACCTTCTCGGGGACCTGAGAGAGAGCCCAAGGGCAAGCAGCAGC 300
QY 572 TCAATAAGGGGGTGTGGGGAGAAACCAAACTTGCCTGAGTACAAAGTAGCGCCATCC 631
Db 301 TCAATAAGGGGGTGTGGGGAGAAACCAAACTTGCCTGAGTACAAAGTAGCGCCATCC 360
QY 632 GGAAGTCGCCCTTTCATCTCTGTGACCTGTGGGCACTGAGAGCCACCTGGGATGGCTTCA 691
Db 361 GGAAGTCGCCCTTTCATCTCTGTGACCTGTGGGCACTGAGAGCCACCTGGGATGGCTTCA 420
QY 692 TCTGTCTGCGCACACTATGTGGCTGTACTGTGCGCTTACAGCGTGTGTGAGCAGCAG 751
Db 421 TCTGTCTGCGCACACTATGTGGCTGTACTGTGCGCTTACAGCGTGTGTGAGCAGCAG 480
QY 752 CAGGGAGCCAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 811
Db 481 CAGGGAGCCAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
QY 812 TCTTCATCTTGTACTGTG 831
Db 541 TCTTCATCTTGTACTGTG 560
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RESULT 10
AW249298
LOCUS 2821074.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821074 5',
DEFINITION mRNA sequence.
ACCESSION AW249298
VERSION AW249298.1 GI:6592291
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 501)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other ESTs: 2821074.3prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/BTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross match from University of Washington Genome Center
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu
Plate: LLCW5 row: N column: 19
High quality sequence stop: 500.
FEATURES
Location/Qualifiers
1..501
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821074"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
adapted to EcoRI/XhoI sites using the following 5'
adapter: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

Query Match	15.1%	Score 492	DB 10	Length 501
Best Local Similarity	100.0%	Pred. No. 6.3e-70		
Matches 492	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY 1263	CAGTCTCGGCGCAGATGACAACTGAGCAGCAGAGCGGCGGCTTGGG			1322
Db 10	CAGTCTCGGCGCAGATGACAACTGAGCAGCAGAGCGGCGGCTTGGG			69
QY 1323	GCTGTGCGGCGCGCGCTGCGTGGCGGCTTGGGCAACGTTGGG			1382
Db 70	GCTGTGCGGCGCGCGCTGCGTGGCGGCTTGGGCAACGTTGGG			129
QY 1383	CAGCTCACCAGCGGTGGGCTTGGGCAACGTTGGGCAACGTTGGG			1442
Db 130	CAGCTCACCAGCGGTGGGCTTGGGCAACGTTGGGCAACGTTGGG			189
QY 1443	CTCATCTGCACCATGCTCATGCGCGCCCTGATGCGCGCTTGGG			1502
Db 190	CTCATCTGCACCATGCTCATGCGCGCCCTGATGCGCGCTTGGG			249
QY 1503	GGCATCATCCAGCGCATGTACGCCCGCGCTTGTCTGTACCAAG			1562
Db 250	GGCATCATCCAGCGCATGTACGCCCGCGCTTGTCTGTACCAAG			309
QY 1563	GGCGGACTATACCGCATCCACCGTATCCCAAGCCCTTCAAGC			1622
Db 310	GGCGGACTATACCGCATCCACCGTATCCCAAGCCCTTCAAGC			369
QY 1623	CTTCCAGGCGACCTGGGCGGTGAACAATGATGATGATGATGAT			1682
Db 370	CTTCCAGGCGACCTGGGCGGTGAACAATGATGATGATGATGAT			429
QY 1683	CCCTGAGCGTGGCGCGCAGACATCGCCATGCACTGCAAGGAGG			1742
Db 430	CCCTGAGCGTGGCGCGCAGACATCGCCATGCACTGCAAGGAGG			489
QY 1743	ACTGTTTGGAGC 1754			
Db 490	ACTGTTTGGAGC 501			

RESULT 11
CD106245
LOCUS CD106245
DEFINITION AGENCOURT 13980050 NIH_MGC_179 Homo sapiens cDNA clone
IMAGE:30368984 5', mRNA sequence.
ACCESSION CD106245
VERSION CD106245.1 GI:30759419
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 865)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: ND4432 row: k column: 09
High quality sequence stop: 548.
Location/Qualifiers
1. .865
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30368984"
/tissue_type="Pituitary"
/lab_host="DH10B-Ton A (T1 and T5 phage resistances)"
/clone_lib="NIH MGC 179"
/notes="Organ: Brain; Vector: pCMV-SPORT6.1; Site 1: EcoRV (destroyed); Site 2: NotI; Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.1 kb. Library was constructed by (Invitrogen). Note: this is a NIH MGC Library."
ORIGIN
Query Match 14.7%; Score 477; DB 14; Length 865;
Best Local Similarity 100.0%; Pred. No. 2.1e-67;
Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2776 CCGTGGCCAGCAGCACCTCCGGGCTTCTGCAGCCCTCTGTGTGTGACACTGGGGCATCC 2835
DB 1 CCGTGGCCAGCAGCACCTCCGGGCTTCTGCAGCCCTCTGTGTGTGACACTGGGGCATCC 60
QY 2836 TCCTACTGCTGAGCCGCCAGCTGGCTCTGTCTTGTAGTGGGACTTGGCCCACTCCCTGCT 2895
DB 61 TCCTACTGCTGAGCCGCCAGCTGGCTCTGTCTTGTAGTGGGACTTGGCCCACTCCCTGCT 220
QY 2896 CCGGGGCTTCCTCCCTCATGGACCCCTGGCCCTGGGGTCCCGACGCTCTAGAGCTCC 2955
DB 121 CCGGGGCTTCCTCCCTCATGGACCCCTGGCCCTGGGGTCCCGACGCTCTAGAGCTCC 180
QY 2955 CCCTGGCTTCGAGCCACAGCTTCTGACCTCCACCTCAGACTCAGAGCCCTCGCTCA 3015
DB 181 CCCTGGCTTCGAGCCACAGCTTCTGACCTCCACCTCAGACTCAGAGCCCTCGCTCA 240
QY 3016 GGAGACCTTGCTCTGAGCCAGCACCTTGCTCCCTTCCTCTTCGAGGAAGGGCT 3075
DB 241 GGAGACCTTGCTCTGAGCCAGCACCTTGCTCCCTTCCTCTTCGAGGAAGGGCT 300
QY 3076 AGGACTGGCCCGCAGAGCCTGTGAGCCAGGCTGAGGCTACAGCACTGGAGGCCCA 3135
DB 301 AGGACTGGCCCGCAGAGCCTGTGAGCCAGGCTGAGGCTACAGCACTGGAGGCCCA 360
QY 3136 CCAGGCTCAGGGGGCTTGGCTTGGCTGGGACCCGCCACAGCCTGGAGATGGCTTATT 3195
DB 361 CCAGGCTCAGGGGGCTTGGCTTGGCTGGGACCCGCCACAGCCTGGAGATGGCTTATT 420
QY 3196 GGCTGCGATGGCTCTGGGCACTGTCCAGTGGAACCCAGGAAGAGGACAGGGGCTTGA 3252
DB 421 GGCTGCGATGGCTCTGGGCACTGTCCAGTCCAGTGGACCCAGGAAGGACAGGGGCTTGA 477
RESULT 12
BE266788
LOCUS 601190482F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3534309 5',
DEFINITION mRNA sequence.
ACCESSION BE266788

VERSION BE266788.1 GI:9140371
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
1 (bases 1 to 482)
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Plate: LLC213 row: d column: 22
High quality sequence stop: 482.
Location/Qualifiers
1. .482
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/tissue_type="small cell carcinoma"
/cell_line="WGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 7"
/notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN
Query Match 14.5%; Score 470; DB 10; Length 482;
Best Local Similarity 99.8%; Pred. No. 2.3e-66;
Matches 481; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 2456 ATCTCAGCCCCCAGGGTAGTAGATGGCATTGAAGAGCGGTGTGGCTCGGACCAAGCCAAAGT 2515
DB 1 ATCTCAGCCCCCAGGGTAGTAGATGGCATTGAAGAGCGGTGTGGCTCGGACCAAGCCAAAGT 60
QY 2516 TCTCTTTTCGGCTGGGCCAGTCTGGCCCGGAATGTAGCAGAGCCCCCTCCCTTGGACCAAG 2575
DB 61 TCTCTTTTCGGCTGGGCCAGTCTGGCCCGGAATGTAGCAGAGCCCCCTCCCTTGGACCAAG 120
QY 2576 AGAGCGGCTGTCTCACTGTTCCCATGGCCCCAGGAGCAAGGAACACAGACACTGG 2635
DB 121 AGAGCGGCTGTCTCACTGTTCCCATGGCCCCAGGAGCAAGGAACACAGACACTGG 180
QY 2636 ACAAGCTTCGGCAGCGGTGACAGAGCTGTACAGAGCTGTGAGATGCGGGAAGGAC 2695
DB 181 ACAAGCTTCGGCAGCGGTGACAGAGCTGTGAGATGCGGGAAGGAC 240
QY 2696 TGCAGTCACTTCGCCAGGCTGTGAGCTTGTCTTGGGCCCCACAGGGAGGGTCC-GTCC 2754
DB 241 TGCAGTCACTTCGCCAGGCTGTGAGCTTGTCTTGGGCCCCACAGGGAGGGTCCGTGTGC 300
QY 2755 CCTCGGGCATCGGAGAGGGCCGTGGCCAGCCAGCACTCCGGGCTTTCGAGCTCTG 2814
DB 301 CCTCGGGCATCGGAGAGGGCCGTGGCCAGCCAGCACTCCGGGCTTTCGAGCTCTG 360
QY 2815 TGTGTGGACACTGGGGCATCTCTCTACTGCTTCAGAGCCCCCAGCTGGGTCTGTCTTGGT 2874
DB 361 TGTGTGGACACTGGGGCATCTCTCTACTGCTTCAGAGCCCCCAGCTGGGTCTGTCTTGGT 420
QY 2875 GGGACTTGGCCCCACCTCTGTCGGGGGCTCTCTCCCTCATGGCACCTTGGCCCTTGGGGT 2934
DB 421 GGGACTTGGCCCCACCTCTGTCGGGGGCTCTCTCCCTCATGGCACCTTGGCCCTTGGGGT 480
QY 2935 CC 2936
DB 481 CC 482

